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 Duclert, Aymeric
 Bougueleret, Lydie
 Jobert, Severin
 Clusel, Catherine

<120> Complementary DNA's Encoding Proteins with Signal Peptides

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Ala Leu Gly Tyr Val Gln Ala Ser Lys Arg Asp Lys Lys Phe Phe Ala
      445              450              455
tgt gct cca aat tac tcg tat gca gcc ctt tgt gag tgc ctt cgt cga      1552
Cys Ala Pro Asn Tyr Ser Tyr Ala Ala Leu Cys Glu Cys Leu Arg Arg
      460              465              470
gta ttc atc tat cgt cag cct gct ccc atg tcc act gta ctt tac aac      1600
Val Phe Ile Tyr Arg Gln Pro Ala Pro Met Ser Thr Val Leu Tyr Asn
      475              480              485              490
aga aag gaa ggc agg caa gta gga cag gtt gct aag cag caa gta gca      1648
Arg Lys Glu Gly Arg Gln Val Gly Gln Val Ala Lys Gln Gln Val Ala
      495              500              505
agc cta gaa acc aat gat cct att tta gga ttt cag gca aca aat gag      1696
Ser Leu Glu Thr Asn Asp Pro Ile Leu Gly Phe Gln Ala Thr Asn Glu
      510              515              520
aga tta ttt gtt ctt act acc aaa aac ctc ttt tta ata aaa gta aat      1744
Arg Leu Phe Val Leu Thr Thr Lys Asn Leu Phe Leu Ile Lys Val Asn
      525              530              535
aca gag aat taattattct aacatattgg cctctttgta ctggaanaag      1793
Thr Glu Asn
      540
attcagtggc acctggagggt ctggacagtt atactgtaac ctcttaagtt ttaatgtgct      1853
aaatatatct tgtatgattt ttattttttt aataacattg gaaatatatt caagagatta      1913
tgattctgta aagctgtgga atgaagctgc agatttagag aacattggct tctgaaaaaa      1973
aaaaagagtg aagatagtac tagcaagtat acttattttt taaaacaggg tagaatctca      2033
tgttttatat gaaagatgta caattcagtg tttaaaaaata aaaaatttta ttgtgtaaaa      2093
aaaaaaaaa a      2104

<210> 6
<211> 515
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 144..440

<220>
<221> sig_peptide
<222> 144..287
<223> Von Heijne matrix
      score 4.10
      seq VFMLIVSVLALIP/ET

<220>
<221> polyA_signal
<222> 457..462

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gcatacctcac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg      176
                                     Met
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc      224
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala
-30 -25 -20
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag      272
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln
-15 -10 -5 1
cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt      320
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val
5 10 15
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc      368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val
20 25 30
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tcg aag cac caa      416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln
35 40 45
agc atc act gtt gct gac act aac aag tagtgccaag ggattgacct      463
Ser Ile Thr Val Ala Asp Thr Asn Lys
50 55
taaggaagat caggagcgga acatctgggt gcaaagaaaa tctttctaata agccccattc      523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gaggtagggga cttaggatgt      583
tttgtttttt taatcaattc agaaaaatat tatgttttgaa ataaaaataa aaataacttga      643
gccaaaaaaa aaaaaaaaaa
661

<210> 8
<211> 694
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 55..399

<220>
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<222> 55..192
<223> Von Heijne matrix
score 4.70
seq ILTGLTVGSAADA/GE

<220>
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<222> 654..659

<220>
<221> polyA_site
<222> 680..694

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                                     Met
aaa acc ttg ttc aat cca gcc cct gcc att gct gac ctg gat ccc cag      105
Lys Thr Leu Phe Asn Pro Ala Pro Ala Ile Ala Asp Leu Asp Pro Gln
-45 -40 -35 -30
ttc tac acc ctc tca gat gtg ttc tgc tgc aat gaa agt gag gct gag      153
Phe Tyr Thr Leu Ser Asp Val Phe Cys Cys Asn Glu Ser Glu Ala Gln
-25 -20 -15
att tta act ggc ctc acg gtg ggc agc gct gca gat gct ggg gag gct      201
Ile Leu Thr Gly Leu Thr Val Gly Ser Ala Ala Asp Ala Gly Glu Ala
-10 -5 1

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00075360.101501

gca tta gtg ctc ttg aaa agg ggc tgc cag gtg gta atc att acc tta 249
 Ala Leu Val Leu Leu Lys Arg Gly Cys Gln Val Val Ile Ile Thr Leu
 5 10 15
 ggg gct gaa gga tgt gtg ctg tca cag aca gaa cct gag cca aag 297
 Gly Ala Glu Gly Cys Val Val Leu Ser Gln Thr Glu Pro Glu Pro Lys
 20 25 30 35
 cac att ccc aca gag aaa gtc aag gct gtg gat acc acg tgt aga cct 345
 His Ile Pro Thr Glu Lys Val Lys Ala Val Asp Thr Thr Cys Arg Pro
 40 45 50
 ggc tca aga ccc aag agt gaa gca gca agt gtg aag aag cag aaa cat 393
 Gly Ser Arg Pro Lys Ser Glu Ala Ala Ser Val Lys Lys Gln Lys His
 55 60 65
 tat aaa taacccagag aatcctttta taacagcaac tgccactga ttttgtggcc 449
 Tyr Lys
 taacagctcg agcaaaaatg aatataaata caacattgtg caatgactaa ttactcaaaa 509
 ttttgtgcat cagcagaagt ggaacctgtg gttggtgcta atattatgaa atgcctttgc 569
 tgtttaataa tctggtagct ctgtattatt tagcatgcat ttttcttgga gaacaatgat 629
 ttattttcaa gtacctctca ctgaataaaa aaagcagctg ttagaagacg aaaaaaaaaa 689
 aaaaa 694

 <210> 9
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 <212> DNA
 <213> Homo Sapiens

 <220>
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 <222> 90..287

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 seq VFVFLFLWDPVLA/GI

 <220>
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 <222> 1078..1083

 <220>
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 <222> 1096..1110

 <400> 9
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 actagcctcc ttaacagaag ttcccagcc atg aag cct ctc ctt gtt gtg ttt 113
 Met Lys Pro Leu Leu Val Val Phe
 -15
 gtc ttt ctt ttc ctt tgg gat cca gtg ctg gca ggt ata aat tca tta 161
 Val Phe Leu Phe Leu Trp Asp Pro Val Leu Ala Gly Ile Asn Ser Leu
 -10 -5 1 5
 tca tca gaa atg cac aag aaa tgc tat aaa aat ggc atc tgc aga ctt 209
 Ser Ser Glu Met His Lys Lys Cys Tyr Lys Asn Gly Ile Cys Arg Leu
 10 15 20
 gaa tgc tat gag agt gaa atg tta gtt gcc tac tgt atg ttt cag ctg 257
 Glu Cys Tyr Glu Ser Glu Met Leu Val Ala Tyr Cys Met Phe Gln Leu
 25 30 35
 gag tgc tgt gtc aaa gga aat cct gca ccc tgacataaga aaccaatgaa 307
 Glu Cys Cys Val Lys Gly Asn Pro Ala Pro
 40 45


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tggccactat cctgtaggcc cttgattctg ccatctttca caaaaccagg gaatttagat 367
caaaactgtga caccatgatg tgtccatgac tactgggttt tagcattttt ataggccagc 427
agactcttgt ggtctttaaata ttaaagagct gagctgtagc cttcttttaa agagctcggt 487
ttttcacaaa aacaatgtag aagatatttt ctcacctcaa cgtgatgtcc agtgtgctca 547
tcagcacctg tttctccctc taatcataga ggataattctt attattttaga aaggcttcaa 607
gggaacaacac tttttggcac taagtctgtg cctacottcg cttcagcttc gcattttcca 667
tttctgtgaa attcccaact ttagagaagc agatttgcca tggcctttct acaaccttgt 727
acatctctca cataaacgcg ataggcaggg cttaactaca ggctggcccg agtctggact 787
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<210> 10
<211> 623
<212> DNA
<213> Homo Sapiens

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<220>
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<222> 49..447

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<222> 49..111
<223> Von Heijne matrix
score 5.00
seq LIVIFFYCWSSS/HE

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<222> 579..584

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<220>
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<222> 602..623

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Met Ser Cys
-20
tcc cta aag ttt act ttg att gta att ttt ttt tac tgt tgg ctt tca 105
Ser Leu Lys Phe Thr Leu Ile Val Ile Phe Phe Tyr Cys Trp Leu Ser
-15 -10 -5
tcc agc cat gag gag tta gaa ggt ggt aca tgc aag tct ttt gac ctc 153
Ser Ser His Glu Glu Leu Glu Gly Gly Thr Ser Lys Ser Phe Asp Leu
1 5 10
cat aca gtg att atg ctt gtc atc gct ggt ggt atc ctg gcg gcc ttg 201
His Thr Val Ile Met Leu Val Ile Ala Gly Gly Ile Leu Ala Ala Leu
15 20 25 30
ctc ctg ctg ata gtt gtc gtg ctc tgt ctt tac ttc aaa ata cac aac 249
Leu Leu Leu Ile Val Val Leu Cys Leu Tyr Phe Lys Ile His Asn
35 40 45
gcg cta aaa gct gca aag gaa cct gaa gct gtg gct gta aaa aat cac 297
Ala Leu Lys Ala Ala Lys Glu Pro Glu Ala Val Ala Val Lys Asn His
50 55 60
aac cca gac aag gtg tgg tgg gcc aag aac agc cag gcc aaa acc att 345
Asn Pro Asp Lys Val Trp Trp Ala Lys Asn Ser Gln Ala Lys Thr Ile
65 70 75

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Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr	
75 80 85	
ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg	678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp	
90 95 100	
aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag	726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu	
105 110 115 120	
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga	774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg	
125 130 135	
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc	822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu	
140 145 150	
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg	870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met	
155 160 165	
gag aac aat gcc cac att gcc gga gag cag atg ctc gaa gat ggg ccc	918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro	
170 175 180	
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg	966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg	
185 190 195 200	
gcg tagccagcat gcaggtgcag ggccctgtgg tccagatccc cctgggttgg	1019
Ala	
gattcaagtc cagggtgagc ccatgtgctg gagaaaaatac acatcattg gtctccttgc	1079
tttgaaagat ccaataaagt cctgaggcaaa ggtttggaaa accaaaaaaa aaaaaaaa	1137

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 <212> DNA
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<220>
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 <222> 192..440

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 <222> 192..278
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 score 5.20
 seq VVFMIVAAGGASS/FA

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 <222> 590..595

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gttcggggcg ttaccatcgt cgtgcgcac cgcccgcgct ccagatttgg caattcttcg	180
ctgaagtcac c atg agc ttt ttc caa ctc ctg atg aaa agg aag gaa ctc	230
Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu	
-25 -20	
att ccc ttg gtg gtg ttc atg act gtg gcg gcg ggt gga gcc tca tct	278
Ile Pro Leu Val Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser	

-15	-10	-5	
ttc gct gtg tat tct ctt tgg aaa acc gat gtg atc ctt gat cga aaa	326		
Phe Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys			
1 5 10 15			
aaa aat cca gaa cct tgg gaa act gtg gac cct act gta cct caa aag	374		
Lys Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys			
20 25 30			
ctt ata aca atc aac caa caa tgg aaa ccc att gaa gag ttg caa aat	422		
Leu Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn			
35 40 45			
gtc caa agg gtg acc aaa tgacgagccc tgcctctttt cttctgaaga	470		
Val Gln Arg Val Thr Lys			
50			
gtactctata aatctagtgg aaacattttct gcacaaacta gattctggac accagtgctgc	530		
ggaaatgctt ctgctacatt tttagggttt gtctacattt tttagggctct ggataaggaa	590		
ttaaaggagt gcagcaataa ctgcactgtc caaaaaaaaa aaaaaa	636		

<210> 14
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 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 59..703

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 <222> 59..181
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 score 6.80
 seq LVSCLSQSSALS/QS

<220>
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 <222> 783..788

<220>
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 <222> 804..818

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atg gtc tca gct ctg cgg gga gca ccc ctg atc agg gtg cac tca agc	106
Met Val Ser Ala Leu Arg Gly Ala Pro Leu Ile Arg Val His Ser Ser	
-40 -35 -30	
cct gtt tct tct cct tct gtg agt gga cca cgg agg ctg gtg agc tgc	154
Pro Val Ser Ser Pro Ser Val Ser Gly Pro Arg Arg Leu Val Ser Cys	
-25 -20 -15 -10	
ctg tca tcc caa agc tca gct ctg agc cag agt ggt ggt gcc tcc acc	202
Leu Ser Ser Gln Ser Ser Ala Leu Ser Gln Ser Gly Gly Gly Ser Thr	
-5 1 5	
tct gcc gcc gcc ata gaa gcc agg agc agg gct ctc aga agg cgg tgg	250
Ser Ala Ala Gly Ile Glu Ala Arg Ser Arg Ala Leu Arg Arg Arg Trp	
10 15 20	
tgc cca gct ggg atc atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc	298
Cys Pro Ala Gly Ile Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys	
25 30 35	
ctg cta ccc tcc agt gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc	346
Leu Leu Pro Ser Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala	
40 45 50 55	

09973260.101501

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aga gtg cta cat gac ttc ggg ctg gac gga tac cgg gga tac agc ctg      394
Arg Val Leu His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu
60
gct gac tgg gtc tgc ctt gct tat ttc aca agc ggt ttc aac gca gct      442
Ala Asp Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala
75
gct ttg gac tac gag gct gat ggg agc acc aac aac ggg atc ttc cag      490
Ala Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
90
atc aac agc cgg agg tgg tgc agc aac ctc acc ccg aac gtc ccc aac      538
Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn
105
gtg tgc cgg atg tac tgc tca gat ttg ttg aat cct aat ctc aag gat      586
Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp
120
acc gtt atc tgt gcc atg aag ata acc caa gag cct cag ggt ctg ggt      634
Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly
140
tac tgg gag gcc tgg agg cat cac tgc cag gga aaa gac ctc act gaa      682
Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys Asp Leu Thr Glu
155
tgg gtg gat ggc tgt gac ttc taggatggac ggaaccatgc acagcaggct      733
Trp Val Asp Gly Cys Asp Phe
170
gggaaatgtg gtttggttcc tgacctagcg ttgggaagac aagccagcga ataaaggatg      793
gttgaacgtg aaaaaaaaaa aaaaa
818

<210> 15
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<212> DNA
<213> Homo Sapiens

<220>
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<222> 139..1389

<220>
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<222> 139..198
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<221> polyA_signal
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<220>
<221> polyA_site
<222> 1873..1888

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ctatcagggc acagtctctca ggaatgttctc gggagaatag gagccagaac ctgagccctc      120
aagccattcc cctcacca atg atg ggg tcc cca gtg agt cat ctg ctg gcc      171
Met Met Gly Ser Pro Val Ser His Leu Leu Ala
-20 -15 -10
ggc ttc tgt gtg tgg gtc gtc ttg ggc tgg gta ggg ggc tca gtc ccc      219
Gly Phe Cys Val Trp Val Val Leu Gly Trp Val Gly Gly Ser Val Pro
-5 1 5
aac ctg ggc cct gct gag cag gag cag aac cat tac ctg gcc cag ctg      267

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09978350.161501

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Phe	Gly	Leu	Tyr	Gly	Glu	Asn	Gly	Thr	Leu	Thr	Ala	Gly	Gly	Leu	Ala		
25						30					35						
cgg	ctt	ctc	cac	agc	ctg	ggg	cta	ggc	cga	gtt	cag	ggg	ctt	cgc	ctg	363	
Arg	Leu	Leu	His	Ser	Leu	Gly	Leu	Gly	Arg	Val	Gln	Gly	Leu	Arg	Leu		
40					45					50					55		
gga	cag	cat	ggg	cct	ctg	act	gga	cgg	gct	gca	tcc	cca	gct	gca	gac	411	
Gly	Gln	His	Gly	Pro	Leu	Thr	Gly	Arg	Ala	Ala	Ser	Pro	Ala	Ala	Asp		
60									65					70			
aat	tcc	aca	cac	agg	cca	cag	aac	cct	gag	ctg	agt	gtg	gat	gtc	tgg	459	
Asn	Ser	Thr	His	Arg	Pro	Gln	Asn	Pro	Glu	Leu	Ser	Val	Asp	Val	Trp		
75								80					85				
gca	ggg	atg	cct	ctg	ggg	ccc	tca	ggg	tgg	ggg	gac	ctg	gaa	gag	tca	507	
Ala	Gly	Met	Pro	Leu	Gly	Pro	Ser	Gly	Trp	Gly	Asp	Leu	Glu	Glu	Ser		
90						95						100					
aag	gcc	cct	cac	cta	ccc	cgt	ggg	cca	gcc	ccc	tcg	ggc	ctg	gac	ctc	555	
Lys	Ala	Pro	His	Leu	Pro	Arg	Gly	Pro	Ala	Pro	Ser	Gly	Leu	Asp	Leu		
105						110					115						
ctt	cac	agg	ctt	ctg	ttg	ctg	gac	cac	tca	ttg	gct	gac	cac	ctg	aat	603	
Leu	His	Arg	Leu	Leu	Leu	Leu	Asp	His	Ser	Leu	Ala	Asp	His	Leu	Asn		
120					125					130				135			
gag	gat	tgt	ctg	aac	ggc	tcc	cag	ctg	ctg	gtc	aat	ttt	ggc	ttg	agc	651	
Glu	Asp	Cys	Leu	Asn	Gly	Ser	Gln	Leu	Leu	Val	Asn	Phe	Gly	Leu	Ser		
140								145					150				
ccc	gct	gct	cct	ctg	acc	cct	cgt	cag	ttt	gct	ctg	ctg	tgc	cca	gcc	699	
Pro	Ala	Ala	Pro	Leu	Thr	Pro	Arg	Gln	Phe	Ala	Leu	Leu	Cys	Pro	Ala		
155								160					165				
ctg	ctt	tat	cag	atc	gac	agc	cgc	gtc	tgc	atc	ggc	gct	ccg	gcc	cct	747	
Leu	Leu	Tyr	Gln	Ile	Asp	Ser	Arg	Val	Cys	Ile	Gly	Ala	Pro	Ala	Pro		
170						175					180						
gca	ccc	cca	ggg	gat	cta	cta	tct	gcc	ctg	ctt	cag	agt	gcc	ctg	gca	795	
Ala	Pro	Pro	Pro	Gly	Asp	Leu	Leu	Ser	Ala	Leu	Leu	Gln	Ser	Ala	Leu	Ala	
185						190						195					
gtc	ctg	ttg	ctc	agc	ctc	cct	tct	ccc	cta	tcc	ctg	ctg	ctg	ctg	cgg	843	
Val	Leu	Leu	Leu	Ser	Leu	Pro	Ser	Pro	Leu	Ser	Leu	Leu	Leu	Leu	Arg		
200					205					210				215			
cct	ctg	gga	cct	cgt	cta	cta	cgg	ccc	ttg	ctg	ggc	ttc	ctg	ggg	gcc	891	
Leu	Leu	Gly	Pro	Arg	Leu	Leu	Arg	Pro	Leu	Leu	Gly	Phe	Leu	Gly	Ala		
220								225					230				
ctg	gcg	gtg	ggc	act	ctt	tgt	ggg	gat	gca	ctg	cta	cat	ctg	cta	ccg	939	
Leu	Ala	Val	Gly	Thr	Leu	Cys	Gly	Asp	Ala	Leu	Leu	His	Leu	Leu	Pro		
235								240				245					
cat	gca	caa	gaa	ggg	cgg	cac	gca	gga	cct	ggc	gga	cta	cca	gag	aag	987	
His	Ala	Gln	Glu	Gly	Arg	His	Ala	Gly	Pro	Gly	Gly	Leu	Pro	Glu	Lys		
250						255						260					
gac	ctg	ggc	ccg	ggg	ctg	tca	gtg	ctc	gga	ggc	ctc	ttc	ctg	ctc	ttt	1035	
Asp	Leu	Gly	Pro	Gly	Leu	Ser	Val	Leu	Gly	Gly	Leu	Phe	Leu	Leu	Phe		
265						270					275						
gtg	ctg	gag	aac	atg	ctg	ggg	ctt	ttg	cgg	cac	cga	ggg	ctc	agg	cca	1083	
Val	Leu	Glu	Asn	Met	Leu	Gly	Leu	Leu	Arg	His	Arg	Gly	Leu	Arg	Pro		
280					285					290				295			
aga	tgc	tgc	agg	cga	aaa	cga	agg	aat	ctc	gaa	aca	cgc	aac	ttg	gat	1131	
Arg	Gly	Cys	Arg	Arg	Lys	Arg	Arg	Asn	Leu	Glu	Thr	Arg	Asn	Leu	Asp		
300								305					310				
ccg	gag	aat	ggc	agt	ggg	atg	gcc	ctt	cag	ccc	cta	cag	gca	gct	cca	1179	
Pro	Glu	Asn	Gly	Ser	Gly	Met	Ala	Leu	Gln	Pro	Leu	Gln	Ala	Ala	Pro		
315								320					325				
gag	cca	ggg	gct	cag	ggc	cag	agg	gag	aag	aac	agc	cag	cac	cca	cca	1227	
Glu	Pro	Gly	Ala	Gln	Gly	Gln	Arg	Glu	Lys	Asn	Ser	Gln	His	Pro	Pro		

330 335 340
 gct ctg gcc cct cct ggg cac caa ggc cac agt cat ggg cac cag ggt 1275
 Ala Leu Ala Pro Pro Gly His Gln Gly His Ser His Gly His Gln Gly
 345 350 355
 ggc act gat atc acg tgg atg gtc ctc ctg gga gat ggt cta cac aac 1323
 Gly Thr Asp Ile Thr Trp Met Val Leu Leu Gly Asp Gly Leu His Asn
 360 365 370 375
 ctc act gat ggg ctg gcc ata ggt gct gcc ttc tct gat ggc ttc tcc 1371
 Leu Thr Asp Gly Leu Ala Ile Gly Ala Ala Phe Ser Asp Gly Phe Ser
 380 385 390
 gcg gcc tca gta cca cct tagcgggtctt ctgccatgag ctgccccacg 1419
 Ala Ala Ser Val Pro Pro
 395
 aactgggtga ctttgccatg ctgctccagt cagggctgtc ctttcggcgg ctgctgctgc 1479
 tgagcctcgt gtctggagcc ctgggattgg ggggtgcagt cctgggggtg gggctcagcc 1539
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 tgctggagga gccgctaact gccgtgacca ctgagggctg atggggccag tggaaagggg 1779
 tcggggtgcc ctctcttccc cccaaccaca ggaatggagg cgggacacag ggccagtagg 1839
 agcaatagga ttttaataaa cagaacccat cccaaaaaaa aaaaaaaaaa 1888

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 <212> DNA
 <213> Homo Sapiens

 <220>
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 <222> 21..1118

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 <222> 21..89
 <223> Von Heijne matrix
 score 10.80
 seq ALALLSAFSATQA/RK

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 <222> 1858..1863

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 <222> 1879..1894

 <220>
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 <222> 1695
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 Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala
 -20 -15
 ctg gct ctt ctt tca gcg ttt tgg gcc acc cag gca cgg aaa ggc ttc 101
 Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe
 -10 -5 1
 tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag 149
 Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln
 5 10 15 20

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atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc	197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser	
25 30 35	
ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg	245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg	
40 45 50	
cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac cgg gtg ggc	293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly	
55 60 65	
atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc	341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu	
70 75 80	
cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag	389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu	
85 90 95 100	
ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag	437
Gly Leu Arg Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln	
105 110 115	
gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg	485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly	
120 125 130	
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct	533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala	
135 140 145	
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc	581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe	
150 155 160	
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg	629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly	
165 170 175 180	
cgc cac gtg cag gag ctg cac cgc agt gtg gct cgg cac gcc ccc gcc	677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala	
185 190 195	
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc	725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu	
200 205 210	
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac	773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp	
215 220 225	
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag	821
Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu	
230 235 240	
gaa ggg gcc ggc cgg gac ccc cag atg ctc tcc gag gag gtg cgc cag	869
Glu Gly Ala Gln Gly Pro Asp Pro Gln Met Leu Ser Glu Val Arg Gln	
245 250 255 260	
cga ctt gag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc	917
Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe	
265 270 275	
act cgc gcc atc gac cag gag act gag gag gtc cag cag cag ctg gcg	965
Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala	
280 285 290	
cca cct cca cca gcc cac agt gcc ttc gcc cca gag ttt caa caa aca	1013
Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr	
295 300 305	
gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg	1061
Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu	
310 315 320	
tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg	1109
Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu	
325 330 335 340	
ggg gac ccc tgaggatcta cctgcccagg cccattccca gctccttgtc	1158

09970360-102603

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<222> 143..592
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<222> 1877..1882
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<220>
<221> polyA_site
<222> 1899..1913
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[illegible]

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Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Thr	Trp	Ala	Val	Gly		
			65					70					75				
gtg	ggg	ctg	gga	cgc	tgt	ttg	tgc	tca	gcg	ggg	aca	gcc	agg	gtt	gat	556	
Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp		
			80				85					90					
ctg	gcc	ccg	agg	gtt	ttg	gat	gtt	ttt	agg	atg	aca	taaaaagcaa				602	
Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr						
			95				100				105						
gtgttttccc	cattttctct	tatgaacac	cgtctgagcc	caaggtacac	attgggcggc	662											
ctgcaggaac	ctgctccagg	tggaacacg	ggccagcagc	cgcgaacctt	gaagctgggg	722											
tgaccgcagg	agaccctgtg	aggcctgtga	gcggagccct	cgaccccgtg	acaccctggc	782											
cagacacccct	gcttggactg	gggtggcctc	tgctaccacc	gggtctggca	cgggggaggg	842											
ctgggggtttt	ctctgcctcg	tacacacgga	aaggcggctg	tgccgacgca	gggtcacctg	902											
gctccgggttt	ttctgacagt	cgggtgtttcc	tgggcctttg	gagtggctgc	gaggcctgaa	962											
cgctctgtgg	atccgctgtg	tccagcccg	ctgagcatcg	ccagggttag	ctcatgctgc	1022											
ttctgtcagc	ctctggttct	cctcgagtc	ttggggagct	ggcagatgcc	agcgaccatc	1082											
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tgctctgtcc	actgccaccc	cccgtgtgct	ggctccctca	cttctggctg	cagtgggagc	1442											
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atgtcagcagc	ctctgcaactg	accgcagccg	gccccccaggc	ctcagagttc	tgagtgcttc	1562											
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caatctgagct	ctgtgcccgg	gcccgtggcca	tgggaagatg	ttccacgctg	cctcctctct	1682											
gagtttttct	cggaacacct	cttgaatgtc	tgagtgaagg	tcctgcttag	ctcttttgcc	1742											
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<210> 18
<211> 1744
<212> DNA
<213> Homo Sapiens

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<221> CDS
<222> 76..999

<220>
<221> sig_peptide
<222> 76..279
<223> Von Heijne matrix
score 5.10
seq LSLPVCTVSLVSS/VS

<220>
<221> polyA_signal
<222> 1711..1716

<220>
<221> polyA_site
<222> 1729..1744

<220>
<221> misc_feature
<222> 336

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<223> n=a, g, c or t

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cgccacacct	tgcttc	atg gat ttt gtc gct	gga gcc atc gga ggc gtc tgc			111
	Met Asp Phe Val Ala Gly Ala Ile Gly Gly Val Cys					
		-65		-60		
ggt gtt gct gtg ggc tac ccc ctg gac acg gtg aag gtc agg atc cag						159
Gly Val Ala Val Gly Tyr Pro Leu Asp Thr Val Lys Val Arg Ile Gln						
-55	-50	-45				
acg gag cca aag tac aca ggc atc tgg cac tgc gtc cgg gat acg tat						207
Thr Glu Pro Lys Tyr Thr Gly Ile Trp His Cys Val Arg Asp Thr Tyr						
-40	-35	-30				
cac cga gag cgc gtg tgg ggc ttc tac cgg ggc ctc tgc ctg ccc gtg						255
His Arg Glu Arg Val Trp Gly Phe Tyr Arg Gly Leu Ser Leu Pro Val						
-20	-15	-10				
tgc acg gtg tcc ctg gta tct tcc gtg tct ttt ggc acc tac cgc cac						303
Cys Thr Val Ser Leu Val Ser Ser Val Ser Phe Gly Thr Tyr Arg His						
-5	1	5				
tgc ctg cgc cac atc tgc cgg ctc cgg tac ggn aac cct gac gcc aag						351
Cys Leu Ala His Ile Cys Arg Leu Arg Tyr Gly Asn Pro Asp Ala Lys						
10	15	20				
ccc acc aag gcc gac atc acg ctc tgc gga tgc gcc tcc ggc ctc gtc						399
Pro Thr Lys Ala Asp Ile Thr Leu Ser Gly Cys Ala Ser Gly Leu Val						
25	30	35				
cgc gtg ttc ctg acg tgc ccc act gag gtg gcc aaa gtc cgc ttg cag						447
Arg Val Phe Leu Thr Ser Pro Thr Glu Val Ala Lys Val Arg Leu Gln						
45	50	55				
acg cag aca cag cgc cag aag cag cag cgg ctg ctt tgc gcc tgc ggg						495
Thr Gln Thr Gln Ala Gln Lys Gln Gln Arg Leu Leu Ser Ala Ser Gly						
60	65	70				
cgc ttg gct gtg ccc ccc atg tgt cct gtg ccc cca gcc tgc cca gag						543
Pro Leu Ala Val Pro Pro Met Cys Pro Val Pro Ala Cys Pro Glu						
75	80	85				
ccc aag tac cgc ggg cca ctg cac tgc ctg gcc acg gta gcc cgt gag						591
Pro Lys Tyr Arg Gly Pro Leu His Cys Leu Ala Thr Val Ala Arg Glu						
90	95	100				
gag ggg ctg tgc ggc ctc tac aag ggc agc tgc gcc ctg gtc tta cgg						639
Glu Gly Leu Cys Gly Leu Tyr Lys Gly Ser Ser Ala Leu Val Leu Arg						
105	110	115				
gac ggc cac tcc ttt gcc acc tac ttc ctt tcc tac cgc gtc ctc tgc						687
Asp Gly His Ser Phe Ala Thr Tyr Phe Leu Ser Tyr Ala Val Leu Cys						
125	130	135				
gag tgg ctc agc ccc gct ggc cac agc cgg cca gat gtc ccg ggc gtg						735
Glu Trp Leu Ser Pro Ala Gly His Ser Arg Pro Asp Val Pro Gly Val						
140	145	150				
ctg gtg gcc ggg ggc tgt gca gga gtc ctg gcc tgg gct gtg gcc acc						783
Leu Val Ala Gly Gly Cys Ala Gly Val Leu Ala Trp Ala Val Ala Thr						
155	160	165				
ccc atg gac gtg atc aag tgc aga ctg cag gca gac ggg cag ggc cag						831
Pro Met Asp Val Ile Lys Ser Arg Leu Gln Ala Asp Gly Gln Gly Gln						
170	175	180				
agg cgc tac cgg ggt ctc ctg cac tgt atg gtg acc agc gtt cga gag						879
Arg Arg Tyr Arg Gly Leu Leu His Cys Met Val Thr Ser Val Arg Glu						
185	190	195				
gag gga ccc cgg gtc ctt ttc aag ggg ctg gta ctc aat tgc tgc cgc						927
Glu Gly Leu Cys Gly Val Leu Phe Lys Gly Leu Val Leu Asn Cys Cys Arg						
205	210	215				
gcc ttc cct gtc aac atg gtg gtc ttc gtc gcc tat gag gca gtg ctg						975
Ala Phe Pro Val Asn Met Val Val Phe Val Ala Tyr Glu Ala Val Leu						
220	225	230				

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agg ctc gcc cgg ggt ctg ctc aca tagccgggtcc ccacgcccag cggccccacc 1029
 Arg Leu Ala Arg Gly Leu Leu Thr
 235 240

accagcagct gctggagggtc gtagtggtctg gaggaggcaa ggggtagtgt ggctgggttc 1089
 gggacccccc agggccattg cccaggagaa taggagcct cctgcagtg ttgtcgcccg 1149
 aggcctaagc tcgccctgcc cagctactga cctcaggtcg agggggccgc cagccatcag 1209
 ccagggttgg cctagggtgg caggagccag ggaggagtgg gcctctttga tgagagcggt 1269
 gagtgtcatg gagtgggtg ttcatccag cctcccatg gcctcgccct cccatgtctt 1329
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 gccacactga gaggggcctg ggggtggcctg cctcggccgg ttagggaatt tgggtgagg 1629
 tctctcagga gccctcactc tgctgtgga cgctgcacct gccacttaa gaccccaag 1689
 actctgttgg gaactgttgt caataaaatg tttctgagga aaaaaaaaa aaaaa 1744

<210> 19
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 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> 123..464

<220>
 <221> sig_peptide
 <222> 123..269
 <223> Von Heijne matrix
 score 4.90
 seq PSLAAGLLFGSLA/GL

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 <222> 908..913

<220>
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 <222> 931..946

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 ga atg gag aag ccc ctc ttc cca tta gtg cct ttg cat tgg ttt ggc 167
 Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
 -45 -40 -35

ttt ggc tac aca gca ctg gtt gtt tct ggt ggg atc gtt ggc tat gta 215
 Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
 -30 -25 -20

aaa aca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttc ggc agt 263
 Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
 -15 -10 -5

cta gcc ggc ctg ggt gct tac cag ctg tat cag gat cca agc aac gtt 311
 Leu Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
 1 5 10

tgg ggt ttc cta gcc gct aca tct gtt act ttt gtt ggt gtt atg gga 359
 Trp Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly
 15 20 25 30

atg aga tcc tac tac tat gga aaa ttc atg cct gta ggt tta att gca 407
 Met Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala
 35 40 45

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ggt gcc agt ttg ctg atg gcc gcc aaa gtt gga gtt cgt atg ttg atg 455
 Gly Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met
 50 55 60
 aca tct gat tagcagaagt catgttccag cttggactca tgaaggatta 504
 Thr Ser Asp
 65
 aaaaatctgca tcttccacta ttttcaatgt attaagagaa ataagtcgac catttttgc 564
 tctgacattt tacctaaaaa aaaaaagaca ccaattttgg cggagggggtg gaaaatcagt 624
 tgttaccatt ataaccctac agagggtgggt agcatgtaac atgagcttat tgagaccatc 684
 atagagatcg attcttggat attgatttta tctctttctg tatctatagg taaatctcaa 744
 gggtaaaatg ttaggtgttg acattgagaa ccttgaacc ccatccctg ctcagaggaa 804
 cagtgtgaaa aaaaatctct tgagagattt agaatatctt tctctttgct catcttagac 864
 cacagactga ctttgaatt atgttaagt aaatatcaat gaaaataaag ttactataa 924
 ataattaaaa aaaaaaaaaa aa 946

 <210> 20
 <211> 1622
 <212> DNA
 <213> Homo Sapiens

 <220>
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 <222> 85..1230

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 <221> sig_peptide
 <222> 85..129
 <223> Von Heijne matrix
 score 10.10
 seq LLLPLALCILVLC/CG

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 <221> polyA_signal
 <222> 1589..1594

 <220>
 <221> polyA_site
 <222> 1607..1622

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 atcctctggcc ttgttctcca caga atg ggt ctg ctc ctt ccc ctg gca ctc 111
 Met Gly Leu Leu Leu Pro Leu Ala Leu
 -15 -10
 tgc atc cta gtc ctg tgc tgc gga gca atg tct cca ccc cag ctg gcc 159
 Cys Ile Leu Val Leu Cys Cys Gly Ala Met Ser Pro Pro Gln Leu Ala
 -5 1 5 10
 ctc aac ccc tgc gct ctg ctc tcc cgg ggc tgc aat gac tca gat gtg 207
 Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp Ser Asp Val
 15 20 25
 ctg gca gtt gca ggc ttt gcc ctg cgg gat att aac aaa gac aga aag 255
 Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys Asp Arg Lys
 30 35 40
 gat ggc tat gtg ctg aga ctc aac cga gtg aac gac gcc cag gaa tac 303
 Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala Gln Glu Tyr
 45 50 55
 aga cgg ggt ggc ctg gga tct ctg ttc tat ctt aca ctg gat gtg cta 351
 Arg Arg Gly Gly Leu Gly Ser Leu Phe Tyr Leu Thr Leu Asp Val Leu
 60 65 70
 gag act gac tgc cat gtg ctc aga aag aag gca tgg caa gac tgt gga 399
 Glu Thr Asp Cys His Val Leu Arg Lys Lys Ala Trp Gln Asp Cys Gly

75	80	85	90	
atg agg ata ttt ttt gaa tca gtt tat ggt caa tgc aaa gca ata ttt				447
Met Arg Ile Phe Phe Glu Ser Val Tyr Gly Gln Cys Lys Ala Ile Phe				
95	100	105		
tat atg aac aac cca agt aga gtt ctc tat tta gct gct tat aac tgt				495
Tyr Met Asn Asn Pro Ser Arg Val Leu Tyr Leu Ala Ala Tyr Asn Cys				
110	115	120		
act ctt cgc cca gtt tca aaa aaa aag att tac atg acg tgc cct gac				543
Thr Leu Arg Pro Val Ser Lys Lys Lys Ile Tyr Met Thr Cys Pro Asp				
125	130	135		
tgc cca agc tcc ata ccc act gac tct tcc aat cac caa gtg ctg gag				591
Cys Pro Ser Ser Ile Pro Thr Asp Ser Ser Asn His Gln Val Leu Glu				
140	145	150		
gct gcc acc gag tct ctt gcg aaa tac aac aat gag aac aca tcc aag				639
Ala Ala Thr Glu Ser Leu Ala Lys Tyr Asn Asn Glu Asn Thr Ser Lys				
155	160	165		
cag tat tct ctc ttc aaa gtc acc agg gct tct agc cag tgg gtg gtc				687
Gln Tyr Ser Leu Phe Lys Val Thr Arg Ala Ser Ser Gln Trp Val Val				
175	180	185		
ggc cct tct tac ttt gtg gaa tac tta att aaa gaa tca cca tgt act				735
Gly Pro Ser Tyr Phe Val Glu Tyr Leu Ile Lys Glu Ser Pro Cys Thr				
190	195	200		
aaa tcc cag gcc agc agc tgt tca ctt cag tcc tcc gac tct gtg cct				783
Lys Ser Gln Ala Ser Ser Cys Ser Ser Leu Gln Ser Ser Asp Ser Val Pro				
205	210	215		
gtt ggt ctt tgc aaa ggt tct ctg act cga aca cac tgg gaa aag ttt				831
Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp Glu Lys Phe				
220	225	230		
gtc tct gtg act tgt gac ttc ttt gaa tca cag gct cca gcc act gga				879
Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro Ala Thr Gly				
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agt gaa aac tct gct gtt aac cag aaa cct aca aac ctt ccc aag gtg				927
Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu Pro Lys Val				
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gaa gaa tcc cag cag aaa aac acc ccc cca aca gac tcc ccc aaa				975
Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser Pro Ser Lys				
270	275	280		
gct ggg cca aga gga tct gtc caa tat ctt cct gac ttg gat gat aaa				1023
Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu Asp Asp Lys				
285	290	295		
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Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val His Leu Asp				
300	305	310		
cta acc acg aat ccc cag gga gaa acc ctg gat att tcc ttc ctc ttc				1119
Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser Phe Leu Phe				
315	320	325		
ctg gag cct atg gag gag aag ctg gtg gtc ctg cct ttc ccc aaa gaa				1167
Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Phe Pro Lys Glu				
335	340	345		
aaa gca cgc act gct gag tgc cca ggg cca gcc cag aat gcc agc cct				1215
Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn Ala Ser Pro				
350	355	360		
ctt gtc ctt ccg cca tgagaatcac acagagtctt ctgtagggggt ttgtgcgcc				1270
Leu Val Leu Pro Pro				
365				
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 ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg 100
 Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala
 -185 -180 -175
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 Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala
 -170 -165 -160
 cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc 196
 His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe
 -155 -150 -145
 agc tcg cag aag gcc aag atc ttg gag cat gat gat gtg agc tac ctg 244
 Ser Ser Gln Lys Ala Lys Ile Leu Glu His Asp Asp Val Ser Tyr Leu
 -140 -135 -130
 aag aag atc ctc ggg gaa ctg gcc atg gtg ctg gac cag att gag gcg 292
 Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln Ile Glu Ala
 -125 -120 -115 -110
 gan ctg gag aag agg aag ctg gag aac gag ggg cag aaa tgc gag ctg 340
 Xaa Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu

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Tyr	Leu	Val	Arg	Arg	Ser	Arg	Arg	Pro	Gln	Val	Thr	Leu	Leu	Asp	Pro	
aat	gaa	aag	5	ctg	cta	cga	ctg	cta	gac	aag	acg	ctc	tct	gca	cgg	194
Asn	Glu	Lys	20	Tyr	Leu	Leu	Arg	Leu	Asp	Lys	Thr	Leu	Ser	Ala	Arg	
tcc	cca	ggc	aaa	cat	atc	tac	ctc	tcc	acc	cga	att	gat	ggc	agc	ctg	242
Ser	Pro	Gly	Lys	His	Ile	His	Ile	Ser	Thr	Arg	Ile	Asp	Gly	Ser	Leu	
gtc	atc	agg	cca	tac	act	cct	gtc	acc	agt	gat	gag	gat	caa	ggc	tat	290
Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr	
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Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe	
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg	386
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly	
gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga	434
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly	
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Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro	
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Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr	
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Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	lys	Val	Pro	Glu	Asp	Pro	
acc	cag	tcg	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc	626
Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile	
ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	cgc	ttt	674
Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe	
aag	ctc	trg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	arg	722
Lys	Leu	Tyr	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Tyr	Gly	Ala	Tyr	
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Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro	
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Gly	Asp	Asp	Val	Leu	Val	Leu	Cys	Gly	Gly	ccc	ccc	Pro	Met	Val	Gln	
ctg	gcc	tcg	cat	ccc	aac	ttt	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg	866
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met	
cga	ttc	acc	tac	tgagcatctct	ccagctttccc	tggtgctgttt	cgtgcaggtt									918
Arg	Phe	Thr	Tyr													
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ccatggagaaga	gggcccaaggcc	tcagttacata	ctttgtagtgc	ctctctaaatc	ttcccgtgtgc											1098
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gttccaccatc	agtaactcaag	caactanaagc	cttgatattcc	ttctctcaga	gtttccaggtt	978
tttccatctg	catctatagac	tgaattattcg	attatgactct	caggaataact	attctctgtg	1038
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 Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
 -25 -20 -15
 act ctc tta ctg ctg ctg acg ctg cta gcc ttt gcc ggg tac tca ggg 159
 Thr Leu Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
 -10 -5 1
 cta ctg gct ggg gtg gaa gtg agt gct ggg tca ccc ccc atc cgc aac 207
 Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 5 10 15 20
 gtc act gtg gcc tac aag ttc cac atg ggg ctc tat ggt gag act ggg 255
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
 25 30 35
 cgg ctt ttc act gag agc tgc atc tct ccc aag ctc cgc tcc atc gct 303
 Arg Leu Phe Thr Glu Ser Cys Ile Ser Pro Lys Leu Arg Ser Ile Ala
 40 45 50
 gtc tac tat gac aac ccc cac atg gtg ccc cct gat aag tgc cga tgt 351
 Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys
 55 60 65
 gcc gtg ggc agc atc ctg agt gaa ggt gag gaa tgc ccc tcc cct gag 399
 Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu Ser Pro Ser Pro Glu
 70 75 80
 ctc atc gac ctc tac cag aaa ttt ggc ttc aag gtg ttc tcc ttc ccg 447
 Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe Lys Val Phe Ser Phe Pro
 85 90 95 100
 gca ccc agc cat gtg gtg aca gcc acc ttc ccc tac acc acc att ctg 495
 Ala Pro Ser His Val Val Thr Ala Thr Phe Pro Tyr Thr Thr Ile Leu
 105 110 115
 tcc atc tgg ctg gct acc cgc cgt gtc cat cct gcc ttg gac acc tac 543
 Ser Ile Trp Leu Ala Thr Arg Arg Val His Pro Ala Leu Asp Thr Tyr
 120 125 130
 atc aag gag cgg aag ctg tgt gcc tat cct cgg ctg gag atc tac cag 591
 Ile Lys Glu Arg Lys Leu Cys Ala Tyr Pro Arg Leu Glu Ile Tyr Gln
 135 140 145
 gaa gac cag atc cat ttc atg tgc cca ctg gca cgg cag gga gac ttc 639

Glu Asp Gln Ile His Phe Met Cys Pro Leu Ala Arg Gln Gly Asp Phe	
150 155 160	
tat gtg cct gag atg aag gag aca gag tgg aaa tgg cgg ggg ctt gtg	687
Tyr Val Pro Glu Met Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val	
165 170 175 180	
gag gcc att gac acc cag gtg gat ggc aca gga gct gac aca atg agt	735
Glu Ala Ile Asp Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser	
185 190 195	
gac acg agt tct gta agc ttg gaa gtg agc cct ggc agc cgg gag act	783
Asp Thr Ser Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr	
200 205 210	
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Ser Ala Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp	
215 220 225	
ggg gac acc cgc agc gag cac agc tac agc gag tca ggt gcc agc ggc	879
Gly Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly	
230 235 240	
tcc tct ttt gag gag ctg gac ttg gag ggc gag ggg ccc tta ggg gag	927
Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Trp Leu Gly Glu	
245 250 255 260	
tca cgg ctg gac cct ggg act gag ccc ctg ggg act acc aag tgg ctc	975
Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys Trp Leu	
265 270 275	
tgg gag ccc act gcc cct gag aag ggc aag gag taacccatgg cctgcaccct	1028
Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu	
280 285	
cctgcagtgc agttgctgag gaactgagca gactctccag cagactctcc agccctcttc	1088
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tgaggaggat gtgaccggga ctgagtcagg agccctctgg aagc atg gag act gtg	176
Met Glu Thr Val	

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Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile Phe Leu Ala Ser Phe
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Ala Ala Leu Val Leu Val Cys Arg Gln Arg Tyr Cys Arg Pro Arg Asp
      -5      1      5
ctg ctg cag cgc tat gat tct aag ccc att gtg gac ctc att ggt gcc      320
Leu Leu Gln Arg Tyr Asp Ser Lys Pro Ile Val Asp Leu Ile Gly Ala
      10      15      20
atg gag acc cag tct gag ccc tct gag tta gaa ctg gac gat gtc gtt      368
Met Glu Thr Gln Ser Glu Pro Ser Glu Leu Glu Leu Asp Asp Val Val
      25      30      35
atc acc aac ccc cac att gag gcc att ctg gag aat gaa gac tgg atc      416
Ile Thr Asn Pro His Ile Glu Ala Ile Leu Glu Asn Glu Asp Trp Ile
      40      45      50      55
gaa gat gcc tgc ggt ctc atg tcc cac tgc att gcc atc ttg aag att      464
Glu Asp Ala Ser Gly Leu Met Ser His Cys Ile Ala Ile Leu Lys Ile
      60      65      70
tgt cac act ctg aca gag aag ctt gtt gcc atg aca atg ggc tct ggg      512
Cys His Thr Leu Thr Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly
      75      80      85
gcc aag atg aag act tca gcc agt gtc agc gac atc att gtg gtg gcc      560
Ala Lys Met Lys Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala
      90      95      100
aag cgg atc agc ccc agg gtg gat gat gtt gtg aag tgc atg tac cct      608
Lys Arg Ile Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro
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ccg ttg gac ccc aaa ctc ctg gac gca cgg acg act gcc ctg ctc ctg      656
Pro Leu Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Leu
      120      125      130      135
tct gtc agt cac ctg gtg ctg gtg aca agg aat gcc tgc cat ctg acg      704
Ser Val Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr
      140      145      150
gga ggc ctg gac tgg att gac cag tct ctg tgc gct gct gag gag cat      752
Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu His
      155      160      165
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Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp Lys Gly
      170      175      180
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Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala Ile
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Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Trp Thr Leu
-25 -20 -15

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Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln
-10 -5 1 5

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Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu
10 15 20

ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg 246
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp
25 30 35

agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc 294
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro
40 45 50

cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc 342
His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro
55 60 65

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Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser
70 75 80 85

gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc 438
Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser
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gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg 486
Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Tyr Ser Leu
105 110 115

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Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr
120 125 130

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Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr
135 140 145

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Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser
150 155 160 165

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Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys
170 175 180

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Ser Met Gln Glu His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val	
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Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala	
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Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser	
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Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn	
280 285 290	
ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat	1062
Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr	
295 300 305	
tgg gac caa cac tac ctc agc tgg tgg atg ctc ctg ggt gtg ggc ttc	1110
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe	
310 315 320 325	
cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg	1158
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val	
330 335 340	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg	1206
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu	
345 350 355	
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat	1248
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn	
360 365 370	
taaggccgc tctctggagg gaaggacatt actgaacctg tcttgcgtg ctcgaaact	1308
ctggagggtt gagcatcaag ttccagcccc ctccactccc ccactcttgc tttctgtgga	1368
acctcagagg ccagcctcga ctctcctggag acccccagggt ggggcttcct tcatactttg	1428
ttgggggact ttggaggcgg gcagggggaca gggctattga taagggtcccc ttggtgttgc	1488
cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaata gagaggcatt	1548
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<222> 131..490

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<221> sig_peptide

<222> 131..301

<223> Von Heijne matrix

score 5.30

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 tcagcgtgtt atg atg cgg tcc cgt acc aac ctg gct act gga atc ccc 169
 Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro
 -55 -50 -45
 agt agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac 217
 Ser Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr
 -40 -35 -30
 att gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc 265
 Ile Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala
 -25 -20 -15
 atc gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att 313
 Ile Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile
 -10 -5 1
 ata ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac 361
 Ile Gly Ser Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp
 5 10 15 20
 cgg gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga 409
 Arg Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly
 25 30 35
 ttt tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt 457
 Phe Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly
 40 45 50
 tac tcc tat gat gac att cca gac ttt gat gac tagcaccac cccatagctg 510
 Tyr Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp
 55 60
 aggaggagtc acagtggaac tgtccagct ttaagatatc tagcagaac tatagctgag 570
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 cctggggccc tgacaagtgt ttccaccagg atagtgtatc tggaaagata gagggttatc 750
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 agtaggttgg acagcatata atttgcacaa ttttgtccct tgaataatcaa gatgttctgc 1170
 agattattcc tttaacggcc ggacttttgg cgtgttcccta atgaaacatg tagtggttat 1230
 tattttagagt ttatagccgt attgctagca cctttagtaga tgtcatcatt ctgctcatga 1290
 ttcaaggat cagcctggat gcctagagga ctagatcacc ttagtttgat tctatttttt 1350
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 score 4.60
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Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu
-35 -30 -25
cgc tat tgc atg aca gtc agc ggc aca gtg gtt ctg gtg gcc ggg acg      156
Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr
-20 -15 -10 -5
ctc tgc ttc gct tgg tgg agc gaa ggg gat gca acc gcc cag cct ggc      204
Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly
1 5 10
cag ctg gcc cca ccc acg gag tat ccg gtg cct gag ggc ccc agc ccc      252
Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro
15 20 25
ctg ctc agg tcc gtc agc ttc gtc tgc tgc ggt gca ggt ggc ctg ctg      300
Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu
30 35 40
ctc ctg att ggc ctg ctg tgg tcc gtc aag gcc agc atc cca ggg cca      348
Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro
45 50 55 60
cct cga tgg gac ccc tat cac ctc tcc aga gac ctg tac tac ctc act      396
Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr
65 70 75
gtg gag tcc tca gag aag gag agc tgc agg acc ccc aaa gtg gtt gac      444
Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp
80 85 90
atc ccc act tac gag gaa gcc gtg agc ttc cca gtg gcc gag ggg ccc      492
Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro
95 100 105
cca aca cca cct gca tac cct acg gag gaa gcc ctg gag cca agt gga      540
Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly
110 115 120
tcg agg gat gcc ctg ctc agc acc cag ccc gcc tgg cct cca ccc agc      588
Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Ser
125 130 135 140
tat gag agc atc agc ctt gct ctt gat gcc gtt tct gca gag acg aca      636
Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr
145 150 155
cgc agt gcc aca cgc tcc tgc tca ggc ctg gtt cag act gca cgg gga      684
Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly
160 165 170
gga agt taaagctcc tagcaggtcc tgaattccaga gacaaaaatg ctgtgccttc      740
Gly Ser
tcacagagtct tatgcagtgc ctgggacaca gtaggcactc agcaaacggt cggtgttgaa      800
ggctgttcta tttatctatt gctgtataac aaaccaccc agaatttagt ggctttaaatt      860
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 <223> Von Heijne matrix
 score 4.10
 seq LPSLAHLLPALDC/LE

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 <222> 243,252,278,285,387,1429
 <223> n=a, g, c or t

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 gctgcgcagc gcagctatag acattctgcg tcagggtccgg gctcctggac ttgaccttct 180
 ccgagccctg gagggtggga gaaaagggtc accaattttt aaatccaaa tatatctcat 240
 ggntacagtg gnaagaactg gccagagagt ctgggaagntt tgggnttctg gtccctggctg 300
 tgccactgac tcaactgtgac cttgggatct tgtgctgtga agacatttcc caagtgtctc 360
 atgttagcca gcaaatctga cccacanggc ctggaaagag gtgattgtta ggttgccgag 420
 aggtggtctt atccagctca gcttcccctg ggaccaccg tgggacctga ggcagaactg 480
 ggggtgactt ggccctctcc atg gca cac cgg ctg cag ata cga ctg ctg acg 533
 Met Ala His Arg Leu Gln Ile Arg Leu Leu Thr
 -240 -235
 tgg gat gtg aag gac acg ctg ctc agg ctc cgc cac ccc tta ggg gag 581
 Trp Asp Val Lys Asp Thr Leu Leu Arg Leu Arg His Pro Leu Gly Glu
 -230 -225 -220
 gcc tat gcc acc aag gcc cgg gcc cat ggg ctg gag gtg gag ccc tca 629
 Ala Tyr Ala Thr Lys Ala Arg Ala His Gly Leu Glu Val Glu Pro Ser
 -215 -210 -205
 gcc ctg gaa caa ggc ttc agg cag gca tac agg gct cag agc cac agc 677
 Ala Leu Glu Gln Gly Phe Arg Gln Ala Tyr Arg Ala Gln Ser His Ser
 -200 -195 -190 -185
 ttc ccc aac tac ggc ctg agc cac ggc cta acc tcc cgc cag tgg tgg 725
 Phe Pro Asn Tyr Gly Leu Ser His Gly Leu Thr Ser Arg Gln Trp Trp
 -180 -175 -170
 ctg gat gtg gtc ctg cag acc ttc cac ctg gcg ggt gtc cag gat gct 773
 Leu Asp Val Val Leu Gln Thr Phe His Leu Ala Gly Val Gln Asp Ala
 -165 -160 -155
 cag gct gta gcc ccc atc gct gaa cag ctt tat aaa gac ttc agc cac 821
 Gln Ala Val Ala Pro Ile Ala Glu Gln Leu Tyr Lys Asp Phe Ser His
 -150 -145 -140
 ccc tgc acc tgg cag gtg ttg gat ggg gct gag gac acc ctg agg gag 869
 Pro Cys Thr Trp Gln Val Leu Asp Gly Ala Glu Asp Thr Leu Arg Glu

-135	-130	-125	
tgc cgc aca cgg ggt ctg aga ctg gca gtg atc tcc aac ttt gac cga			917
Cys Arg Thr Arg Gly Leu Arg Leu Ala Val Ile Ser Asn Phe Asp Arg			
-120	-115	-110	-105
cgg cta gag ggc atc ctg gag ggc ctt ggc ctg cgt gaa cac ttc gac			965
Arg Leu Glu Gly Ile Leu Glu Gly Leu Gly Leu Arg Glu His Phe Asp			
-100	-95	-90	
ttt gtg ctg acc tcc gag gct gct ggc tgg ccc aag cgg gac ccc cgc			1013
Phe Val Leu Thr Ser Glu Ala Ala Gly Trp Pro Lys Pro Asp Pro Arg			
-85	-80	-75	
att ttc cag gag gcc ttg cgg ctt gct cat atg gaa cca gta gtg gca			1061
Ile Phe Gln Glu Ala Leu Arg Leu Ala His Met Glu Pro Val Val Ala			
-70	-65	-60	
gcc cat gtt ggg gat aat tac ctc tgc gat tac cag ggg cct cgg gct			1109
Ala His Val Gly Asp Asn Tyr Leu Cys Asp Tyr Gln Gly Pro Arg Ala			
-55	-50	-45	
gtg ggc atg cac agc ttc ctg gtg gtt ggc cca cag gca ctg gac ccc			1157
Val Gly Met His Ser Phe Leu Val Val Gly Pro Gln Ala Leu Asp Pro			
-40	-35	-30	-25
gtg gtc agg gat tct gta cct aaa gaa cac atc ctc ccc tct ctg gcc			1205
Val Val Arg Asp Ser Val Pro Lys Glu His Ile Leu Pro Ser Leu Ala			
-20	-15	-10	
cat ctc ctg cct gcc ctt gac tgc cta gag ggc tca act cca ggg ctt			1253
His Leu Leu Pro Ala Leu Asp Cys Leu Glu Gly Ser Thr Pro Gly Leu			
-5	1	5	
tgaggccagt gaggaagtg gctgggccct agggccatgga gaaaacctta aacaaaccct			1313
ggagacaggg agccccctct tctccacag ctctggacct ttccccctct cctgcgggc			1373
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 <213> Homo Sapiens

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 <222> 25..402

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 <222> 25..96
 <223> Von Heijne matrix
 score 7.00
 seq LLCCFRALSGSLs/MR

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 <222> 1500..1505

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 <222> 1525..1540
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 <222> 625,1411,1432,1440,1450,1506
 <223> n=a, g, c or t

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Met Asp Lys Ser Leu Leu Leu Glu Leu

-20

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ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg      99
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met
-15                                     -10                                     -5                                     1
aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct      147
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro
5                                     10                                     15
gtg ata gaa att att cag tgt agg atg tgc cac ctc cag ttc cca gga      195
Val Ile Glu Ile Ile Gln Cys Arg Met Cys His Leu Gln Phe Pro Gly
20                                     25                                     30
gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag      243
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu
35                                     40                                     45
gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta      291
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu
50                                     55                                     60                                     65
acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg      339
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg
70                                     75                                     80
tgg agt gtc tat ttg gtg aac ttc agg tgc tgc agg agc cat gac ctg      387
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Cys Arg Ser His Asp Leu
85                                     90                                     95
tgc aat gaa gac ctt tagaagttaa tgggttcttct gtgactccaa tttctgggtg      442
Cys Asn Glu Asp Leu
100
aggtgtgttc ctcagcctct tcacaatgac ttcttaaaaa aaatcacaca cacacacaca      502
cacactacag aagaggattg caaacacatg gctccatctt ctgcacacga aaggaaaagt      562
cctctccttt tctcagctct ctgtcagccg ccttaaaata agtaaaataa taaccttgag      622
agnaaagaac aagatcaata tatcctgcag gttgctacaa acccttgtgc tttcactgta      682
tagccagttc attcagaaaa ggaggaaaagg gtagtttaat ttcaaaaaag aatcccttcc      742
tctttcctct gctgctttcc ttccctctgt ggcagggtat tttaatatat ttttcaaat      802
tttttctctt ctgtgtttat cttcttatcc cactccaaag aaagcacata actgtggcct      862
gaagggatgg ggagtagcaa cataaaaaa agtggtctcaa gtctctcttg agtttgttca      922
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catgaacaga gaaagattgt ctaccttcta gaatcagatc tgtttggggc tgggggttgg      1042
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gccaaactca caaggagaca tcaacctcta gacagggaac agcttcagga tacttccagg      1162
agacagagcc accagcagca aaacaaatat tcccatgcct ggagcatggc atagaggaaag      1222
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cgaacctgnt tcacaagggt agaggctgan ttctaacnga aacttgttag aatgaagcct      1462
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<211> 1643

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<213> Homo Sapiens

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<221> CDS

<222> 280..678

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<221> sig_peptide

<222> 280..411

<223> Von Heijne matrix

score 3.90

seq LSDSLWSPHCSWS/ER

03970360.10501

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 <222> 1628..1643

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 atccattttt catgccatta ctttatttta aaacctgggc caaccaggt ctcaaaaggt 180
 attggacatc ctcagaaaag atgactgtct tatgttgaa cacaacactg attcttacag 240
 gttttcttct caactgttct ctggctgtgg cagccagat atg gac agg aga gct 294
 Met Asp Arg Arg Ala
 -40
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 Thr Ser Phe Pro Pro Leu Pro Ala Lys Glu Arg Arg Ala Gly Ile Ser
 -35 -30 -25
 agt gcc ctc ccc tgc cca ccc act atg tca ctt tct gac tcc ctt tgg 390
 Ser Ala Leu Pro Cys Pro Pro Thr Met Ser Leu Ser Asp Ser Leu Trp
 -20 -15 -10
 tcc cct cat tgc tct tgg agt gag aga cct cat tcc ttc tct cac tgg 438
 Ser Pro His Cys Ser Trp Ser Glu Arg Pro His Ser Phe Ser His Trp
 -5 1 5
 agg cag cca aga atg gga tcc tct ggt ggg tct ttg gat tat gta agt 486
 Arg Gln Pro Arg Met Gly Ser Ser Gly Gly Ser Leu Asp Tyr Val Ser
 10 15 20 25
 ttc aaa cac tgg ata cac agc tcc aga tct aaa ggc aag att gct gct 534
 Phe Lys His Trp Ile His Ser Ser Arg Ser Lys Gly Lys Ile Ala Ala
 30 35 40
 cta gag gca gga ctg ttc att tcc tgc ctt ggg gat gca ccc aga ggc 582
 Leu Glu Ala Gly Leu Phe Ile Ser Cys Leu Gly Asp Ala Pro Arg Gly
 45 50 55
 ctg aat gct tcc caa gga aac caa aga aag aac atg gtc tgt ttc aga 630
 Leu Asn Ala Ser Gln Gly Asn Gln Arg Lys Asn Met Val Cys Phe Arg
 60 65 70
 ggt gga gtg gcc agt cta gct ctg cca tct ctc act cct tcc tgc ctt 678
 Gly Gly Val Ala Ser Leu Ala Leu Pro Ser Leu Thr Pro Ser Cys Leu
 75 80 85
 tagggtagca ctgagggtga aagcctgaac tgctgtctct gctctggctt gtgctcaagg 738
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Met Glu Ala Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys
-25 -20 -15
gtg gtc ttc acc ctt ggc atg ttc tcc gcc ggc ctc tcg gac ctc agg 156
Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg
-10 -5 1
cac atg cga atg acc cgg agt gtg gac aac gtc cag ttc ctg ccc ttt 204
His Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe
5 10 15
ctc acc acg gaa gtc aac aac ctg ggc tgg ctg agt tat ggg gct ttg 252
Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu
20 25 30 35
aag gga gac ggg atc ctc atc gtc gtc aac aca gtg ggt gct gcg ctt 300
Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu
40 45 50
cag acc ctg tat atc ttg gca tat ctg cat tac tgc cct cgg aag cgt 348
Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg
55 60 65
gtt gtg ctc cta cag act gca acc ctg cta ggg gtc ctt ctc ctg ggt 396
Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly
70 75 80
tat ggc tac ttt tgg ctc ctg gta ccc aac cct gag gcc cgg ctt cag 444
Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln
85 90 95
cag ttg ggc ctc ttc tgc agt gtc ttc acc atc agc atg tac ctc tca 492
Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser
100 105 110 115
cca ctg gct gac ttg gct aag gtg att caa act aaa tca acc caa tgt 540
Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys
120 125 130
ctc tcc tac cca ctc acc att gct acc ctt ctc acc tct gcc tcc tgg 588
Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp
135 140 145
tgc ctc tat ggg ttt cga ctc aga gat ccc tat atc atg gtg tcc aac 636
Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn
150 155 160
ttt cca gga atc gtc acc agc ttt atc cgc ttc tgg ctt ttc tgg aag 684

09978360.101501

Phe	Pro	Gly	Ile	Val	Thr	Ser	Phe	Ile	Arg	Phe	Trp	Leu	Phe	Trp	Lys		
	165					170				175							
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Tyr	Pro	Gln	Glu	Gln	Asp	Arg	Asn	Tyr	Trp	Leu	Leu	Gln	Thr				
180					185			190									
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 Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val Val
 -15 -10 -5
 acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc caa 152
 Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser Gln
 1 5 10
 gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag agt 200
 Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys Ser
 15 20 25 30
 att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata gaa 248
 Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile Glu
 35 40 45
 gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg gaa 296
 Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val Glu
 50 55 60
 aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag atg 344
 Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys Met

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Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile Ile			
80	85	90	
cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag gat			440
His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Gln Asp			
95	100	105	
ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg gat			488
Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val Asp			
115	120	125	
ctg ggt cta gag act gtg tat gag aag ttc cac ccc tct att cag tcc			536
Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln Ser			
130	135	140	
ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa ggc			584
Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys Gly			
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atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca ggg			632
Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr Gly			
160	165	170	
gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg ccc			680
Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro Pro			
175	180	185	
aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc ctg			728
Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser Leu			
195	200	205	
ctg cag agg cag gag tgc agc gtc agg ctc tgg aag gtg ctg gcc ctg			776
Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala Leu			
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Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg Lys			
225	230	235	
cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag gag			872
Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln Glu			
240	245	250	
gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct gag			920
Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro Glu			
255	260	265	
gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc ttc			968
Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser Phe			
275	280	285	
aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc acc gag			1016
Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr Glu			
290	295	300	
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Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg Gln			
305	310	315	
cgc atc acc cgg gtg ata ccc ctg tac aac agc taatagtgtt gaagccgcac			1117
Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser			
320	325		
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tgctccatgtg cagcctcctc agagcctcac ctggggaggga tgccgtggcg tctctcccca			1357
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cacttggggag agctcgggggt ggtccctggt ttccctcctt ggagaatgag gcgcagaggc 1897
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 tggatgtcac aacatgatct aatcccgga gacttgaggg acctccgagt agaacctgtt 180
 acaactagtgt ttgcaacagg ggactattca attttgatga atgtaagctg ggtaactcgg 240
 gcag atg tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac aca 289
 Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr
 -180 -175 -170
 gtc tat ttc att ggg gcc cat aaa att cct aat gca aat atg aat gaa 337
 Val Tyr Phe Ile Gly Ala His Lys Ile Pro Asn Ala Asn Met Asn Glu
 -165 -160 -155
 gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta gac 385
 Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp
 -150 -145 -140
 cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg tgg 433
 His Ile Met Lys Tyr Lys Lys Cys Val Lys Ala Gly Ser Leu Trp
 -135 -130 -125
 gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa gtg 481
 Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val
 -120 -115 -110
 aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc caa 529
 Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln
 -105 -100 -95
 cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag aag 577
 His Ser Thr Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys
 -85 -80 -75
 aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt gaa 625

Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	
ggt	gct	acg	gtg	cag	ctg	act	cca	tat	ttt	cct	act	tgt	ggc	agc	gac	673
Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	
		-55					-50					-45				
tgc	atc	cga	cat	aaa	gga	aca	gtt	gtg	ctc	tgc	cca	caa	aca	ggc	gtc	721
Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val		
		-40					-35					-30				
cct	ttc	cct	ctg	gat	aac	aac	aaa	agc	aag	ccg	gga	ggc	tgg	ctg	cct	769
Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	
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ctc	ctc	ctg	ctg	tct	ctg	ctg	gtg	gcc	aca	tgg	gtg	ctg	gtg	gca	ggg	817
Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	Val	Leu	Val	Ala	Gly	
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atc	tat	cta	atg	tgg	agg	cac	gaa	agg	atc	aag	aag	act	tcc	ttt	tct	865
Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	Lys	Thr	Ser	She		
		10					15					20				
acc	acc	aca	cta	ctg	ccc	ccc	att	aag	gtt	ctt	gtg	gtt	tac	cca	tct	913
Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val	Val	Tyr	Pro	Ser	
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gaa	ata	tgt	ttc	cat	cac	aca	att	tgt	tac	ttc	act	gaa	ttt	ctt	caa	961
Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr	Glu	Phe	Leu	Gln	
		40				45				50				55		
aac	cat	tgc	aga	agt	gag	gtc	atc	ctt	gaa	aag	tgg	cag	aaa	aag	aaa	1009
Asn	His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys	
			60						65				70			
ata	gca	gag	atg	ggc	cta	gtg	cag	tgg	ctt	gcc	act	caa	aag	aag	gca	1057
Ile	Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	Gln	Lys	Lys	Ala	
			75					80					85			
yca	gac	aaa	gtc	gtc	ttc	ctt	ctt	tcc	aat	gac	gtc	aac	agt	gtg	tcg	1105
Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	Asn	Ser	Val	Cys	
		90					95					100				
gat	ggt	acc	tgt	ggc	aag	agc	gag	ggc	agt	ccc	agt	gag	aac	tct	caa	1153
Asp	Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Arg	Glu	Asn	Ser	Gln	
		105					110				115					
gac	ctc	ttc	ccc	ctt	gcc	ttt	aac	ctt	tte	tgc	agt	gat	cta	aga	agc	1201
Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	Asp	Leu	Arg	Ser	
		120				125				130					135	
cag	att	cat	ctg	cac	aaa	tac	gtg	gtg	gtc	tac	ttt	aga	gag	att	gat	1249
Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	Arg	Glu	Ile	Asp	
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<222> 573
<223> n=a, g, c or t

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gaggcaacggy ggattccatt tctactagga gtatcaacct ctgagaggga tatatccatc      180
tctgtggatg tcattctgctc tgcagaaaaac cctttcttgg aataccagg aaac atg      237
                                     Met
aat ctg atg tgg acc ctc ctc ctt ttc ctc ctt ttg gac gta act gtc      285
Asn Leu Met Trp Thr Leu Leu Leu Phe Leu Leu Leu Asp Val Thr Val
-20 -15 -10
ttc att cca gcc ctg ccc ttc tca aca cga cat ata gac aac ccc agg      333
Phe Ile Pro Ala Leu Pro Phe Ser Thr Arg His Ile Asp Asn Pro Arg
-5 1 5 10
tcg tgg gtc cct aga gga cac cac cga tac tgt gat gtg atg atg agg      381
Ser Trp Val Pro Arg Gly His His Arg Tyr Cys Asp Val Met Met Arg
15 20 25
cgc cgt tgg ctg atc tat agg ggt aaa tgc gag cag atc cac aca ttc      429
Arg Arg Trp Leu Ile Tyr Arg Gly Lys Cys Glu Gln Ile His Thr Phe
30 35 40
att cat aga atc tgaccacccat agcagatttc tgcagaactc caccactgcc      481
Ile His Arg Ile
45
tggtaccaac agcccoctcca tgtgcagctg ccacaacagt actcatgatg tcaatgtcac      541
ctactgcttt gccagcacag ggaccgcgacc tnttctactgc cactacccaaa aataaggagt      601
ccaccaggcc catgcgagtg ggctgcaaga agggggcatc tgttcacctg gatggctagg      661
ttcctcctga caacggcacc tgaatgaact gcacctacg ccttcaaatc tgtgcagcac      721
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 <222> 828,832
 <223> n=a, g, c or t

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 Met Asn Lys Thr His Lys Asp Cys Ser
 -45
 tca ccc cag tat tcc att tac aac atc ctg aat gaa ctc ccg acc agg 162
 Ser Pro Gln Tyr Ser Ile Tyr Asn Ile Leu Asn Glu Leu Pro Thr Arg
 -40 -35 -30 -25
 cct ata att ctc tct tgc agc caa ata tcc tgc tta ctc ctg gta tct 210
 Pro Ile Ile Leu Ser Cys Ser Gln Ile Ser Cys Leu Leu Val Ser
 -20 -15 -10
 acc tgg tca gca gac ctc atg agt tat cgc cca gtg aca aaa cca tcc 258
 Thr Trp Ser Ala Asp Leu Met Ser Tyr Arg Pro Val Thr Lys Pro Ser
 -5 1 5
 caa aga tgc acc agt cca gca caa agt atg act gtc aat ctc aca aaa 306
 Gln Arg Cys Thr Ser Pro Ala Gln Ser Met Thr Val Asn Leu Thr Lys
 10 15 20
 gat gta ggg ttc tac gag gat act cag agt ata aga att acg cta agt 354
 Asp Val Gly Phe Tyr Glu Asp Thr Gln Ser Ile Arg Ile Thr Leu Ser
 25 30 35 40
 gaa ata agc caa gcc cag aaa gac aca tac ttt att att tca tgt atc 402
 Glu Ile Ser Gln Ala Gln Lys Asp Thr Tyr Phe Ile Ile Ser Cys Ile
 45 50 55
 tgt gga atc taaaagagtc aaattcatgg cagcagggag agggctgaag 451
 Cys Gly Ile
 aagggggaga tgttgatcaa agtttctatg tatacaaaga ccaaaccatc acattatgcc 511
 tcataaatat atacaattat tatttgctaa ttacaagtaa agcaatacaa gaagaaaaaa 571
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 seq LDIVISFVGAVSS/ST

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<220>
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 <222> 1309..1324

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 <222> 888,1080
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 aaaaataaa atg tat ttt cat ttt cta ggt gcc gga gca att ctt att cct 170
 Met Tyr Phe His Phe Leu Gly Ala Gly Ala Ile Leu Ile Pro
 -25 -20 -15
 cgt tta gac att gtg att tcc ttc gtt gga gct gtg agc agc agc aca 218
 Arg Leu Asp Ile Val Ile Ser Phe Val Gly Ala Val Ser Ser Ser Thr
 -10 -5 1
 ttg gcc cta atc ctg cca cct ttg gtt gaa att ctt aca ttt tcg aag 266
 Leu Ala Leu Ile Leu Pro Pro Leu Val Glu Ile Leu Thr Phe Ser Lys
 5 10 15
 gaa cat tat aat ata tgg atg gtc ctg aaa aat att tct ata gca ttc 314
 Glu His Tyr Asn Ile Trp Met Val Leu Lys Asn Ile Ser Ile Ala Phe
 20 25 30
 act gga gtt gtt gcc ttc tta tta ggt aca tat ata act gtt gaa gaa 362
 Thr Gly Val Val Gly Phe Leu Leu Gly Thr Tyr Ile Thr Val Glu Glu
 35 40 45 50
 att att tat cct act ccc aaa gtt gta gct ggc act cca cag agt cct 410
 Ile Ile Tyr Pro Thr Pro Lys Val Val Ala Gly Thr Pro Gln Ser Pro
 55 60 65
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 Phe Leu Asn Leu Asn Ser Thr Cys Leu Thr Ser Gly Leu Lys
 70 75 80
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 tcattccctgt gaatgnocaa agtaaaacttt atgtacagtg taaaaaaaaaa aaaattctcag 932
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 aacataaatat aagcatcaga aaattgcata cactagaatt aattttacac tctaattgga 1052
 gtgtgacttc atagtcaaga ggcactgntc aagatcatga cttagtgttt caatgaaatt 1112
 tgacaaggga ctttaaaact fatccagtg aactcccttg tttttcgtca gaggaagagg 1172
 aggcctagaa aggttaagta acttggtcga gaccactcag ccttgagatc aagaaaacct 1232
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<210> 37
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 <213> Homo Sapiens

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 tgataggcag cttctcttct ttccaacagt gatacctacg aaaatcaaaa taaatgcaag 180
 ctgaggtttt gtgctcactg aaagggctgt caaccctcaga aggcgcgacac aaaaaaaa 237
 atg gta tgt gaa gat gca ccg tct ttt caa atg gcc tgg gag agt caa 285
 Met Val Cys Glu Asp Ala Pro Ser Phe Gln Met Ala Trp Glu Ser Gln
 -35 -30 -25
 atg gcc tgg gag agg ggg cct gcc ctt ctg tgc tgt gtc ctt tcg gct 333
 Met Ala Trp Glu Arg Gly Pro Ala Leu Leu Cys Val Leu Ser Ala
 -20 -15 -10
 tcc cag ttg agc tcc caa gac cag gac cca ctg ggg cat ata aaa tct 381
 Ser Gln Leu Ser Ser Gln Asp Gln Asp Pro Leu Gly His Ile Lys Ser
 -5 1 5 10
 ctg ctg tat cct ttc ggc ttc cca gtt gag ctg cca aga cca gga ccc 429
 Leu Leu Tyr Pro Phe Gly Phe Pro Val Glu Leu Pro Arg Pro Gly Pro
 15 20 25
 act ggg gca tat aaa aaa gtc aaa aat caa aat caa aca aca agt tct 477
 Thr Gly Ala Tyr Lys Val Lys Asn Gln Asn Gln Thr Thr Ser Ser
 30 35 40
 gag tta ctt agg aaa cag act tcg cat ttc aat cag aga ggc cac aga 525
 Glu Leu Leu Arg Lys Gln Thr Ser His Phe Asn Gln Arg Gly His Arg
 45 50 55
 gca agg tct aaa ctt ctg gct tct aga caa att cct gat aga aca ttt 573
 Ala Arg Ser Lys Leu Leu Ala Ser Arg Gln Ile Pro Asp Arg Thr Phe
 60 65 70 75
 aaa tgt ggg aag tgg ctt ccc cag gtc cca tcc cct gtt tagggataga 622
 Lys Cys Gly Lys Trp Leu Pro Gln Val Pro Ser Pro Val
 80 85
 gttgatatca tttttatagt tgccatgtat gcctctgcct gaattttttt aattgacttt 682
 tgagcttttg agattgcacg agggagaaca aggcctttgc tgttgtggat aggaagagact 742
 taacctaaaa ttaaccacgc aagaagcat tagtaaaaat ctaacaatat gaagggctct 802

tatgagtc	at	ttttttc	agatgaaa	ccagaaa	cacaggaac	aaatacctc	862
cagaacat	g	aagcaat	cgaagact	ctcggta	ttttaaaa	tatacagat	922
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aagcctgac	g	cctgtcagt	gaaaaggg	tcaatgaat	acgggtgtg	tgcattggc	1282
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atgcgcctgt	g	agtcgccag	gtccaggag	ctgaggcagg	agaattgatt	gaacccggg	1522
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gattccgttc	g	ccaagaaaa	aaaattgtc	aacaataagg	gncaaaagg	gagaatcata	1642
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ctgtgtcaaa	g	aggaagctg	tttgaatac	gtgtgcataa	aaattaaata	gaggtgaaca	1762
caattatttt	g	aaggcagtt	aattatctc	gtattgtgaa	ctaagacttt	ctagaatttt	1822
acttattcat	g	tctgtacta	aattttttc	aatgaacaca	tatactttt	taatcagaaa	1882
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 <222> 229..492
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 score 6.70
 seq VFALSSFLNKASA/VY

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 <222> 841..852

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	aacagctcct
	cccagatcat
	atactcct atg
	aaa gga
	Met Lys Gly
gga atc tcc	aat gta tgg
Gly Ile Ser	Asn Val Trp
-85	-80
cca gaa cac	ctt gaa tca
Pro Glu Ser	Leu Glu Ser
-65	-60
ttg att gat	gaa gaa gta
Leu Ile Asp	Glu Glu Val
-50	-45
ata gga gga	ttc tct atg
Ile Gly Gly	Phe Ser Met
	Gly Gly Cys
	Met Ala Met
	His Leu Ala
	Tyr

0007350.101501

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      -35              -30              -25
aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg      477
Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu
      -20              -15              -10
aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta      525
Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val
      -5              1              5              10
ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt      573
Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu
      15              20              25
cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg      621
His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val
      30              35              40
acc acg aag ttt cat agt ttt cca aat gtt tac cat gag cta agc aaa      669
Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys
      45              50              55
act gag tta gac ata ttg aag tta tgg att ctt aca aag ctg cca gga      717
Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys Leu Pro Gly
      60              65              70              75
gaa atg gaa aaa caa aaa tgaatgaatc aagagtgatt tgттаатgта      765
Glu Met Glu Lys Gln Lys
      80
agtgтаатgt ctttgtgaaa agtgattttt actgccaaat tataatgata attaaaaat      825
тааgааатag caaaaaaa aaaaaa      852

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seq QMIMLVCFNLSRG/CL

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<222> 708..726

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<222> 723
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acaaccagac actgtcagaa ccaactttgt gagaaccggg aaaataatca aagggtacg      120
gcaactaaaaaatgtctgga tcaacacaaa ggaacttaa aatgat atg aaa gct      176
Met Lys Ala
-55
gtg tgg cat ttt tgc ttg tcc cac aag tcc agc ttg gtg ata gtc ttg      224

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Val	Trp	His	Phe	Cys	Leu	Ser	His	Lys	Ser	Ser	Leu	Val	Ile	Val	Leu		
			-50					-45					-40				
aag	acg	gca	ggc	tgg	att	ccc	cag	gct	ggg	acc	ctt	atc	cct	cct	ggg	tcc	272
Lys	Thr	Ala	Gly	Trp	Ile	Pro	Gln	Ala	Gly	Thr	Leu	Ile	Pro	Gly	Ser		
			-35					-30					-25				
aga	gag	gag	agc	aga	tct	gat	tca	caa	atg	att	atg	ctt	gtc	tgt	ttt	320	
Arg	Glu	Glu	Ser	Arg	Ser	Asp	Ser	Gln	Met	Ile	Met	Leu	Val	Cys	Phe		
			-20				-15				-10						
aat	ctt	tcc	aga	ggc	tgt	ctg	aag	aag	gta	ttc	atc	atc	tct	gtt	tta	368	
Asn	Leu	Ser	Ser	Arg	Gly	Cys	Leu	Lys	Lys	Val	Phe	Ile	Ile	Ser	Val	Leu	
			-5			1			5					10			
cct	gac	cca	gaa	acc	att	ctg	cta	gga	aaa	aca	gtg	ggc	att	gct		413	
Pro	Asp	Pro	Glu	Thr	Ile	Leu	Leu	Gly	Lys	Thr	Val	Gly	Ile	Ala			
			15				20				25						
tgaaaacagt	gttctgtggt	tgaaaaaccc	acagtcacct	tgggctggtg	ggaatgtaaa											473	
atggcgccctc	ttcttgatca	tcgtttggca	gtttctcaaa	agggtcaaacg	tagaatcact											533	
atttgatcca	acaattctac	tcctaggtat	atccccaaaa	gaattgaaaa	caaggatgca											593	
aacatatgcy	tgtaacataa	tgtttataga	aaaaatatct	acaataatca	aaaggcagaa											653	
acaacccaag	gtgtccaataa	cagaagaatg	aataaacagt	gtgatataaa	cataaaaaaa											713	
aaaaaaaaaa	aaa															726	

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 <222> 1019..1039

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				Met Asp Lys Val Gln													
				-20													
agt ggt ttc ctc att ttg ttt ttg ttt tta atg gaa tgc caa ctt cat																162	
Ser Gly Phe Leu Ile Leu Phe Leu Phe Leu Met Glu Cys Gln Leu His																	
			-15			-10			-5					1			
tta tgc ttg ccg tat gca gat gga ctc cat ccc act gga aac ata aca																210	
Leu Cys Leu Pro Tyr Ala Asp Gly Leu His Pro Thr Gly Asn Ile Thr																	
			5			10			15								
ggc tta cca ggt agc ttc aac cac tgg ttt tat gtg act cag gga gaa																258	
Gly Leu Pro Gly Ser Phe Asn His Trp Phe Tyr Val Thr Gln Gly Glu																	
			20			25			30								
ttg aaa agc tgt ttc agg gga gat aaa aag aag gta att aca ttt cac																306	
Leu Lys Ser Cys Phe Arg Gly Asp Lys Lys Lys Val Ile Thr Phe His																	

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      35              40              45
cgc aaa aag ttt tct ttt caa ggc agt aaa cgg tca caa cca ccc aga      354
Arg Lys Lys Phe Ser Phe Gln Gly Ser Lys Arg Ser Gln Pro Pro Arg
50              55              60              65
aac atc acc aaa gag ccc aaa gtg ttc ttt cat aaa acc cag ttg cct      402
Asn Ile Thr Lys Lys Glu Pro Lys Val Phe Phe His Lys Thr Gln Leu Pro
70              75              80
ggg att caa ggg gct gcc tcg aga tcc acg gct gca tcc cct acg aac      450
Gly Ile Gln Gly Ala Ala Ser Arg Ser Thr Ala Ala Ser Pro Thr Asn
85              90              95
ccc atg aaa ttc ctg agg aat aaa gca ata att cgg cat aga cct gct      498
Pro Met Lys Phe Leu Arg Asn Lys Ala Ile Ile Arg His Arg Pro Ala
100             105             110
ctt gtt aaa gta att tta att tcg agc gta gcc ttc agc att gcc ctg      546
Leu Val Lys Val Ile Leu Ile Ser Ser Val Ala Phe Ser Ile Ala Leu
115             120             125
ata tgt ggg atg gca atc tcc tat atg ata tat cga ctg gca cag gct      594
Ile Cys Gly Met Ala Ile Ser Tyr Met Ile Tyr Arg Leu Ala Gln Ala
130             135             140             145
gag gaa aga caa cag ctc gag tca ctt tat aag aac ctc agg ata ccg      642
Glu Glu Arg Gln Gln Leu Glu Ser Leu Tyr Lys Asn Leu Arg Ile Pro
150             155             160
tta tta gga gat gaa gaa gag ggc tca gag gac gag ggt gag tcc acg      690
Leu Leu Gly Asp Glu Glu Gly Ser Glu Asp Glu Gly Glu Ser Thr
165             170             175
cac cta ctt cca aag aac gaa aat gag ctg gaa aag ttc atc cac tca      738
His Leu Leu Pro Lys Asn Glu Asn Glu Leu Glu Lys Phe Ile His Ser
180             185             190
gtt att ata tca aaa aga agc aaa aat att aag aag aaa ctg aag gaa      786
Val Ile Ile Ser Lys Arg Ser Lys Asn Ile Lys Lys Lys Leu Lys Glu
195             200             205
gag caa aac tca gta aca gaa aac aaa aca aag aat gcg tca cat aat      834
Glu Gln Asn Ser Val Thr Glu Asn Lys Thr Lys Asn Ala Ser His Asn
210             215             220             225
gga aaa atg gaa gac ttg tgaacgcaga cgacagaggt gccggctgag      882
Gly Lys Met Glu Asp Leu
230
gcagaggaga aactatgggg gtgctgggag actgagcctg tgggcgtggc ttgctccag      942
agaaccttat ggaagaggac atcaagaaaa gaaatgccag acctgtatcc cagaaaaataa      1002
agccacatga tatagcaaaa aaaaaaaaaa aaaaaaa      1039

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 <223> Von Heijne matrix
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 <222> 1324..1355

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 ccttttccat ttatgtgctt tagtaatctg ccgccaaaca gctatcttct ttatgttctt 180
 ctacaactga tgggtgtttt tttttctcat ttgtctctt aatagacaaa tggagggc 237
 atg agc ttc ctt aga att acc cct tgc acg cat agt tct gtt tca tct 285
 Met Ser Phe Leu Arg Ile Thr Pro Ser Thr His Ser Ser Val Ser Ser
 -30 -25 -20
 gga ctt ttg agg ctt agt atc ttt cta cta ctt agc ttt cct gac tca 333
 Gly Leu Leu Arg Leu Ser Ile Phe Leu Leu Leu Ser Phe Pro Asp Ser
 -15 -10 -5
 aac gga aaa gcc att tgg aca gct cac ctg aat ata aca ttt cag gtt 381
 Asn Gly Lys Ala Ile Trp Thr Ala His Leu Asn Ile Thr Phe Gln Val
 1 5 10
 gga aat gac atc aca tgc gaa tta gga gag agt gga gtg ttc ggg aat 429
 Gly Asn Glu Ile Thr Ser Glu Leu Gly Glu Ser Gly Val Phe Gly Asn
 15 20 25 30
 cat tct cct ctg gaa agg gtg tct ggt gtg gca ctt cct gaa gaa 477
 His Ser Pro Leu Glu Arg Val Ser Gly Val Val Ala Leu Pro Glu Glu
 35 40 45
 tgg aat cag aat gcc tgt cat cct ttg acc aat ttc agc agg ccc aaa 525
 Trp Asn Gln Asn Ala Cys His Pro Leu Thr Asn Phe Ser Arg Pro Lys
 50 55 60
 cag gca gac tca tgg ctg gcc ctc atc gaa cgt gga ggc tgt act ttt 573
 Gln Ala Asp Ser Trp Leu Ala Leu Ile Glu Arg Gly Gly Cys Thr Phe
 65 70 75
 aca cat aaa atc aac gtg gca gca gag aag gga gca aat ggg gtg atc 621
 Thr His Lys Ile Asn Val Ala Ala Glu Lys Gly Ala Asn Gly Val Ile
 80 85 90
 atc tac aac tat caa ggt acg ggc agt aaa gta ttt ccc atg tct cac 669
 Ile Tyr Asn Tyr Gln Gly Thr Gly Ser Lys Val Phe Pro Met Ser His
 95 100 105 110
 cag ggg acg gaa aat ata gtc gcg gtg atg ata agc aac ctg aaa ggc 717
 Gln Gly Thr Glu Asn Ile Val Ala Val Met Ile Ser Asn Leu Lys Gly
 115 120 125
 atg gaa att ttg cac tgc att cag aaa gga gtc tat gtg aca gtc atc 765
 Met Glu Ile Leu His Ser Ile Gln Lys Gly Val Tyr Val Thr Val Ile
 130 135 140
 att gaa gtg ggg aga atg cac atg cag tgg gtg agc cat tac atc atg 813
 Ile Glu Val Gly Arg Met His Met Gln Trp Val Ser His Tyr Ile Met
 145 150 155
 tat cta ttt acc ttc ctg gct gcc aca att gcc tac ttt tac tta gat 861
 Tyr Leu Phe Thr Phe Leu Ala Ala Thr Ile Ala Tyr Phe Tyr Leu Asp
 160 165 170
 tgc gtc tgg aga ctt aca cct aga gtg ccc aat tct ttc acc agg agg 909
 Cys Val Trp Arg Leu Thr Pro Arg Val Pro Asn Ser Phe Thr Arg Arg
 175 180 185 190
 cga agt caa ata aag aca gat gtg aag aaa gct att gac cag ctt caa 957
 Arg Ser Gln Ile Lys Thr Asp Val Lys Lys Ala Ile Asp Gln Leu Gln
 195 200 205
 ctg cga gtt ctc aaa gaa ggg gat gag gaa tta gac cta aat gaa gac 1005
 Leu Arg Val Leu Lys Glu Gly Asp Glu Glu Leu Asp Leu Asn Glu Asp
 210 215 220
 aac tgt gtt gtt tgc ttt gac aca tac aaa ccc caa gat gta gta cgc 1053
 Asn Cys Val Val Cys Phe Asp Thr Tyr Lys Pro Gln Asp Val Val Arg
 225 230 235
 att tta act tgc aaa cat ttt ttc cat aag gca tgc att gac ccc tgg 1101

Ile Leu Thr Cys Lys His Phe Phe His Lys Ala Cys Ile Asp Pro Trp
240 245 250
ctt tta gcc cat agg aca tgt ccc atg tgc aag tgt gac atc ctg aaa 1149
Leu Leu Ala His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys
255 260 265 270
act taagaaatct ggagaatttt ctgaagatgt aaccagatct ttccaataac 1202
Thr
aaagattaga taaattgtct tattgtactt tatgtagaga gaaaatttca gcttctctac 1262
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taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1355

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<222> 187..312
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seq LLPCSSVLTCGQA/SQ

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<222> 489..494

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<222> 558..572

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<222> 94,527,537..538
<223> n=a, g, c or t

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tgaacagtca atttagttta acatttgctt aacnagccat tatgtatgcc aggtaatgtg 120
ctagatgctg gtgggttcaaa gaaaggaacg atgtggacct gacctcaaag aaatccattg 180
gagaat atg aca gat tta gat tta atg atc aac ttt act ttt cct ata 228
Met Thr Asp Leu Asp Leu Met Ile Asn Phe Thr Phe Pro Ile
-40 -35 -30
cag tgg gtc aac caa aac cgc atg gcg tac tac tct ctg aag cct cta 276
Gln Trp Val Asn Gln Asn Arg Met Ala Tyr Tyr Ser Leu Lys Pro Leu
-25 -20 -15
cta ccc tgc tcc tcc gtg ttg aca tgt ggt cag gca agc cag gac tta 324
Leu Pro Cys Ser Ser Val Leu Thr Cys Gly Gln Ala Ser Gln Asp Leu
-10 -5 1
ctc aca tca gct aca tca gtt act ggg atg gag aaa att gaa gcc 369
Leu Thr Ser Ala Thr Ser Val Thr Gly Met Glu Lys Ile Glu Ala
5 10 15
tagaaagatc aagaaacttt ctccaggcca taaatagagg aatcaggatt caaatcagat 429
agacccacag gcttgttctc ttcaacacca cattacccta cattattatt caattattaa 489
ataaaacctt gcattagtgg catttccaaa tgcataanca aaaaaatnna aaaaaaagta 549
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09978260.101501

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 <213> Homo Sapiens

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 score 4.20
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 <222> 497..502

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 <222> 521..535

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 <222> 486,489
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 atg aac ttc tat tta ctc cta gcg agc agc att ctg tgt gcc ttg att 168
 Met Asn Phe Tyr Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
 -15 -10 -5 1
 gtc ttc tgg aaa tat cgc cgc ttt cag aga aac act ggc gaa atg tca 216
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
 5 10 15
 tca aat tca act gct ctt gca cta gtg aga ccc tct tct tct ggg tta 264
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
 20 25 30
 att aac agc aat aca gac aac aat ctt gca gtc tac gac ctc tct cgg 312
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
 35 40 45
 gat att tta aat aat ttc cca cac tca ata gcc agg cag aag cga ata 360
 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
 50 55 60 65
 ttg gta aac ctc agt atg gtg gaa aac aag ctg gtt gaa ctg gaa cat 408
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
 70 75 80
 act cta ctt agc aag ggt ttc aga ggt gca tca cct cac cgg aaa tcc 456
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
 85 90 95
 acc taaaagcgta caggatgtaa tgccagnggn ggaatcatt aaagacactt 509
 Thr
 tgagtagatt caaaaaaaaa aaaaaa 535

<210> 44
 <211> 572
 <212> DNA
 <213> Homo Sapiens

00078360.101501

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<220>
<221> CDS
<222> 34...336

<220>
<221> sig_peptide
<222> 34...123
<223> Von Heijne matrix
      score 7.80
      seq SVTLAQLQLLVQQ/GQ

<220>
<221> polyA_signal
<222> 536..541

<220>
<221> polyA_site
<222> 556..572

<220>
<221> misc_feature
<222> 545
<223> n=a, g, c or t

<400> 44
gcattacacg ccggtcagga ttcgcgaccc gac atg gag cgt ccc cgc agt ccc      54
                                Met Glu Arg Pro Arg Ser Pro
                                -30                                -25
caa tgc tgc gcc ccg gcc tct gcc tca gct tgc gtt acc ctg gcg cag      102
Gln Cys Ser Ala Pro Ala Ser Ala Ser Ala Ser Val Thr Leu Ala Gln
                                -20                                -15                                -10
ctc ctg cag ctg gtc cag cag gcc cag gaa ctc ccg gcc ctg gag aaa      150
Leu Leu Gln Leu Val Gln Gln Gly Gln Glu Leu Pro Gly Leu Glu Lys
                                -5                                1                                5
cgc cac atc gcg gcg atc cac gcc gaa ccc aca gcg tcc cgg ctg ccg      198
Arg His Ile Ala Ala Ile His Gly Glu Pro Thr Ala Ser Arg Leu Pro
                                10                                15                                20                                25
cgg agg ccc aag ccc tgg gag gcc gcg gct ttg gct gag tcc ctt ccc      246
Arg Arg Pro Lys Pro Trp Glu Ala Ala Ala Leu Ala Glu Ser Leu Pro
                                30                                35                                40
cct ccg acc ctc agg ata gga acg gcc ccg gcg gag cct gcc ttg gtt      294
Pro Pro Thr Leu Arg Ile Gly Thr Ala Pro Ala Glu Pro Gly Leu Val
                                45                                50                                55
gag gca gcg act gcg cct tct tca tgg cat aca gtg gcc ccc      336
Glu Ala Ala Thr Ala Pro Ser Ser Trp His Thr Val Gly Pro
                                60                                65                                70
tgaggttcca ggtccttttc gccgcgcgac tggagggcgt ggctacagga cccgggatgc      396
cattcagtta ctcacctttt atgctttcgt cctgacctgt ctcaactaga cttgctcctg      456
caaccaccat gggggttttg catttacatt tgtggacatc gttacagtta agaaaaatcc      516
tgtttcagtc cttatatgta ataaaatgnt ttatgatgca aaaaaaaaaa aaaaaa      572

<210> 45
<211> 804
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 119..409

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<220>
 <221> sig_peptide
 <222> 119..388
 <223> Von Heijne matrix
 score 4.30
 seq TCLTACWTALCCCC/CL

<220>
 <221> polyA_signal
 <222> 769..774

<220>
 <221> polyA_site
 <222> 789..804

<220>
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 <222> 274
 <223> n=a, g, c or t

<220>
 <221> unsure
 <222> -39
 <223> Xaa = His,Gln

<400> 45
 acctgctctg agacaggtgc ggcaagtcta ctgcgggctg gtcggggctc ctcaggttca 60
 gaccgacccg ttatccagtc ggttcgtgga gaggagaggt gcactttaca ggtcccca 118
 atg aac caa gag aac cct cca cca tat cca ggc cct ggt cca acg gcc 166
 Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
 -90 -85 -80 -75
 cca tac cca cct tat cca cca caa cca atg ggt cca gga cct atg ggg 214
 Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Pro Met Gly
 -70 -65 -60
 gga ccc tac cca cct cct cca ggg tac ccc tac cca gga tac cta cag 262
 Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Leu Gln
 -55 -50 -45
 tac ggc tgg can ggt gga cct cag gag cct cct aaa acc aca gtg tat 310
 Tyr Gly Trp Xaa Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
 -40 -35 -30
 gtg gta gaa gac caa aga aga gat gag cta gga cca tcc acc tgc ctc 358
 Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
 -25 -20 -15
 aca gcc tgc tgg acg gct ctc tgt tgc tgc tgt ctc tgg gac atg ctc 406
 Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp Asp Met Leu
 -10 -5 1 5
 acc tgaccagacc agcccagccg tctgtctctg ccagctctgc tgccacctct 459
 Thr
 gacaggtgtg cctgcccca tctcttctga ttgctgttaa caaatgacta gctttgcaca 519
 gacacctcta ccttcagcac tatgggattc tagattaatg ggggttgcta ctgtttaatt 579
 cagtgaactt atctttttaa tgtccaaaat ccatttctta ttgactotta aagatgtgct 639
 aaatgacttt ttgtggcaca ggcttagttg tgaaaaatat aattttttaa ttatacatc 699
 aaggtagtgg ccaaatgtaa cacatcaatc atggaatgat ttctctgcta acagccgcct 759
 gtatgtttca ataaatttgt ccaaagctca aaaaaaaaaa aaaaa 804

<210> 46
 <211> 629
 <212> DNA
 <213> Homo Sapiens

<220>

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<221> CDS
<222> 232..534

<220>
<221> sig_peptide
<222> 232..306
<223> Von Heijne matrix
      score 3.70
      seq AKTCLVLCRSVLS/VI

<220>
<221> polyA_signal
<222> 595..600

<220>
<221> polyA_site
<222> 615..629

<400> 46
tatcaactggt acgaaccaag gatttacaga tcactggcaa aaattctgag aactttcaca      60
ccagtagact gtccaagccc attaatgggc atcacacctc tcttttatgt agctcagaca      120
agacagctta atactctcaa aatactactg caatatggaa tcttagaaga agaaaaaaac      180
cctatcaaca ttgtcttaac aatagtactc tacccttcga gagtaagagt a atg gtt      237
                                         Met Val
                                         -25
gat cgt gaa ttg gct gac atc cat gaa gat gcc aaa aca tgt ttg gta      285
Asp Arg Glu Leu Ala Asp Ile His Glu Asp Ala Lys Thr Cys Leu Val
      -20      -15      -10
cta tgt tcc aga gtg ctt tct gtc att tca gtc aag gaa ata aag aca      333
Leu Cys Ser Arg Val Leu Ser Val Ile Ser Val Lys Glu Ile Lys Thr
      -5      1      5
cag ctg agt tta gga aga cat cca att att tca aat tgg ttt gat tac      381
Gln Leu Ser Leu Gly Arg His Pro Ile Ile Ser Asn Trp Phe Asp Tyr
      10      15      20      25
att cct tca aca aga tac aaa gat cca tgt gaa cta tta cat ctt tgc      429
Ile Pro Ser Thr Arg Tyr Lys Asp Pro Cys Glu Leu Leu His Leu Cys
      30      35      40
aga cta acc atc agg aat caa cta tta acc aac aat atg ctg cca gat      477
Arg Leu Thr Ile Arg Asn Gln Leu Leu Thr Asn Asn Met Leu Pro Asp
      45      50      55
gga ata ttt tca ctt cta att cct gct cgt cta caa aac tat ctg aat      525
Gly Ile Phe Ser Leu Leu Ile Pro Ala Arg Leu Gln Asn Tyr Leu Asn
      60      65      70
tta gaa atc taacatacgt cagtgctcta agttccttaa caatgcttac      574
Leu Glu Ile
      75
caatgtatgg cttagaagtt aataaaaaatt cacttcatgc aaaaaaaaaa aaaaa      629

<210> 47
<211> 669
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 140..595

<220>
<221> sig_peptide
<222> 140..442
<223> Von Heijne matrix

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score 4.10
seq VFMLIVSVLALIP/ET

<220>
<221> polyA_signal
<222> 630..635

<220>
<221> polyA_site
<222> 655..669

<400> 47
gagcggaag cagagctggg cgagaagtag gggagggcgg tgctccgccc cggtggcggt 60
tgctatcgct tcgcagaacc tactcaggca gccagctgag aagagttgag ggattgctgc 120
tgctgggtct gcagacgcg atg gat aac gtg cag ccg aaa ata aaa cat cgc 172
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg
-100 -95
ccc ttc tgc ttc agt gtg aaa ggc cac gtg aag atg ctg cgg ctg gca 220
Pro Phe Cys Phe Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala
-90 -85 -80 -75
cta act gtg aca tct atg acc ttt ttt atc atc gca caa gcc cct gaa 268
Leu Thr Val Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu
-70 -65 -60
cca tat att gtt atc act gga ttt gaa gtc acc gtt atc tta ttt ttc 316
Pro Tyr Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe
-55 -50 -45
ata ctt tta tat gta ctc aga ctt gat cga tta atg aag tgg tta ttt 364
Ile Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
-40 -35 -30
tgg cct ttg ctt gat att atc aac tca ctg gta aca aca gta ttc atg 412
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
-25 -20 -15
ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca ttg aca 460
Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
-10 -5 1 5
gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgt ctt gcc 508
Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
10 15 20
gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc ggt cct 556
Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
25 30 35
tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg taattttata 605
Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
40 45 50
ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca aaaaaaaaaa 665
aaaa 669

<210> 48
<211> 973
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 32..658

<220>
<221> sig_peptide
<222> 32..289
<223> Von Heijne matrix
score 4.00

05978350.101501

seq KLWKLLFLMKSQG/WI

<220>

<221> polyA_signal

<222> 936..941

<220>

<221> polyA_site

<222> 959..973

<220>

<221> misc_feature

<222> 934

<223> n=a, g, c or t

<400> 48

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agggagaggg atggctatgt aggtttatag c atg ttg agc cct acc ttt gtt      52
                                Met Leu Ser Pro Thr Phe Val
                                -85                    -80
ttg tgg gat gtt gga tat ccc tta tac acc tat gga tcc atc tgc att      100
Leu Trp Asp Val Gly Tyr Pro Leu Tyr Thr Tyr Gly Ser Ile Cys Ile
                                -75                    -70                    -65
att gca tta att att tgg caa gtg aaa aag agc' tgc caa aaa tta agc      148
Ile Ala Leu Ile Ile Trp Gln Val Lys Lys Ser Cys Gln Lys Leu Ser
                                -60                    -55                    -50
ttg gta cct aac agg agc tgt tgc cgg tgt cac cga aga gtc caa caa      196
Leu Val Pro Asn Arg Ser Cys Cys Arg Cys His Arg Arg Val Gln Gln
                                -45                    -40                    -35
aag tct gga gat aga aca tca aga gct agg aga act tca cag gaa gaa      244
Lys Ser Gly Asp Arg Thr Ser Arg Ala Arg Arg Thr Ser Gln Glu Glu
                                -30                    -25                    -20
gcc gag aag ttg tgg aag ctg ctg ttt ctc atg aaa agc cag ggc tgg      292
Ala Glu Lys Leu Trp Lys Leu Leu Phe Leu Met Lys Ser Gln Gly Trp
                                -15                    -10                    -5                    1
att cct cag gaa gga agt gtg cgg cga atc ctg tgt gca gac ccc tgc      340
Ile Pro Gln Glu Gly Ser Val Arg Arg Ile Leu Cys Ala Asp Pro Cys
                                5                    10                    15
tgc caa atc tgc aat gtt atg gct ctg gag att aag caa ttg ctg gca      388
Cys Gln Ile Cys Asn Val Met Ala Leu Glu Ile Lys Gln Leu Leu Ala
                                20                    25                    30
gaa gct cca gaa gtt ggc ttg gat aac aag atg aag ctg ttt ctg cac      436
Glu Ala Pro Glu Val Gly Leu Asp Asn Lys Met Lys Leu Phe Leu His
                                35                    40                    45
tgg att aac cct gaa atg aaa gat cga agg cat gag gaa tcc att ctc      484
Trp Ile Asn Pro Glu Met Lys Asp Arg Arg His Glu Glu Ser Ile Leu
                                50                    55                    60                    65
ctt tct aag gct gag aca gtg acc caa gac agg aca aaa aac att gag      532
Leu Ser Lys Ala Glu Thr Val Thr Gln Asp Arg Thr Lys Asn Ile Glu
                                70                    75                    80
aag agt cca act gtc acc aaa gat cat gtg tgg gga gct aca aca cag      580
Lys Ser Pro Thr Val Thr Lys Asp His Val Trp Gly Ala Thr Thr Gln
                                85                    90                    95
aag aca aca gag gac cct gag gct cag cct cct tct act gag gag gaa      628
Lys Thr Thr Glu Asp Pro Glu Ala Gln Pro Pro Ser Thr Glu Glu Glu
                                100                    105                    110
ggc ctg atc ttc tgt gat gcc ccc agt gcc taaataatct gctctagcaa      678
Gly Leu Ile Phe Cys Asp Ala Pro Ser Ala
                                115                    120
cactcccttc agtccagcca atcctgggtc ctgtgccact cctacaaaatg ctccaaaactc      738
tgtctctaaa tgacttgtgc cactcaacca ggaaatctat ccagggtcta actcactcca      798
gcagaaggca ctgttttatg caagaatacc catcacaaga aaaaggagtt cataggttcc      858

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tgaacctctg caatccctg aaaaaggctt tcattgccat ttccattaac atgcagggtga 918
agcagggcgat tctccnaaat atacctttgta cctttaagct aaaaaaaaaa aaaaa 973

<210> 49
<211> 791
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 14..280

<220>
<221> sig_peptide
<222> 14..76
<223> Von Heijne matrix
score 9.50
seq ALVVLCAFLVAA/LE

<220>
<221> polyA_site
<222> 776..791

<220>
<221> misc_feature
<222> 607
<223> n=a, g, c or t

<400> 49
ataggcgcgc acc atg ggc tcc tgc tcc ggc cgc tgc gcg ctc gtc gtc 49
Met Gly Ser Cys Ser Gly Arg Cys Ala Leu Val Val
-20 -15 -10
ctc tgc gct ttt cag ctg gtc gcc gcc ctg gag agg cag gtg ttt gac 97
Leu Cys Ala Phe Gln Leu Val Ala Ala Leu Glu Arg Gln Val Phe Asp
-5 1 5
ttc ctg ggc tac cag tgg gcg ccc atc ctg gcc aac ttt gtc cac atc 145
Phe Leu Gly Tyr Gln Trp Ala Pro Ile Leu Ala Asn Phe Val His Ile
10 15 20
atc atc gtc atc ctg gga ctc ttc ggc acc atc cag tac cgg ctg cgc 193
Ile Ile Val Ile Leu Gly Leu Phe Gly Thr Ile Gln Tyr Arg Leu Arg
25 30 35
tat gtc atg tgt aca cgc tgt ggg cag ccg tct ggg tca cct gga acg 241
Tyr Val Met Cys Thr Arg Cys Gly Gln Pro Ser Gly Ser Pro Gly Thr
40 45 50 55
tct tca tca tct gct tct acc tgg aag tcg gtg gcc tct taaaggacag 290
Ser Ser Ser Ser Ala Ser Thr Trp Lys Ser Val Ala Ser
60 65
cgagctactg accttcagcc tctcccggca tgcctcctgg tggcgtgagc gctggccagg 350
ctgtctgcgt gaggaggtgc cagcagtgagg cctcgggggcc ccccatggcc aggccctggg 410
gtcaggtgct ggctgtgcc tggagcccag ctatgtggag gccctacaca gttgcctgca 470
gatcctgac gcgcttctgg gctttgtctg tggctgccag gtggcagcgg tgtttacgga 530
ggaagaggac agctgcctgc gtaagtgagg aaacagctga tctctgctct gtggcctcca 590
gcctcagcga cgcacnagt gacaatgaca ggagctccca gcccttgga cgcgccccca 650
cccagcacc cccaggcggc cggcagcacc tgccctgggt tctaagtact ggacaccagg 710
cagggcggca gggcagtgcc acggctgggt gcagcgtcaa gagagtttgt aatttccttt 770
ctcttaaaaa aaaaaaaaaa a 791

<210> 50
<211> 1110
<212> DNA
<213> Homo Sapiens

<220>
 <221> CDS
 <222> 93..290

<220>
 <221> sig_peptide
 <222> 93..149
 <223> Von Heijne matrix
 score 9.30
 seq VFVFLFLWDPVLA/GI

<220>
 <221> polyA_signal
 <222> 1078..1083

<220>
 <221> polyA_site
 <222> 1096..1110

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<400> 50
agtataggac tgtgtgtctca acctcttctc tctgttccct gacagccgat gtcagaccct    60
gccactagcc tccttaacag aagttccag cc atg aag cct ctc ctt gtt gtg    113
                               Met Lys Pro Leu Leu Val Val
                               -15
ttt gtc ttt ctt ttc ctt tgg gat cca gtg ctg gca ggt ata aat tca    161
Phe Val Phe Leu Phe Leu Trp Asp Pro Val Leu Ala Gly Ile Asn Ser
                               -10                               1
tta tca tca gaa atg cac aag aaa tgc tat aaa aat ggc atc tgc aga    209
Leu Ser Ser Glu Met His Lys Lys Cys Tyr Lys Asn Gly Ile Cys Arg
5                               10                               15                               20
ctt gaa tgc tat gag agt gaa atg tta gtt gcc tac tgt atg ttt cag    257
Leu Glu Cys Tyr Glu Ser Glu Met Leu Val Ala Tyr Cys Met Phe Gln
                               25                               30                               35
ctg gag tgc tgt gtc aaa gga aat cct gca ccc tgacataaga aaccaatgaa    310
Leu Glu Cys Cys Val Lys Gly Asn Pro Ala Pro
                               40                               45
tggccactat cctgtaggcc cttgattctg ccatctttca caaaaccagg gaatttagat    370
caaaactgtga caccatgatg tgtccatgac tactggtttt tagcattttt ataggccagc    430
agactcttgt ggtcttaaat ttaaagagct gagctgtagc cttcttttaa agagctcggt    490
ttttcacaaa aacaatgtag aagatatatt ctcacctcaa cgtgatgttc agtgtgtctca    550
tcagcaacctg tttctccctc taatcataga ggatattctt attatttaga aaggcttcaa    610
gggaacaacac ttttgacacc taagtctgtg cctacacttg cttcagcttc gcatttccca    670
ttctgtgtgaa attcccaaca gagaagcaga tttgccatgg ccttctgaca accttgtaca    730
ctctctcacat aaaccgcata ggcagggtct gactacaggc tggcccgagt ctgcaactgag    790
tctgacctctg aagtctcttt ggaacaggag aggccatctt gtgatgggct ggaacaaggt    850
aatttctcat ccacctccct agtttcagtt gagcaatgga acttcccacc tgagccccta    910
gggttcagct acagggtata agactgcgct cctgtggttt agtgttggtt ccttagcagc    970
agagtgtatgc cactctgtct gcccgtoatc tgactcctct ggatgggtgt tatcctgtgg    1030
cttaagagct aacaccatgc tgatcttgct ttgctatatg tgtaactaat aaactgccta    1090
aatccaaaaa aaaaaaaaaa
                               1110

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<210> 51
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix

score 4.19999980926514
seq MLAVSLTVPLLGA/MM

<220>

<221> polyA_site

<222> 1042..1053

<400> 51

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tgatggccag	gccccggagg	ctaaggacgg	cagctccttt	agcggcagag	ttttccgagt	120
gacctttctg	atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc	169				
	Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala					
	-10	-5				
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa	217					
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys						
1	5	10	15			
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga	265					
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg						
	20	25	30			
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata	313					
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile						
	35	40	45			
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc	361					
Ala His Ile Leu Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val						
	50	55	60			
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg	409					
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser						
	65	70	75	80		
ggc cct tgc aaa acc cga ggt gat gag cct gtg tgt ggg aga ccc ctg	457					
Gly Pro Cys Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu						
	85	90	95			
ggt atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tac	505					
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr						
	100	105	110			
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg	553					
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu						
	115	120	125			
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat	601					
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn						
	130	135	140			
gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc gat tct	649					
Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser						
	145	150	155	160		
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc	697					
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Val Met Glu Gly						
	165	170	175			
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta	745					
Thr Asp Asp Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val						
	180	185	190			
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct	793					
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser						
	195	200	205			
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata	841					
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile						
	210	215	220			
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt	889					
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe						
	225	230	235	240		
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct	937					
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser						
	245	250	255			

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ggg ggg tac tgg gtg ggc atg tgc acc atc cgc cct aac cct ggg ttt 985
 Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
 260 265 270
 tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att 1033
 Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
 275 280 285
 ttt aag gta aaaaaaaaa a 1053
 Phe Lys Val
 290

<210> 52
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 638..643

<220>
 <221> polyA_site
 <222> 662..675

<400> 52
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 gtacgagtggt ttcagcacac ttggttatgt tgactgtta atg atg tac gtt tct 114
 Met Met Tyr Val Ser
 1 5
 ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc 162
 Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
 10 15 20
 tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa 210
 Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
 25 30 35
 aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg 258
 Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
 40 45 50
 tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatgggtttat 306
 Tyr Val Cys Val Phe Ile
 55
 ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agattttatca 366
 tattttttcaa taatatgaga agaaaaatggg ccgtaaaattg ttaaccattt tatgttcaga 426
 tattttctcta gtttttacct agtttgcctt aacatagaga ccagcaagtg aatatatatg 486
 cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt 546
 cagagaagaa catttaaagg gttaatatatt ttgaaacggtt ttcagataat atctattttg 606
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 aaaaaaaaa 675

<210> 53
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 <213> Homo sapiens

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 <222> 111..194
 <223> Von Heijne matrix
 score 4.80000019073486
 seq GVLLEPFVHQVGG/HS

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<220>
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<222> 1101..1112

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ccgctggact ccgctgccto ccccatctcc ccgccatctg cgcccgagg atg agc 116
Met Ser
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 164
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
-25 -20 -15
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 212
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
-10 -5 1 5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 260
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
10 15 20
ttc tac gag acc ctg cct gct gag atg cgc aaa ttc tct ccc cag tac 308
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr
25 30 35
aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat 356
Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His
40 45 50
ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag gga agt gtg gcc 401
Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val Ala
55 60 65
tgaatacccc accccggctc ctctgcaccc agagctgggg gccacctcag aagtgtcatc 461
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<210> 54
<211> 547
<212> DNA
<213> Homo sapiens

<220>
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<222> 359..454
<223> Von Heijne matrix
score 4
seq FSPMLLGMMGGCLP/GF

<220>
<221> polyA_site
<222> 536..547

<400> 54
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cagctagcct ctcatccctt ttctactgag aggaagtgga atgcactccg acaaggataa 120

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gggttttattg tgagctgggcc ttggaattaa accaccacca acacactttt ggattatcag 180
aaggtggaag gagtgcacaaa atgtcattcc catgcttgctc tgccaggcaa cctgggtgcc 240
attctttatg acgcctttcc tgaatcacag gtgcattggg gtgcttctcc ctccccagga 300
ctccccacca actttgtgaa cacaaaccac ttagaggagt tatctcagca cattatga 358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct 406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
-30 -25 -20

ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct 454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
-15 -10 -5

gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc 502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1 5 10 15

acc ttt gcc cat taaagtcaat tctccacca taaaaaaaaaaa aaa 547
Thr Phe Ala His
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<210> 55
<211> 1198
<212> DNA
<213> Homo sapiens

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<223> Von Heijne matrix
score 4
seq RLPLVVSFIASSS/AN

<220>
<221> polyA_signal
<222> 1164..1169

<220>
<221> polyA_site
<222> 1187..1198

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Met Ala Asp Asp Leu Lys Arg Phe Leu
-95 -90

tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca 100
Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
-85 -80 -75

gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca 148
Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
-70 -65 -60

gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca 196
Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
-55 -50 -45

gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt 244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
-40 -35 -30 -25

tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg 292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
-20 -15 -10

gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc 340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
-5 1 5

cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg 388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val

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10	15	20	
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Glu Val Ser			
25			
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caagaaaaggg	cccccttttc	caacttatac	taaagagcta gcataatagat gtaatttata 557
gatagatcag	ttgctatatt	ttctgggtga	gggtctttct tatttagtga gatctaggga 617
taccacagaa	atgggttcagt	ctatcacagc	tcccatggag ttagtctggg caccagatat 677
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<210> 56
 <211> 1400
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 36..107
 <223> Von Heijne matrix
 score 5.69999980926514
 seq ILGLLGLGLTVA/ML

<220>
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 <222> 1302..1307

<220>
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 <222> 1389..1400

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			Met Ala Ser Leu Gly Leu
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Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr Leu			
			-15 -10 -5
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Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly Ala			
			1 5 10
agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa tgt 197			
Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu Cys			
			15 20 25 30
gcc aca cag aca ggc atc acc cag tgt gat ctc tat agc acc ctt 245			
Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu			
			35 40 45
ctg ggc ctg ccc gct gac atc cag gct gcc cag gcc atg atg gtg aca 293			
Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr			
			50 55 60
tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc atg 341			
Ser Ser Ala Ile Ser Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met			
			65 70 75
aga tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg gcg 389			

Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	
80						85					90					
gta	gca	ggt	gga	gtc	ttt	ttc	atc	ctt	gga	ggc	ctc	ctg	gga	ttc	att	437
Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	
95					100					105				110		
cct	gtt	gcc	tgg	aat	ctt	cat	ggg	atc	cta	cgg	gac	ttc	tac	tca	cca	485
Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro	
				115					120					125		
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Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	Leu	
				130				135					140			
ggc	att	att	tct	tcc	ctg	ttc	tcc	ctg	ata	gct	gga	atc	atc	ctc	tgc	581
Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	Leu	Cys	
				145			150					155				
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Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	Asp	Ala	Tyr	
				160		165					170					
caa	gcc	caa	cct	ctt	gcc	aca	agg	agc	tct	cca	agg	cct	ggt	caa	cct	677
Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	Pro	Gly	Gln	Pro	
				175		180				185				190		
ccc	aaa	gtc	aag	agt	gag	ttc	aat	tcc	tac	agc	ctg	aca	ggg	tat	gtg	725
Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser	Leu	Thr	Gly	Tyr	Val	
				195				200				205				
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<210> 57
 <211> 538
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 35..130
 <223> Von Heijne matrix
 score 8
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<220>
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 <222> 505..510

<220>
 <221> polyA_site
 <222> 526..538

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 cgt gct ttt cgc aag aac aag act ctc gcc tat gga gtc ccc atg ttg 103

09978350.101501

Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
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 ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc 151
 Leu Leu Ile Ala Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
 -5 1 5
 cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa 199
 Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
 10 15 20
 ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc 247
 Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
 25 30 35
 tgt tgaagggtcta ctatctttcc ttggcccttc tcccttggtg ggactcaatc 300
 Cys
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 caaagactcc aagtttgatg actggaagaa tattcgagga ccagggcctt gggaagatcc 420
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<210> 58
 <211> 1167
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 169..267
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LTFLFLHLPSTS/LF

<220>
 <221> polyA_signal
 <222> 1132..1137

<220>
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 <222> 1155..1167

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 gaaatttgaa gaccagatca tgggtggctt gcattgtgaat gaacagga atg agc cag 177
 Met Ser Gln
 aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct 225
 Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser
 -30 -25 -20 -15
 gcc ctt aca ttt ttg ttt ttc cat cta cca tcc acc agt cta ttt 273
 Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe
 -10 -5 1
 att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg 321
 Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu
 5 10 15
 ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc 369
 Leu Leu Ser Phe Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser
 20 25 30
 tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa 417
 Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys
 35 40 45 50
 aga aaa aca aaa tgc taatgaagcc atcagtcgaag ggtcacatgc caataaacaa 472
 Arg Lys Thr Lys Cys

55
 taaattttcc agaagaaatg aaatccaact agacaaataa agtagagctt atgaaatggt 532
 tcagtaagga tgagcttggt gttttttggt ttgtttttgt ttgttttttt aaagacggag 592
 tctcgctctg tcactcaggc tggagtgagc tggatgatgc ttggctcact gtaacctccg 652
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 gaagaatatg agtcagttat tgccagcctt ggaatttact tctctagctt acaatggacc 1072
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<210> 59
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 <212> DNA
 <213> Homo sapiens

<220>
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 seq VPMLLLIVGGSFG/LR

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 <222> 697..702

<220>
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 <222> 721..730

<220>
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 <222> 1,14,28,52
 <223> n=a, g, c or t

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 gagccgatgg aagagttcac tc atg ttt gca ccc gcg gtg acg cgt gct ttt 172
 Met Phe Ala Pro Ala Val Thr Arg Ala Phe
 -30 -25
 cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att 220
 Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile
 -20 -15 -10
 gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat 268
 Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp
 -5 1 5 10
 gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag 316
 Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu
 15 20 25
 aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag 364
 Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys
 30 35 40
 ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct 412
 Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro
 45 50 55
 gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act 460

Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 60 65 70
 tgactctgct gattctcttt tctttttttt ttttaataaa aaatactatt aactggactt 520
 cctaataat acttctatca agtggaaaagg aaattccagg cccatggaaa cttgggatag 580
 ggtaatttga tgacaaataa tcttcaactaa aggtcatgta cagggtttta tacttcccag 640
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<210> 60
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 108..170
 <223> Von Heijne matrix
 score 5.5
 seq SFLPSALVIWTS/AF

<220>
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<220>
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 <222> 1161..1174

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 Met Trp Trp
 -20
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 Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
 -15 -10 -5
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 Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
 1 5 10
 ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca 260
 Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
 15 20 25 30
 gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc 308
 Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Val Leu Cys
 35 40 45
 att gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct 356
 Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro
 50 55 60
 gaa gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga 404
 Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly
 65 70 75
 ata ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag aaa aca 452
 Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Lys Thr
 80 85 90
 acc ctt ttt gct gca cat gta agt gga gct gtg ctt acc ttt ggt atg 500
 Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr Phe Gly Met
 95 100 105 110
 ggc tca tta tat atg ttt gtt cag acc atc ctt tcc tac caa atg cag 548
 Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln
 115 120 125
 ccc aaa atc cat ggc aaa caa gtc ttc tgg atc aga ctg ttg ttg gtt 596

Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val	
130 135 140	
atc tgg tgt gga gta agt gca ctt agc atg ctg act tgc tca tca gtt	644
Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val	
145 150 155	
ttg cac agt ggc aat ttt ggg act gat tta gaa cag aaa ctg cat tgg	692
Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp	
160 165 170	
aac ccc gag gac aaa ggt tat gcg ctt cac atg atc act act gca gca	740
Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr Thr Ala Ala	
175 180 185 190	
gaa tgg tct atg tca ttt tcc ttc ttt ggt ttt ttc ctg act tac att	788
Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile	
195 200 205	
cgt gat ttt cag aaa att tcc tta cgg gtg gaa gcc aac tta cat gga	836
Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn Leu His Gly	
210 215 220	
tta acc ctg tat gac act gca cct tgc cct att aac aat gaa cga aca	884
Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn Glu Arg Thr	
225 230 235	
cgg cta ctt tcc aga gat att aga tgaagaggata aaatatttct gtaatgatta	938
Arg Leu Leu Ser Arg Asp Ile Arg	
240 245	
tgattctcag ggattgggga aagggttcaca gaagttgctt attcttctct gaaattttca	998
accacttaat caaggctgac agtaacactg atgaatgctg ataatcagga aacatgaaag	1058
aagccatttg atagattatt ctaaaggata tcataagaa gactattaaa aacacctatg	1118
cctatacttt tttatctcag aaaataaagt caaaagacta tgaaaaaa aaaaaa	1174

<210> 61
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 1133..1138

<220>
 <221> polyA_site
 <222> 1146..1158

<220>
 <221> misc_feature
 <222> 652
 <223> n=a, g, c or t

<400> 61	
aarttgagct tggggactgc agctgtgggg agatttcagt gcaattgcctc cccctgggtgc	60
tcttcatctt ggatttgaaa gttgagagca gcattgtttt gccactgaaa ctcatcctgs	120
tgrsagtgtg mtgattatt ccttgggctt gaatgacttg aatgtttccc cgccctgagct	180
aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca	232
Met Gly Cys Val Phe Gln Ser Thr	
1 5	
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag	280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu	
10 15 20	
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctg agt gtg	328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Ser Asn Leu Ser Val	
25 30 35 40	
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta	376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu	

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      45              50              55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
      60              65              70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
      75              80              85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
      90              95              100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag      572
Gln Met Leu Thr
      105
gcaaggaac tgattatctt gagtaaatgc cagcctttgg gctaagtact taccacagag      632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat      692
tttagttaak aataaaaatg tgataattat tgtattatta ctttaaacac acttccccct      752
cacaaaagcc ctgtgaagga tgttttgttc acatataatg tccaaatag ttttggacac      812
atattttata aatggaataa atagtamttg aacccttgga ccthtgacaa caaagtcyat      872
gttyttttta ctatgcccta atacccttsa tcagttatcc acattgatgc tacatytgta      932
ttttataggt accctatggt aggtgttttg ggggatagaa aagaaataag cagkycaggc      992
tcagtgccctc atgcctgtaa tcctagcatt ttggggaggct gagggcagcag aamtgcctga      1052
gccccagggg tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwgga      1112
cagagcaaga ctytgtttaa aataaaaaaa gagaaaaaaa aaaaaa      1158

<210> 62
<211> 754
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 5..142
<223> Von Heijne matrix
      score 6.59999990463257
      seq VCCYLFWLIIAIIA/QL

<220>
<221> polyA_signal
<222> 716..721

<220>
<221> polyA_site
<222> 742..754

<400> 62
tgtg atg agc gtg ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc      49
Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
      -45              -40              -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
      -30              -25              -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa      145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
      -15              -10              -5              1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat      193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
      5              10              15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgtcta      241
Leu Lys Tyr His Trp Pro
      20
gtcttttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc      301

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gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt      595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg
      125      130      135
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag      643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys
      140      145      150
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg      691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met
      155      160      165      170
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca      739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr
      175      180
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg      787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu
      190      195      200
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac      835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr
      205      210      215
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag      890
Met Pro Lys Arg Val
      220
aaggattctg catttctatt cccctcagcc tacccactga agtctttggg tagctcttaa      950
gccataacta aggagcagca tttagtaga tttctgaaaa acgattgtat ttgttgatt
aaaaagaaaa ctgtattttt attaaataaa atttaaacaat cacttcagga aaaaaaaaaa      1010
aaa                                                    1070
                                                    1073

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<210> 64

<211> 413

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 46..189

<223> Von Heijne matrix

score 4.09999990463257

seq VFMLIVSVLALIP/ET

<220>

<221> polyA_signal

<222> 377..382

<220>

<221> polyA_site

<222> 402..413

<400> 64

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tgagaagagt tgagggaag tgctgctgct gggctctgcag acgcg atg gat aac gtg      57
Met Asp Asn Val
      -45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
      -40      -35      -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
      -25      -20      -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
      -10      -5      1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys

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5          10          15          20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc 297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
          25          30          35
ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg 342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
          40          45          50
taattttata ttacttttta gtttgatact aagtattaaa catattctgt tattctttcca 402
aaaaaaaaaa a 413

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<210> 65
<211> 609
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 139..231
<223> Von Heijne matrix
score 4.40000009536743
seq TCCHLGLPHPVRA/PR

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<220>
<221> polyA_signal
<222> 579..584

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<220>
<221> polyA_site
<222> 598..609

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<400> 65
tgctggagtt ggaaggagac gcttggtttc cccccaagcg aaccgggatg ggaagtgact 60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagtccgc ttgccagcag 120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt 171
          Met Ser Asn Thr His Thr Val Leu Val Ser Leu
          -30          -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac 219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20          -15          -10          -5
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct 267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro
          1          5          10
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc 315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe
          15          20          25
cta aat gag ccg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg 363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser
          30          35          40
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta 411
Ala Asp Arg Cys Asp Leu
          45          50
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca 471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttctgct 531
tcccacctcc ttccaataag gaaacgtctt tgggaaccaac tttatggaaat aaataagctg 591
agctgcaaaa aaaaaaaaaa 609

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<210> 66
<211> 522
<212> DNA
<213> Homo sapiens

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<220>
<221> polyA_site
<222> 512..522

<220>
<221> misc_feature
<222> 11
<223> n=a, g, c or t

<400> 66
ccaaactgcag ntctgaattt accgagcggga gaggagatgc acacggcaact cgagtgtgag      60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt      110
          Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys
          1          5          10
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat      158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His
          15          20          25
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa      206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu
          30          35          40          45
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa      254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys
          50          55          60
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta      302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu
          65          70          75
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag      350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu
          80          85          90
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt      398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val
          95          100          105
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca      446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser
          110          115          120          125
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act      494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr
          130          135          140
gtg acc agt gta tcc aca aaaaaaaaaa      522
Val Thr Ser Val Ser Thr
          145

<210> 67
<211> 1322
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..260
<223> Von Heijne matrix
      score 4.59999990463257
      seq VLVYLVTAERVWS/DD

<220>
<221> polyA_signal
<222> 1283..1288

<220>
<221> polyA_site
<222> 1309..1322

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03070360-101501

<400> 67
 ccgaaaacct tccccgcttc tggatatgaa attcaagctg ctgctgagct cctattgccg 60
 gctgctggga gccaggagag ccctgaggag tagtcaactca gtagcagctg acgctgggt 120
 ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag 170
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
 -45 -40 -35
 tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc 218
 Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
 -30 -25 -20 -15
 cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac 266
 Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
 -10 -5 1
 cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc 314
 His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
 5 10 15
 tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg 362
 Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
 20 25 30
 cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg 410
 Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
 35 40 45 50
 gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag 458
 Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
 55 60 65
 aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc 506
 Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
 70 75 80
 tgg tgg aca tat gtc tgc agc cta gtg ttc aag cgc agc gtg gac atc 554
 Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
 85 90 95
 gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct 602
 Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
 100 105 110
 cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc 650
 Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys
 115 120 125 130
 ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg 698
 Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val
 135 140 145
 gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac 746
 Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr
 150 155 160
 ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa 794
 Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln
 165 170 175
 gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa 842
 Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys
 180 185 190
 caa gac gac ctc ctt tgc ggt gac ctc atc ttt ctg ggc tca gac agt 890
 Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser
 195 200 205 210
 cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc 938
 His Pro Trp Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr
 215 220 225
 atc ttg tgaggggctg cctggactgg tctggcaggt tgggctgga tggggaggct 994
 Ile Leu
 ctgactctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag 1054
 gcaagagaga ggattcagac gctctgggag ccagttccta gtccctcaact ccagccact 1114
 gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg ttctcttttc 1174
 tagaatggaa atagtggagg ccaatgccca gggttggagg gaggaggcgc ttcatagaag 1234

aaacacacatg cgggcacactt catcgtgtgt ggcccactgt cagaacttaa taaaagtcaa 1294
ctcatttgcgt ggttaaaaaa aaaaaaaa 1322

<210> 68
<211> 1290
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 50..160
<223> Von Heijne matrix
score 4
seq PLSLDCGHSLCRA/CI

<220>
<221> polyA_site
<222> 1280..1290
<400> 68

gaggagagcc tcaggaggtta ggaccagaag aagccaggga agcagtgc atg gct tca 58
Met Ala Ser
-35
aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg 106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu
-30 -25 -20
gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc 154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys
-15 -10 -5
cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga 202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly
1 5 10
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat 250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His
15 20 25 30
cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag 298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu
35 40 45
gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat 346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Ser Cys Asp His
50 55 60
cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa gtc att 394
His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys Val Ile
65 70 75
tgc tgg ctt tgt gag cgg tct cag gag cac cgt ggt cac cac aca gtc 442
Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr Val
80 85 90
ctc acg gag gaa gta ttc aag gaa tgt cag gag aaa ctc cag gca gtc 490
Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu Gln Ala Val
95 100 105 110
ctc aag agg ctg aag aag gaa gag gag gaa gct gag aag ctg gaa gct 538
Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys Leu Glu Ala
115 120 125
gac atc aga gaa gag aaa act tcc tgg aag tat cag gta caa act gag 586
Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val Gln Thr Glu
130 135 140
aga caa agg ata caa aca gaa ttt gat cag ctt aga agc atc cta aat 634
Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser Ile Leu Asn
145 150 155
aat gag gag cag aga gag ctg caa aga ttg gaa gaa gaa gaa aag aag 682
Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu Lys Lys
160 165 170

00978350.101501

acg ctg gat aag ttt gca gag gct gag gat gag cta gtt cag cag aag 730
 Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val Gln Gln Lys
 175 180 185 190
 cag ttg gtg aga gag ctc atc tca gat gtg gag tgt cgg agt cag tgg 778
 Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg Ser Gln Trp
 195 200 205
 tca aca atg gag ctg ctg cag gac atg agt gga atc atg aaa tgg agt 826
 Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met Lys Trp Ser
 210 215 220
 gag atc tgg agg ctg aaa aag cca aaa atg gtt tcc aag aaa ctg aag 874
 Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys Lys Leu Lys
 225 230 235
 act gta ttc cat gct cca gat ctg agt agg atg ctg caa atg ttt aga 922
 Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln Met Phe Arg
 240 245 250
 gaa ctg aca gct gtc cgg tgc tac tgg gtg gat gtc aca ctg aat tca 970
 Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr Leu Asn Ser
 255 260 265 270
 gtc aac cta aat ttg aat ctt gtc ctt tca gaa gat cag aga caa gtg 1018
 Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln Arg Gln Val
 275 280 285
 ata tct gtg cca att tgg cct ttt cag tgt tat aat tat ggt gtc ttg 1066
 Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr Gly Val Leu
 290 295 300
 gga tcc caa tat ttc tcc tct ggg aaa cat tac tgg gaa gtg gac gtg 1114
 Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu Val Asp Val
 305 310 315
 tcc aag aaa act gcc tgg atc ctg ggg gta tac tgt aga aca tat tcc 1162
 Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg Thr Tyr Ser
 320 325 330
 cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt 1210
 Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu
 335 340 345 350
 tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag 1258
 Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln
 355 360 365
 aat aaa tgt aag tat ggt gcc aaaaaaaaaa a 1290
 Asn Lys Cys Lys Tyr Gly Ala
 370

<210> 69
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 score 8.60000038146973
 seq LLWLALACSPVHT/TL

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 accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt 112
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
 -15 -10

00978350.101501

gcc	ctg	gcc	tgc	agc	cct	gtt	cac	act	acc	ctg	tca	aag	tca	gat	gcc	160
Ala	Leu	Ala	Cys	Ser	Pro	Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	
				-5					1			5				
aaa	aaa	gcc	gcc	tca	aag	acg	ctg	ctg	gag	aag	agt	cag	ttt	tca	gat	208
Lys	Lys	Ala	Ala	Ser	Lys	Thr	Leu	Leu	Glu	Lys	Ser	Gln	Phe	Ser	Asp	
		10				15					20					
aag	ccg	gtg	caa	gac	cgg	ggg	ttg	gtg	gtg	acg	gac	ctc	aaa	gct	gag	256
Lys	Pro	Val	Gln	Asp	Arg	Gly	Leu	Val	Val	Thr	Asp	Leu	Lys	Ala	Glu	
	25				30				35							
agt	gtg	gtt	ctt	gag	cat	cgc	agc	tac	tgc	tcg	gca	aag	gcc	cgg	gac	304
Ser	Val	Val	Leu	Glu	His	Arg	Ser	Tyr	Cys	Ser	Ala	Lys	Ala	Arg	Asp	
	40			45					50							
aga	cac	ttt	gct	ggg	gat	gta	ctg	ggc	tat	gtc	act	cca	tgg	aac	agc	352
Arg	His	Phe	Ala	Gly	Asp	Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	
			60					65					70			
cat	ggc	tac	gat	gtc	acc	aag	gtc	ttt	ggg	agc	aag	ttc	aca	cag	atc	400
His	Gly	Tyr	Asp	Leu	Thr	Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	
	75						80					85				
tca	ccc	gtc	tgg	ctg	cag	ttg	aag	aga	cgt	ggc	cgt	gag	atg	ttt	gag	448
Ser	Pro	Val	Trp	Leu	Gln	Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	
	90					95						100				
gtc	acg	ggc	ctc	cac	gac	gtg	gac	caa	ggg	tgg	atg	cga	gct	gtc	agg	496
Val	Thr	Gly	Leu	His	Asp	Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	
	105				110						115					
aag	cat	gcc	aag	ggc	ctg	cac	ata	gtg	cct	cgg	ctc	ctg	ttt	gag	gac	544
Lys	His	Ala	Lys	Gly	Leu	His	Ile	Val	Pro	Arg	Leu	Phe	Thr	Glu	Ala	
	120			125				130					135			
tgg	act	tac	gat	gat	ttc	cgg	aac	gtc	tta	gac	agt	gag	gat	gag	ata	592
Trp	Thr	Tyr	Asp	Asp	Phe	Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	
			140					145				150				
gag	gag	ctg	agc	aag	acc	gtg	gtc	cag	gtg	gca	aag	aac	cag	cat	ttc	640
Glu	Glu	Leu	Ser	Lys	Thr	Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	
		155					160					165				
gat	ggc	ttc	gtg	gtg	gag	gtc	tgg	aac	cag	ctg	cta	agc	cag	aag	cgc	688
Asp	Gly	Phe	Val	Val	Glu	Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	
	170					175					180					
gtg	ggc	ctc	atc	cac	atg	ctc	acc	cac	ttg	gcc	gag	gcc	ctg	cac	cag	736
Val	Gly	Leu	Ile	His	Met	Leu	Thr	His	Leu	Ala	Glu	Ala	Leu	His	Gln	
	185				190						195					
gcc	cgg	ctg	ctg	gcc	ctc	ctg	gtc	atc	ccg	cct	gcc	atc	acc	ccc	ggg	784
Ala	Arg	Leu	Leu	Ala	Leu	Leu	Val	Ile	Pro	Pro	Ala	Ile	Thr	Pro	Gly	
	200			205					210					215		
acc	gac	cag	ctg	ggc	atg	ttc	acg	cac	aag	gag	ttt	gag	cag	ctg	gcc	832
Thr	Asp	Gln	Leu	Gly	Met	Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	
		220						225				230				
ccc	gtg	ctg	gat	ggg	ttc	agc	ctc	atg	acc	tac	gac	tac	tct	aca	gcg	880
Pro	Val	Leu	Asp	Gly	Phe	Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	
		235						240				245				
cat	cag	cct	ggc	cct	aat	gca	ccc	ctg	tcc	tgg	gtt	cga	gcc	tgc	gtc	928
His	Gln	Pro	Gly	Pro	Asn	Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	
		250			255						260					
cag	gtc	ctg	gac	cgc	aag	tcc	aag	tgg	cga	agc	aaa	atc	ctc	ctg	ggg	976
Gln	Val	Leu	Asp	Pro	Lys	Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	
	265				270					275						
ctc	aac	ttc	tat	ggg	atg	gac	tac	gcg	acc	tcc	aag	gat	gcc	cgt	gag	1024
Leu	Asn	Phe	Tyr	Gly	Met	Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	
	280				285					290				295		
cct	gtt	gtc	ggg	gcc	agg	tac	atc	cag	aca	ctg	aag	gac	cac	agg	ccc	1072
Pro	Val	Val	Gly	Ala	Arg	Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	
			300					305				310				
cgg	atg	gtg	tgg	gac	agc	cag	gcc	tca	gag	cac	ttc	ttc	gag	tac	aag	1120

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Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
      315      320      325
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc      1168
Lys Ser Arg Ser Gly Arg His Val Phe Tyr Pro Thr Leu Lys Ser
      330      335      340
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg gcc gtt ggg gtc tct      1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
      345      350      355
atc tgg gag ctg gcc cag gcc ctg gac tac ttc tac gac ctg ctc      1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
      360      365      370
taggtgggca ttgcggccctc cgcgggtggac gtgttccttt ctaagccatg gagtgagtga      1321
gcagggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa      1364

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<210> 70
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<220>
<221> polyA_site
<222> 1458..1470

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ctg ctc tcc ata ggg atg ctc atg ctg tca gcc aca caa gtc tac acc      107
Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr
      -10      -5      1
gtc ttg act gtc cag ctc ttt gca ttc tta aac cca ctg cct gta gaa      155
Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val Glu
      5      10      15      20
gca gac att tta gca tat aac ttt gaa aat gca tct cag aca ttt gat      203
Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp
      25      30      35
gac ctc cct gca aga ttt ggt tat aga ctt cca gct gaa ggt tta aag      251
Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu Lys
      40      45      50
ggt ttt tta att aac tca aaa cca gag aat gcc tgt gaa ccc ata gtg      299
Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile Val
      55      60      65
cct cca cca gta aaa gac aat tca tct gcc act ttc atc gtg tta att      347
Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu Ile
      70      75      80
aga aga ctt gat tgt aat ttt gat ata aag gtt tta aat gca cag aga      395
Arg Arg Leu Leu Ser Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln Arg
      85      90      95      100
gca gga tac aag gca gcc ata gtt cac aat gtt gat tct gat gac ctc      443
Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp Leu
      105      110      115

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att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att 491
 Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile
 120 125 130
 cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa 539
 Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu
 135 140 145
 ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt 587
 Phe Thr Tyr Glu Lys Gly His Leu Ile Leu Val Pro Glu Phe Ser
 150 155 160
 ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc 635
 Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile
 165 170 175 180
 tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat 683
 Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp
 185 190 195
 aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa 731
 Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Arg Lys Lys Lys
 200 205 210
 ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc 779
 Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala
 215 220 225
 att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc 827
 Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro
 230 235 240
 tgt tcc cat gct tat cat tgc aag tgt gta gac cct tgg cta act aaa 875
 Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys
 245 250 255 260
 acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa 923
 Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln
 265 270 275
 ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg 971
 Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val
 280 285 290
 aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag 1019
 Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln
 295 300 305
 tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa 1067
 Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu
 310 315 320
 tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat 1115
 Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp
 325 330 335 340
 goa gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct 1163
 Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro
 345 350 355
 aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag 1209
 Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
 360 365
 aagatgattg gtttatttcc ctttaaaatg attaggatata tactgtaatt tgattttttg 1269
 ctcccttaaa agattttctgt agaaataact tatttttttag tactctacag tttaatcaaa 1329
 ttactgaaac aggactttttg atctggtatt tatctgccaa gaatatatctt cattcactaa 1389
 ttaatagactg gtgctgtaac tcaagcatca attcagctct tcttttggaa tgaaagtata 1449
 gccaaaacaa aaaaaaaaaa a 1470

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Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys
                230                235                240
aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaa      982
Lys Leu Pro Asn Lys Ala
                245

<210> 72
<211> 455
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<213> Homo sapiens

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<222> 443..455

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Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala
1 5 10 15
gga acc tat ttg cct cag tcc tat ctg att cat gag cac atg gtt att      96
Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile
20 25 30
act gat cgc atc gaa aac att gat cac ctg ggt ttc ttt att tat cga      144
Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg
35 40 45
ctg tgt cat gac aag gaa act tac aaa ctg caa cgc aga gaa act att      192
Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile
50 55 60
aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat      240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His
65 70 75
ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca      289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
80 85 90
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg      349
cagtgattat tttttaaagt cttctttcat gtaagtagca aacagggtct tactatcttt      409
tcattctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa      455

<210> 73
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<212> DNA
<213> Homo sapiens

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score 3.5
seq GLVCAGLADMAPR/AE

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0978360-101501

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acccggctgc caacgatccc tcggcgcgcg atg tcg gcc gcc ggt gcc cga ggc      113
                               Met Ser Ala Ala Gly Ala Arg Gly
                               -60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg      161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55                               -50                               -45                               -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca      209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
                               -35                               -30                               -25
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga      257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
                               -20                               -15                               -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct      305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
                               -5                               1                               5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta      353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10                               15                               20                               25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg      401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
                               30                               35                               40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa      449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
                               45                               50                               55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct      500
Leu Lys Ala Lys Ala His Lys
60
agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaaagcta      560
actgtgtggt tagaaggcac tgtaactggt agctagtctt tgattcaata gaaaaatgca      620
gcaaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta      680
acatttttct accatttgct cgtaataaac cataacttgct cgtaaaaaaa aaaaaaaa      738

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<222> 619..624

<220>
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<222> 637..649

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                               Met Lys Gly Trp Gly Trp Leu Ala Leu

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ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10                                -5                                1                                5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa      210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
10                                15                                20
att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg      258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
25                                30                                35
atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt      306
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
40                                45                                50
ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa      359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
55                                60
aggaccttg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct      419
catttggaag aagctgcagg cttattcccc atgcacttgc ttcttggtg caaaccttaa      479
tactttgttt ctgctgtaga attgttagc aaacagggag tcctgatcag cacccttctc      539
cacatccaca tgactgggtt ttaatgtagc actgtggtat acatgcaaac atccgttcaa      599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa      649

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<211> 714
<212> DNA
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<220>
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seq ALLLGALLGTAWA/RR

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<222> 703..714

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Met Lys Gly Trp Gly Trp Leu
-20                                -15
gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc      101
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser
-10                                -5                                1
cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa      149
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu
5                                10                                15
tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct      197
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser
20                                25                                30                                35
ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat      245
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr
40                                45                                50
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac      293
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp
55                                60                                65
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag      341
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys
70                                75                                80
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac      389

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05978360.104501

Asn	Tyr	Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp		
85						90					95						
cta	caa	ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	437	
Leu	Gln	Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe		
100					105					110					115		
gcg	tgt	ggg	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	485	
Ala	Cys	Gly	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe		
				120					125					130			
ttt	tcc	cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	533	
Phe	Ser	Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg		
			135				140						145				
aca	gat	ctt	tgt	gac	cat	gcc	ctg	cac	ata	tcg	cat	gat	gag	cta		578	
Thr	Asp	Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu			
		150				155				160							
tga	acc	actg	gag	cag	ccca	cactg	gcttg	atgg	atcacc	ccc	agg	aggg	gaaa	atggtg	638		
gca	atg	ccctt	ttat	atatta	tg	ttttt	tact	gaa	attaact	gaaaa	aatat	gaa	acaaaa		698		
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	-25						-20										
tcc	acc	tac	ctg	aaa	atg	ttc	gca	gcc	agt	ctc	ctg	gcc	atg	tgc	gca	101	
Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala	Ser	Leu	Leu	Ala	Met	Cys	Ala		
	-15						-10						-5				
ggg	gca	gaa	gtg	gtg	cac	agg	tac	tac	cga	ccg	gac	ctg	aca	ata	cct	149	
Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr	Arg	Pro	Asp	Leu	Thr	Ile	Pro		
	1				5					10							
gaa	att	cca	cca	aag	cgt	gga	gaa	ctc	aaa	acg	gag	ctt	ttg	gga	ctg	197	
Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu	Lys	Thr	Glu	Leu	Leu	Gly	Leu		
	15				20					25				30			
aaa	gaa	aga	aaa	cac	aaa	cct	caa	gtt	tct	caa	cag	gag	gaa	ctt	aaa	245	
Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val	Ser	Gln	Gln	Glu	Glu	Leu	Lys		
				35				40						45			
ta	actatg	gcc	aaga	attctg	tga	ataatat	aagt	tcttaa	tatg	tatttc	ttaat	tttatt				305	
gca	tcaa	aact	act	gtgcctt	aag	cacttag	tcta	atgcta	actg	caagag	gaggt	gtccta				365	
gt	ggatg	ttt	agcc	gatacg	ttg	aaattta	attac	gggtt	gatt	gatatt	tcttg	aaaaac				425	
tg	ccaa	agca	catat	catca	aacc	atttca	tga	atattg	ttg	gaagatg	tttag	tcttg				485	
aa	tata	acgc	gaa	tga	aat	attgt	taagt	ctact	ata	tg	ggtt	gtctt	att	tcata		545	
aa	ta	agaaa	ttatt	taaaa	ctat	gaacta	gttt	cattaa	aaaa	aaaaa	aga	a				596	

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<210> 77
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> polyA_signal
<222> 375..380

<220>
<221> polyA_site
<222> 390..403

<400> 77
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agagcgcgag gactcggcggg ctgagcgcgcg ccgacagcag ctagaggcgc tgctcaacaa 120
gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt 169
Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
1 5 10 15
ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag 217
Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
20 25 30
ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg 265
Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
35 40 45
ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag 313
Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
50 55 60
agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc 363
Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
65 70
tttcagactt cattaaactt atgacacaaa aaaaaaaaaa 403

<210> 78
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..575
<223> Von Heijne matrix
score 8.60000038146973
seq LELLTSCSPASASQ

<220>
<221> polyA_signal
<222> 670..675

<220>
<221> polyA_site
<222> 721..727

<220>
<221> misc_feature
<222> 257,376..377
<223> n=a, g, c or t

<400> 78
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgtgttag 60
gaccgggggt aggggttttga gcccgtagga gctgccccac gcggcctcgt cctgccaacg 120

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gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag 170
 Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
 -150 -145 -140
 gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 218
 Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
 -135 -130 -125 -120
 gcc cag agg acc ctg tac cga gag gcc atc ggg ttc ccn aaa cca gag 266
 Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
 -115 -110 -105
 ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga 314
 Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
 -100 -95 -90
 ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc 362
 Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
 -85 -80 -75
 tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc 410
 Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
 -70 -65 -60
 gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac 458
 Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
 -55 -50 -45 -40
 agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag 506
 Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
 -35 -30 -25
 acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca 554
 Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
 -20 -15 -10
 tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg 602
 Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
 -5 1 5
 agc cac gct gcc cgg cag aga aaa act gct taaggttgaa aagagaaatt 652
 Ser His Arg Ala Arg Gln Arg Lys Thr Ala
 10 15
 taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga 712
 agcaaaaaaa aaaaa 727

 <210> 79
 <211> 944
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> sig_peptide
 <222> 90..155
 <223> Von Heijne matrix
 score 5.90000009536743
 seq IILGCLALFLLQ/RK

 <220>
 <221> polyA_signal
 <222> 913..918

 <220>
 <221> polyA_site
 <222> 932..944

 <400> 79
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 tctgcttctg gaaggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg 113
 Met Glu Leu Ile Ser Pro Thr Val
 -20 -15

09978260.101501


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att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag      161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
-10 -5 1
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga      209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
5 10 15
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca      257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala
20 25 30
aga atc aag gta tgt ggt gcc aga cgg ggt ctc cag agg aga caa      305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln
35 40 45 50
tgc ttt ctt ttt taaactttct ttcattgact cttaagtgaac gggctagaac      357
Cys Phe Leu Phe
acggggaaca taccgtcttg cctcaactaa aggatctagt catttctgaa ttcctctact      417
aacaattaac aacaatatcc tgtgcaaaat ttgcgaaag aaatgaaata caattgcagc      477
gtgcatgcac atttttgaaa gtagagatta acttttcgta tttttacttc atcgaaagtta      537
agttccaagt gtgtatgtgt taagtaaatg ttttcagtaa ttgggaaaga taaagtgtaa      597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta      657
ttgtacaagt tgcttgcaca gttggtccgt acacaataga caggctctgt atttttagct      717
gacgttgtta ttgatgatg atgtactcca ttttcactac gggccgaaga gactagtaat      777
cctccttgta gtatgtgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag      837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat      897
ggattttgat tgtctaataa atttgtatga tattaataaaa aaaaaaaa      944

<210> 80
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..287
<223> Von Heijne matrix
score 3.90000009536743
seq LETCGLVSLVES/IW

<220>
<221> polyA_signal
<222> 561..566

<220>
<221> polyA_site
<222> 587..598

<400> 80
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gaccgggggt aggtgttttga gcccgtagga gctgccccac gggcctctgt cctgccaaag      120
gtcgg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      170
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
-50 -45 -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-35 -30 -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      266
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
-20 -15 -10
ctg gtt tca cta gtg gaa agc att tgg ctg cat ata aca gaa aac cag      314
Leu Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln
-5 1 5
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      362

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Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
 10 15 20 25
 aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag 410
 Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Gln
 30 35 40
 tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg ctcttgattg 470
 tcttcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc 530
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 aaaaaaaa 598

<210> 81
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 85..150
 <223> Von Heijne matrix
 score 5.90000009536743
 seq IILGCLALFLLQ/RK

<220>
 <221> polyA_site
 <222> 349..360

<400> 81
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 ttctggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att 111
 Met Glu Leu Ile Ser Pro Thr Val Ile
 -20 -15
 ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat 159
 Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn
 -10 -5 1
 ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt 207
 Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val
 5 10 15
 gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga 255
 Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg
 20 25 30 35
 atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg 303
 Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met
 40 45 50
 acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc 348
 Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser
 55 60 65
 aaaaaaaaa aa 360

<210> 82
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 77..124
 <223> Von Heijne matrix
 score 4.80000019073486
 seq SLFIYIFLTCSNT/SP

<220>

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Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys
 75 80 85
 gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa 343
 Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln
 90 95 100
 gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga 394
 Glu Lys Leu Ser Phe Phe Arg
 105
 tgtctgagtc ctcaaggtga ctggggactt ggaaccccta ggacctgaac aaccaagact 454
 ttaataataa tttataatgc aaaaaaaaaa aaaa 488

 <210> 84
 <211> 771
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> sig_peptide
 <222> 48..356
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFGLTAPSGS/KE

 <220>
 <221> polyA_signal
 <222> 742..747

 <220>
 <221> polyA_site
 <222> 760..771

 <400> 84
 ccacagccct tttcaggacc caaacaacog cagccgctgt tcccagg atg gtg atc 56
 Met Val Ile
 cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa 104
 Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys
 -100 -95 -90 -85
 caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa 152
 Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu
 -80 -75 -70
 gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa 200
 Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu
 -65 -60 -55
 aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct 248
 Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro
 -50 -45 -40
 cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt 296
 Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe
 -35 -30 -25
 gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc 344
 Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala
 -20 -15 -10 -5
 cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca 389
 Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala
 1 5 10
 tgaacctga gcaactgtgct ttaagcatcc tgaataatga gtctccattg cttttataaa 449
 atagcagaat tagcttttgc tcaaaagaaa taggcttaat gttgaaataa tagattagtt 509
 ggggttttcc atgcaaacac tcaaaatgaa tacaaaaatta aaatttgtaac attatggtag 569
 ttatggtag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa 629
 atagtggtgt tacctgccaa gccatcctgt atacaccaat gattttacaa agaaaaaccc 689
 cttccctcct tctgccatta ctatggcaac ctaagtgtat ctgcagctct acattaaaaa 749

ggagaaagag aaaaaaaaaa aa

771

<210> 85
<211> 959
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 69..359
<223> Von Heijne matrix
score 4
seq RLPLVVSFIASSS/AN

<220>
<221> polyA_signal
<222> 927..932

<220>
<221> polyA_site
<222> 947..959

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<400> 85
cgagagagaac caggcagccc agaaacccca gccgtggaga ttgatcctgc gagagaaggg      60
ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca      110
           Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro
           -95                    -90                    -85
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta      158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val
           -80                    -75                    -70
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga      206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg
           -65                    -60                    -55
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa      254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys
           -50                    -45                    -40
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac      302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr
           -35                    -30                    -25                    -20
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc      350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala
           -15                    -10                    -5
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt      398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
           1                    5                    10
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct      440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
           15                    20                    25
taatctgaca gtgggtttcag tgtgtacctt atcttctatta taacaacaca atatcaatcc      500
agcaaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc      560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt      620
ttctgtgtga ggggtctttct tatttagtga gatctaggga taccacagaa atgggttcagt      680
ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga ttctattcag      740
tggatcagaa tcaaaactggt acattgatcc acttgagccg ttaagtgctg ccaattgtac      800
aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa taaggacata      860
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aaaaataata aaatcagtac aatcactaaa aaaaaaaaaa      959

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<210> 86
<211> 464
<212> DNA

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<213> Homo sapiens

<220>

<221> sig_peptide

<222> 33..98

<223> Von Heijne matrix

score 9.80000019073486

seq LVVFCLALQLVPG/SP

<220>

<221> polyA_signal

<222> 437..442

<220>

<221> polyA_site

<222> 455..464

<400> 86

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Met Lys Pro Val Leu Pro Leu

-20

cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt 101

Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser

-15 -10 -5 1

ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata 149

Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile

5 10 15

tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc 197

Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys

20 25 30

gag aaa gga ttt cag tgc tgt tcc ttc tgt ggg ata gtc tgt tca 245

Glu Lys Gly Phe Gln Cys Ser Ser Phe Cys Gly Ile Val Cys Ser

35 40 45

tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa 293

Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu

50 55 60 65

gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc 341

Val Ile Met Pro Ala Asn

70

tacgatgttt tttcttggtc cacctttagg aagggtattga gaagcaagaa actggaggcc 401

caatatctaa cctgcacaatc gtttttgagt ttggcaataa aggctaattc accaaaaaaa 461

aaa 464

<210> 87

<211> 799

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 110..235

<223> Von Heijne matrix

score 5.19999980926514

seq LLFDLVCHRFQCS/DD

<220>

<221> polyA_signal

<222> 764..769

<220>

<221> polyA_site

09978760.101501

<222> 787..799

<400> 87

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agctgccaaa caagtacgtt ctgaaaatcc agaattggctt gatgtttac atg cac att 118
Met His Ile
-40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat 166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His
-35 -30 -25
tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc 214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val
-20 -15 -10
tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa 262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu
-5 1 5
cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat 310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr
10 15 20 25
gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt 358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu
30 35 40
cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt 406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys
45 50 55
cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa 454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys
60 65 70
agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat 502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp
75 80 85
att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag 550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu
90 95 100 105
acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt 598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys
110 115 120
tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa 646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu
125 130 135
gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac 694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp
140 145 150
ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga 740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155 160 165
attggaatta cttctgtaca agaaataaac tttatttttc tcactgaaaa aaaaaaaaaa 799

<210> 88

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_site

<222> 308..320

<400> 88

tcacatcca gagcagccag tgtccgggag gcagaag atg ccc cac tcc aag cct 55
Met Pro His Ser Lys Pro
1 5

00978380.101501

ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt 103
 Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
 10 15 20
 cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta 151
 Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
 25 30 35
 aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc 199
 Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
 40 45 50
 ggt gtc ttc aac ctg tgaatggga tcataatcac tgccttacct cctcaccgt 254
 Gly Val Phe Asn Leu
 55
 tgtgtgagg actgagtggt tggaagtttt tcataaaactt tggatgctag tgtaaaaaaa 314
 aaaaaa 320

<210> 89
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 score 4.90000009536743
 seq CLLSYIALGAIHA/KI

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 caccctcagc ctgctcattt ccagctcaga aattctacta atggcggttt ttcttctcga 120
 aaaaggaat atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc 170
 Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
 -25 -20 -15
 tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt 218
 Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
 -10 -5 1
 agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg 266
 Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
 5 10 15
 aga gct tgg tgc ata cag cca tgg gcc aaa taaagtgttc ttggaatagc 316
 Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
 20 25
 caaaaaaaaa aaaaa 331

<210> 90
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 <212> DNA
 <213> Homo sapiens

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 seq IILTAVYFALSIS/LH

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<220>
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gagaaaacag aaggaag atg ctc cag acc agt aac tac agc ctg gtg ctc 110
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu
-80 -75 -70 -65 -60 -55 -50
tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc 158
Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe
-80 -75 -70 -65 -60 -55 -50
tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc 206
Ser Glu Leu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile
-65 -60 -55 -50
atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg 254
Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Phe Leu Met
-50 -45 -40
ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc 302
Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe
-35 -30 -25 -20
cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc 350
His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu
-15 -10 -5
agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc 398
Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser
1 5 10
aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag 446
Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln
15 20 25
aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta 494
Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val
30 35 40 45
aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag 542
Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys
50 55 60
gag ttc atg caa gtt cga agg tgacctcttg tcacactgat ggatactttt 593
Glu Phe Met Gln Val Arg Arg
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ccttctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcattgggca 653
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tccccctctt tgcacaatta gagggtcccc atcgggtctcc agtgccggcat ccttctcttg 773
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tgatagttac gtgctctcga ctgatcacac cgcagacatt tagattttta taccacaaggc 1013
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00975350.101501

score 4.59999990463257
seq LPFSLVSMVLVTQG/LV

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c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt 109
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
-65 -60 -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg 157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
-50 -45 -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa 205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
-35 -30 -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt 253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20 -15 -10 -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga 301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
1 5 10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc 349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
15 20 25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt 397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
30 35 40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg 445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
45 50 55 60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt 493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
65 70 75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact 543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
80 85
ttcgaagttt tttaaacctt tgaatttgta cacattttaa atttcaagtg tacttttaaaa 603
taaaatactt ctaagtgtaaa aaaaaaaaaa 632

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<220>
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00073360 101511

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ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata 101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile
15      20      25
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt 149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser
30      35      40
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat 197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp
45      50      55
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt 245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe
60      65      70
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa 293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln
75      80      85      90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcgaatgac 340
Gly Arg His Thr Lys Leu Gly Asn
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ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaacaatt gtaatttttg 400
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score 3.70000004768372
seq ILFNLLIFLCGFT/NY

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<222> 172..185

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Met Gln Cys Phe Ser
-20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt 104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
-15 -10 -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg 152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
1 5 10
cat aaa cct gtt aca atg taaaaaaaa aaaaa 185
His Lys Pro Val Thr Met
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<223> Von Heijne matrix
score 5.5
seq SFLPSALVIWNTSA/AF

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<221> polyA_site
<222> 574..585

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tgaagactaa cattttgtga agttgtataaa cagaaaaacct gttagaa atg tgg tgg 116
Met Trp Trp
-20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca 164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ser Thr Ala Leu Val Ile Trp Thr
-15 -10 -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat 212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
1 5 10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca 260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15 20 25 30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt 308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
35 40 45
caa aaa tagaatacag gaagataatt caacttaaag aagttcattt catgaccaaa 364
Gln Lys
ctcttcagaa acatgtctttt acaagcatat ctcttgattt gctttctaca ctgttgaaat 424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg 484
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa 544
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seq ALALLWSLPASDL/GR

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<222> 602..613

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atg agc ccc gcc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct 165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser

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-15          -10          -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
      1          5          10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
      15          20          25          30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt      309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
      35          40          45
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca      351
Val Thr Val Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50          55          60
tgagtgcgatg ggtcagaact ttagtatacgc catgcgcctct ctgagtgcaca gggcattttg      411
tcgaaaaataa gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt      471
attgattaag ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt      531
agaacatagc aagggggctc ctctgttggg gtaatgtaaa ttgtaattat aaataaacat      591
gcaaaccttt aaaaaaaaaa aa      613

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<212> DNA
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<223> Von Heijne matrix
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      seq SALLFFARPCVFC/FK

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<222> 410..415

<220>
<221> polyA_site
<222> 424..427

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caaacctggc taataaaactt gaagaaatta aaaaggactt ggatgccaaag aagaaacccc      120
ctagtgcg atg aga ctg cct cca gca ctg cct tca gga tat act gat tct      169
      Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser
      -45          -40          -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt      217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe
      -30          -25          -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt      265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe
      -15          -10          -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca      313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr
      1          5          10          15
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg      361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly
      20          25          30
agg ttc taagactgga attatgggtc tagattagta aacatgactt ttaatgaaaa      417
Arg Phe
aaaaacaaaaa      427

<210> 97

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 tgggtgtcaa caataaacgg cttgggtgt atg tgg ctg gat cct gtt ttc cct 172
 Met Trp Leu Asp Pro Val Phe Pro
 -100
 ctc ttt cot gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg 220
 Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
 -95 -90 -85 -80
 ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa 268
 Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
 -75 -70 -65
 gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc 316
 Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
 -60 -55 -50
 acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga 364
 Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
 -45 -40 -35
 atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa 412
 Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln
 -30 -25 -20
 gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca 460
 Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
 -15 -10 -5 1
 cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc 508
 Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
 5 10 15
 atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg 556
 Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
 20 25 30
 gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga 604
 Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
 35 40 45
 tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc 652
 Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
 50 55 60 65
 ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc 700
 Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
 70 75 80
 tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg 748
 Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
 85 90 95
 cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt 796
 Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
 100 105 110
 cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat 844

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Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp
115 120 125
aac cac aag aag ctt cca aat aaa gcc tgaggtcttc ttgcggtagt 891
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130 135
caaaaaaaaa aaaa 905

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cta aca gaa aag ctg agg aaa ttc cgc ttc cga aaa gag aca gac aat 97
Leu Thr Glu Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn
15 20 25
gca gcc atc ata atg aag gtg gac aaa gac cgg cag atg gtg gtg ctg 145
Ala Ala Ile Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu
30 35 40 45
gag gaa gaa ttt cgg aac att tcc cca gag gag ctc aaa atg gag ttg 193
Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu Leu Lys Met Glu Leu
50 55 60
ccg gag aga cag ccc agg ttc gtg gtt tac agc tac aag tac gtg cgt 241
Pro Glu Arg Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg
65 70 75
gac gat ggc cga gtg tcc tac cct ttg tgt ttc atc ttc tcc agc cct 289
Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro
80 85 90
gtg ggc tgc aag cgg gaa caa cag atg atg tat gca ggg agt aaa aac 337
Val Gly Cys Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn
95 100 105
agg ctg gtg cag aca gca gag ctc aca aag gtg ttc gaa atc cgc acc 385
Arg Leu Val Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr
110 115 120 125
act gat gac ctc act gag gcc tgg ctc caa gaa aag ttg tct ttc ttt 433
Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe
130 135 140
cgt tga tctctgggct ggggactgaa ttctgatgt ctgagtcctc aaggtgactg 489
Arg

gggacttgga acccctagga cctgaacaac caagacttta aataaaatttt aaatgcaaa 549
aaaaaaaaa a

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<213> Homo sapiens

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<222> 7..471

<221> sig_peptide

<222> 7..99

<223> Von Heijne matrix

score 6.9

seq LLLVPSALSLLLA/LL

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<222> 537..542

<221> polyA_site

<222> 554..568

<400> 99

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Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro

-30

-25

-20

ctg tcg aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc 96

Leu Ser Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu

-15

-10

-5

gcc ctc ctc ctg cct cac tgc cag aag ccc ttt gtg tat gac ctt cac 144

Ala Leu Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His

1

5

10

15

gca gtc aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata 192

Ala Val Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile

20

25

30

att tgc ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat 240

Ile Cys Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr

35

40

45

aat ttt agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc 288

Asn Phe Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser

50

55

60

ttt ttg ctg ggt acc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc 336

Phe Leu Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu

65

70

75

att gaa gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg 384

Ile Glu Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu

80

85

90

95

cct tct gga tta atc ttt tgt tgt gct ttt tgc tct gag act aaa ctc 432

Pro Ser Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu

100

105

110

ttc tta tca aga caa gct atg gca gag aac ttt tcc atc taataaaattt 481

Phe Leu Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile

115

120

aagagtagat tcatctgtat gggttgagagt aggctctgac tatgtatatg tgtataataa 541

acctacatat ccaaaaaaaaa aaaaaaa 568

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gatacggcgc ccagcggggt cagaaagcaa cattgaatgc agaagaa atg gcg gac 176
                                     Met Ala Asp
                                     1
ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cgc atg tat tat 224
Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg Met Tyr Tyr
5 10 15
aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg gga 272
Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly
20 25 30 35
aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa aag 320
Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys
40 45 50
aag agg agc aac taggagtcca ctctgaccga gccagagtcc aggtttccac 372
Lys Arg Ser Asn
55
aggaagcaga tggagctcct ttcacagggt ctctgagaaa aactggagcc gatctcaaga 432
agccccacat cttcctaagg ggcgccatgg cctgtttggg ggcagggtag gtcctggggc 492
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Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile
-15 -10 -5
ggc gcc gcc ttc tat ccc atc tac ttc cgg ccc cta atg aga ttg gag 152
Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg Leu Glu
1 5 10
gag tac aag aag gaa caa gct ata aat cgg gct gga att gtt caa gag 200
Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val Gln Glu
15 20 25 30
gat gtg cag cca cca ggg tta aaa gtg tgg tct gat cca ttt ggc agg 248

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Lys																	
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ctctgtaata	ccataaataa	gagtgcttgt	aataaaagac	tgtgcacaag	gattaatatt											421	
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		-20						-15									

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Leu	Ala	Met	Val	Thr	Arg	Pro	Ala	Ser	Ala	Ala	Pro	Met	Gly	Gly	Pro		
-10					-5				1				5				

gaa	ctg	gca	cag	cat	gag	gag	ctg	acc	ctg	ctc	ttc	cat	ggg	acc	ctg		148
Glu	Leu	Ala	Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu		
10					15				20								

cag	ctg	ggc	cag	gcc	ctc	aac	ggg	gtg	tac	agg	acc	acg	gag	gga	tgg		196
Gln	Leu	Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Trp		
25					30				35								

ctg	aca	aag	gcc	agg	aac	agc	ctg	ggg	ctc	tat	ggc	cgc	aca	ata	gaa		244
Leu	Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu		
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Leu	Leu	Gly	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu	Leu			
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Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu	Gln	Leu		
				75				80					85				

cag	gca	gag	gcc	aca	gct	gag	gtg	ctg	ggg	gag	gtg	gcc	cag	gca	cag		388
Gln	Ala	Glu	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala	Gln	Ala	Gln		
90					95				100								

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Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Glu	Val	Gln	Leu	Arg	Ser		
105					110				115								

gcc	tgg	ctg	ggc	cct	gcc	tac	cga	gaa	ttt	gag	gtc	tta	aag	gct	cac		484
Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Glu	Phe	Glu	Val	Leu	Lys	Ala	His		
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cgg cag agg cgg gag atg gtg gca cag cag cat cgg ctg cga cag atc      580
Arg Gln Arg Arg Glu Met Val Ala Gln Gln His Arg Leu Arg Gln Ile
      155      160      165
cag gag aga ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac      633
Gln Glu Arg Leu His Thr Ala Ala Leu Pro Ala
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gtt gtt atg gtc cct tta gtt ggg ctc ata cat ttg ggg tgg tac aga      98
Val Val Met Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg
      -10      -5      1
atc aaa agc agc cct gtt ttc caa ata cct aaa aac gac gac att cct      146
Ile Lys Ser Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro
5      10      15      20
gag caa gat agt ctg gga ctt tca aat ctt cag aag agc caa atc cag      194
Glu Gln Asp Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln
      25      30      35
ggg aag nta gca ggc ttg caa tct tca ggt aaa gaa gca gct ttg aat      242
Gly Lys Xaa Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn
      40      45      50
ctg agc ttc ata tcg aaa gaa gag atg aaa aat acc agt tgg att aga      290
Leu Ser Phe Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg
      55      60      65
aag aac tgg ctt ctt gta gct ggg ata tct ttc ata ggt gac cat ctt      338
Lys Asn Trp Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu
      70      75      80
gga aca tac ttt ttg cag agg tct gca aag cag tct gta aaa ttt cag      386
Gly Thr Tyr Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln
85      90      95      100
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tcgtcgtgt	ggctggattg	ccgagggaa	aagcagatgc	tcctctatgaa	gcctctgaaga										240
atcttacacc	atatgtggct	attgaggaca	aagac atg	cag caa aaa gaa	cag										293
			Met	Gln	Gln	Lys	Glu	Gln							
			-70												
cag ttt agg gag	tgg ttt ttg aaa	gag ttt cct	caa atc aga	tgg aag											341
Gln Phe Arg Glu	Trp Phe Leu Lys	Glu Phe Pro	Gln Ile Arg	Trp Lys											
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att cag gag tcc	ata gaa agg ctt	cgt gtc att	gca aat gag	att gaa											389
Ile Gln Glu Ser	Ile Glu Arg Leu	Arg Val Ile	Ala Asn Glu	Ile Glu											
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aag tgc cac aga	ggc tgc gtc	atc gcc aat	gtg tct ggc	tcc act											437
Lys Val His Arg	Gly Cys Val Ile	Ala Asn Val	Val Ser Gly	Ser Thr											
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Gly Ile Leu Ser	Val Ile Gly	Val Met Leu	Ala Pro Phe	Thr Ala Gly											
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Leu Ser Leu Ser	Ile Thr Ala	Gly Val Gly	Lys Gly Ile	Ala Ser											
1	5	10	15												
gcc acg gct ggg	atc gcc tcc	agc atc gtg	gag aac	aca tac	aca agg										581
Ala Thr Ala Gly	Ile Ala Ser	Ile Val Glu	Asn Thr Tyr	Thr Arg											
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Leu Glu Ala Thr	Arg Asp Ile	Lys Glu Asp	Ile Thr Pro	Asn Val	Leu										
	50	55	60												
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Ser Phe Ala Leu	Asp Phe Asp	Glu Ala Thr	Lys Met Ile	Ala Asn	Asp										
	65	70	75	80											
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Val His Thr Leu	Arg Arg Ser	Lys Ala Thr	Val Gly Arg	Pro Leu	Ile										
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Ala Trp Arg Tyr	Pro Ile Asn	Val Val Glu	Lys Thr Leu	Arg Thr	Arg										
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Asp	Ser	Leu	Asp	Leu	His	Lys	Gly	Glu	Lys	Ser	Glu	Ser	Ala	Glu	Leu	
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Leu	Arg	Gln	Trp	Ala	Gln	Glu	Leu	Glu	Glu	Asn	Leu	Asn	Glu	Leu	Thr	
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His	Ile	His	Gln	Ser	Leu	Lys	Ala	Gly								
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gga ggc tct gtg att tca atg att gtg ctt tta atc tgt gtt gtt tgt 568
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 -20 -15 -10

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 His
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 Met Cys Ile Ser Gly Leu Cys Gln Ile
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 Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys
 10 15 20 25

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 Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln
 30 35 40

tat aaa tcc cag ctc tcc gca acc aaa tgc gat gat act gtg gtt gca 376
 Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala
 45 50 55

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 Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp
 60 65 70

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 His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn
 75 80 85

agt ctc agc tcc aca gga act ttc ctt gtg gac aat tct agt gtg gac 520
 Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp
 90 95 100 105

ttc cag aaa ttt cca gag aaa gag ata ctg aga atg gct gga cca ctc 568
 Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu
 110 115 120

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 Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser
 125 130 135
 aca gtc cag ttc atc ttc tat caa ccc atc atc cac cga tgg agg gag 664
 Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu
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 Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Tyr Gln Leu
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 Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
 1 5 10 15
 acc ctt ccc gcc gcc cag aag gag tgc ttc tac cag ccc atg ccc ctg 197
 Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
 20 25 30
 aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta 245
 Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
 35 40 45
 gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt 293
 Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
 50 55 60
 gaa caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt 341
 Glu Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Glu
 65 70 75
 gat tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag 389
 Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
 80 85 90 95
 gtg att ttc ttt gaa tta atc ccg gat aat atg gga gaa cag gca caa 437
 Val Ile Phe Phe Glu Leu Ile Pro Asp Asn Met Gly Glu Gln Ala Gln

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          100          105          110
gaa caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat      485
Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp
          115          120          125
atg aaa ctg gaa gac atc ctg gtc agt atg gtc ttc taataaaata      531
Met Lys Leu Glu Asp Ile Leu Val Ser Met Val Phe
          130          135
aaaattatttta acagccaaaa aaaaaaaaaa      561

<210> 108
<211> 632
<212> DNA
<213> Homo sapiens

<220>
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<222> 36..395

<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
      score 7.4
      seq VLLLAALPVLPP/GA

<221> polyA_signal
<222> 599..604

<221> polyA_site
<222> 619..632

<400> 108
gacgcctctt tcagcccgagg atcgcccccag caggg atg ggc gac aag atc tgg      53
                               Met Gly Asp Lys Ile Trp
                               -20
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg      101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu
          -15          -10          -5
cct ggg gcg gcc gcc ttc aca cct tcc ctg gat agc gac ttc acc ttt      149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
          1          5          10          15
acc ctt ccc gcc gcc cag aag gag tgc ttc tac cag ccc atg ccc ctg      197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
          20          25          30
aag gcc tgg ctg gag atc gag tac caa gtt tta gat gga gca gga tta      245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
          35          40          45
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt      293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
          50          55          60
gaa caa aga aaa tca gat gga gtt cac acg tgt ata aga agt aaa aat      341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Cys Ile Arg Ser Lys Asn
          65          70          75
ggg cca ggc act gcg gtt cac gcc tat aat ccc agc act ttc cga ggc      389
Gly Pro Gly Thr Ala Val His Ala Tyr Asn Pro Ser Thr Phe Arg Gly
          80          85          90          95
caa gtg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc      445
Gln Val
accatttctg agaaggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca      505
caaggacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg      565
gaagacatcc tgggtcagtat ggtcttcttaa taaaataaaa attattaaca gccaaaaaaa      625
aaaaaaaaa
      632

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0976030

<221> CDS

<222> 21. .41

<221> polyA signal

<222> 328..333

<221> polyA site

<222> 357. .370

<400> 109

ctgggacttc	tggcctcaca	atg gtt gag	atg act ggg	gtg tagcagtgc	51	
		Met Val Glu	Met Thr Gly	Val		
			5			
aagtcgaggc	tgtgaaagcc	cttccacctt	tactctcgtg	ctcgtgcctt	ccccattgt	111
taggagaagg	gcatgctcag	gccagcccat	tagcccagga	ggagagacaag	aaacacacgg	171
agcagacaga	agccacactca	caaccccga	caaggctctg	ctgaattagg	aacactgtaca	231
ctgttgagca	agttccaacgg	ccctccgaag	cttaaccttag	ctaacgccca	caacagatcg	291
caagactgcc	aagctgcacca	cttaaggcgc	atgaggaata	aacactctgt	gctgcatgcc	351
attgcaaaaa	aaaaaaaaa					370

 $\langle 210 \rangle$ 110

<211> 994

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 35.,.631

<221> sig peptide

<222> 35..160

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<223> Von Heijne matrix
      score 8.6
      seq ASLFLLLSLTVFS/IV
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<221> polyA signal

<222> 901..906

<221> polyA site

<222> 979, 994

 $\langle 400 \rangle$ 110

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				Met	Asp	Gly	Gln	Lys	Lys	Asn						
						-40										
trp	aag	gac	aag	gtt	gtt	gac	ctc	ctg	tac	tgg	aga	gac	att	aag	aag	103
Tyr	Lys	Asp	Lys	Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	
-35						-30				-25					-20	
act	gga	gtg	gtg	ttt	ggg	gcc	agc	cta	ttc	ctg	ctg	ctt	tca	ttg	aca	151
Thr	Gly	Val	Val	Phe	Gly	Ala	Ser	Leu	Phe	Leu	Leu	Ser	Ser	Leu	Thr	
				-15					-10					-5		
gta	ttc	agc	att	gtg	agc	gta	aca	gcc	tac	att	gcc	ttg	gcc	ctg	ctc	199
Val	Phe	Ser	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	
			1				5					10				

[illegible] $\langle 210 \rangle$ 111

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<222> 271

 $\langle 400 \rangle$ 111

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acgtctctct	atggccgcgtt	agggcattct	ttggactatca	tgcacctctcg	cacactcttt	120
ctgactgaga	gacgtcctgc	agaggtcttg	cagctgtctg	aggactataa	gcgtgggac	180
ctgcgcccg	gggtcaccaa	tgaacagctc	ttgagtcac	agaaataatc	cgagctgtt	240
ctacatccgg	acaccaatga	gaagatcttc	atg tca ttt	aga atg tca	ggt tat	294
			Met Pro Phe Arg Met Ser Gly Tyr			
			1	5		

11e Pro Phe Gly Thr Pro Ile Val Ser Val Thr Phe Lys Gly Phe Pro

Phe Leu Lys Asn Tyr Phe Lys Cys Leu Thr Leu Cys Tyr Cys Ser Arg
25 30 35 40

Val Phe Asp

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<210> 112
<211> 597
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..252

<221> sig_peptide
<222> 103..213
<223> Von Heijne matrix
      score 3.9
      seq PGPSLRRLFSGSQA/SV

<221> polyA_site
<222> 588..597

<400> 112
gaaaggtcag aggaagggagc tgtgggaagc tgcgagcagg tatcggagct taagccagtg      60
gatttggggg ccctggggctc cctagccggc tgcggtgtga ga atg gag tgg gca      114
                                     Met Glu Trp Ala
                                     -35
gga aag cag cgg gac ttt cag gta agg gca gct ccg ggc tgg gat cat      162
Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro Gly Trp Asp His
      -30      -25      -20
ttg gcc tcc ttt cct ggc cct tct ctc cgg ctg ttt tct ggg agt cag      210
Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe Ser Gly Ser Gln
      -15      -10      -5
gcg agt gtc tgt agt ctc tgc tgc ggg ttt ggg gct cag gaa      252
Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala Gln Glu
      1      5      10
tgatgtcatg ctccaacagt tggattctat tagcttaagg aggagggaaa cagccaattt      312
tcttgacttt gcaaatctag ctgatctcac tcttgctgaa tctgaggtgt ttagacttca      372
ctctaaaaag catcatttta cttttattta gcacaaaggc acaggatatt ttacaggaa      432
gaatctttta tatggaaaaa tctgagttaa catcactccc gtggtgtttg tagttcttac      492
agggaaactc cagtgccttt tgagccgctt gttcgtccta gtgaacactg tctgttttgt      552
ctcttggtgc tgctatgtct gacctgtaat gggagaaaaa aagaa      597

<210> 113
<211> 748
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..460

<221> polyA_signal
<222> 713..718

<221> polyA_site
<222> 735..748

<400> 113
c aca gtt cct ctc ctc cta gag cct gcc gac cat gcc cgc ggg cgt gcc      49
  Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
  1      5      10      15
cat gtc cac cta cct gaa aat gtt cgc agc cag tct cct gcc cat gtg      97
His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
      20      25      30

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cgc agg ggc aga agt ggt gca cag gta cta ccg acc gga cct gat gag      145
Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
      35      40      45
aaa cag gtt gag aag agt gaa gtt gat ttc tca aag tca cat agc tta      193
Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
      50      55      60
gtg aga cga ttt gag gat ctg aag ccc aag ctt tct gtt tgc aaa act      241
Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
      65      70      75      80
gga tca caa gtc ttt cgg tcg gag aac tgg aag gtc tgg gca gag tcg      289
Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
      85      90      95
agc aga gga gac cat gat gac tgc cta gac ttg tgc tca gtg ctg tgt      337
Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
      100      105      110
tgg gga gaa ctg cta cgg aca ata cct gaa att cca cca aag cgt gga      385
Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
      115      120      125
gaa ctc aaa acg gag ctt ttg gga ctg aaa gaa aga aaa cac aaa cct      433
Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
      130      135      140
caa gtt tct caa cag gag gaa ctt aaa taactatgcc aagaattctg      480
Gln Val Ser Gln Gln Glu Leu Lys
      145      150
tgaataatat aagtcttaaa tatgtatttc ttaatttatt gcatacaact acttgctcct      540
aagcacttag tctaagtcta actgcaagag gaggtgctca gtggatgttt agccgatacg      600
ttgaaattta attacggttt gattgatatt tcttgaanaac cgccaaagca catatcatca      660
aaccatttca tgaatatggt ttggaagatg tttagtcttg aatataatgc gaaatagaat      720
atttgaagt ctaccaaaaa aaaaaaaa      748

<210> 114
<211> 703
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..231

<221> polyA_signal
<222> 769..774

<221> polyA_site
<222> 690..703

<400> 114
ctctgggtggc tctgctactcg cggcgcagaa atg agg cag aag cgg aaa gga gat      54
Met Arg Gln Lys Arg Lys Gly Asp
      1      5
ctc agc cct gct aag ctg atg atg ctg act ata gga gat gtt att aaa      102
Leu Ser Pro Ala Lys Leu Met Met Leu Thr Ile Gly Asp Val Ile Lys
      10      15      20
caa ctg att gaa gcc cac gag cag ggg aaa gac atc gat cta aat aag      150
Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp Leu Asn Lys
      25      30      35      40
gtg aga acc aag aca gct gcc aaa tat ggc ctt tct gcc cag ccc cgc      198
Val Arg Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala Gln Pro Arg
      45      50      55
ctg gtg gat atc att gct gcc gtc cct cct gag tagctgggat tacaggcacc      251
Leu Val Asp Ile Ile Ala Ala Val Pro Pro Glu
      60      65

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<221> polyA_site
<222> 1694..1705
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tgtgccccctg gccagctgat aatcctaggt tcatgacct tcacctcccc taacccccaaa	1013
catagatcac acccttctcta gggaggagtc aaatgtaggt catgtttttg ttggtacttt	1073
ctgtttttttg tgacttcattg tgttccattg ctccccgctg ccactgctctc tccctgtgtt	1133
ctttaagagc tcagcatctg tccctgttca ttacatgtca ttgagtaggt gggtagccct	1193
gatgggggtc gctctgtctg gaggcataacc cacaggcgtt ttttctgcca cccctccct	1253
gcatgcctga tccccagttc ctatacccta cccctgacct attgagcagc ctctgaagag	1313
ccatagggcc catgttgaga gatgattctt tcttgccct ggccatctcg ggaagcttga	1373
ggagtcactg gacatgttca tcttagaact ctgtcaact acagtcattt cttttctct	1433
ctctggccct tgggtcctcg gaatgctgct gcttcaaccc cagagcctaa gaatggcagc	1493
cgtttcttaa catgttgaga gatgattctt tcttgccct ggccatctcg ggaagcttga	1553
tggcaatcct ggaagggttt aatctctctt tgtgagttg gtgggggaag gaagggtata	1613
tagattatat taaaaaaaaa aagggtatata tgcatatatc tatatataat atgacgcaga	1673
aataaatcta tgagaaatcc aaaaaaaaaa aa	1705

<210> 117

<211> 1069

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 135..206

<221> polyA_signal

<222> 850..855

<221> polyA_site

<222> 1056..1069

<400> 117

cccactccg	tctcagact	aagctctcac	gattaaggca	cgctgcctc	gattgtccag	60
ctcttgccag	aagaaaagctt	agcagccagc	gcctcagtag	agacctaaag	gcgctgaatg	120
agtgggaaag	ggaa atg ccg acc aat tgc gct gcg	gcg ggc tgt gcc act				170

Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr

1 5 10

acc tac aac aag cac att aac atc agc ttc cac agg taacctgggc	216
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg	

15

20

agggagtggtg	ggtgacggaa	actggagttc	ctattgtggc	tatcgcttgt	gtggaaggaa	276
caggaggatt	ctgctaattc	taataacttt	cccagctggt	agcagggaag	catcgtatgt	336
cccttgtggt	tctcaaatct	gcccaattgt	tctctgcttt	cggggaagct	tactcattt	396
tctaaaagaa	atccaagtac	tgtttgttca	ttaccctcta	gtaaaaaaa	gtaacaggag	456
gatatcgtaa	ttttctactg	ttttattcct	ctggttagacc	gggacctgac	atgaatgacg	516
cgtaaggaga	gaaagagatc	ttcccaatca	gcaatcacgc	taaaagcctg	ctgtgttccc	576
gttaaaatta	ggaaaattctc	actagatgaa	gttgacatgg	aggcatttag	atttctaata	636
gtcacatagt	aattctgcgg	aggaatttag	tcatctttga	tagccatgga	attaaagcat	696
gttaattaaa	gtgcaaacga	taacctttct	gtttcttacta	gtacaaagta	ataaaaagaa	756
cctagggtttt	cttttgtttg	ctggaagaaa	aatcaaaatt	cttttagttct	gtcaaacccag	816
aactcttgaa	agcaacttga	acaatgcctg	gaaaaataca	ggtactctgt	aaatgtttac	876
cttctctgca	agtgctctgc	acgtgcctga	agaaaaagaca	cattaaaaag	taaagtgaca	936
ccagtctctga	tttttatatat	tttatatacc	taacaacgtg	tatgttagta	tgtagaaatt	996
atatccttga	ctcttttccc	tacctattac	gaactgttact	tttattaaaa	gctgccacta	1056
aaaaaaaaa	aaa					1069

<210> 118

<211> 1084

<212> DNA

<213> Homo sapiens

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<220>
<221> CDS
<222> 135..818

<221> polyA_signal
<222> 909..914

<221> polyA_site
<222> 1071..1084

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cctctgccag aagaaagctt agcagccagc gcctcagtag aggcctaagg gcgctgaatg      120
agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act      170
               Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr
                   1               5               10
acc tac aac aag cac att aac atc agc ttc cac agg ttt cct ttg gat      218
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp
                   15               20               25
cct aaa aga aga aaa gaa tgg gtt cgc ctg gtt agg cgc aaa aat ttt      266
Pro Lys Arg Arg Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe
                   30               35               40
gtg cca gga aaa cac act ttt ctt tgt tca aag cac ttt gaa gcc tcc      314
Val Pro Gly Lys His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser
                   45               50               55               60
tgt ttt gac cta aca gga caa act cga cga ctt aaa atg gat gct gtt      362
Cys Phe Asp Leu Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val
                   65               70               75
cca acc att ttt gat ttt tgt acc cat ata aag tct atg aaa ctc aag      410
Pro Thr Ile Phe Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys
                   80               85               90
tca agg aat ctt ttg aag aaa aac aac agt tgt tct cca gct gga cca      458
Ser Arg Asn Leu Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro
                   95               100               105
tct agt tta aaa tca aac att agt agt cag caa gta cta ctt gaa cac      506
Ser Ser Leu Lys Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Gln His
                   110               115               120
agc tat gcc ttt agg aat cct atg gag gca aaa aag agg atc att aaa      554
Ser Tyr Ala Phe Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys
                   125               130               135               140
ctg gaa aaa gaa ata gca agc tta aga aga aaa atg aaa act tgc cta      602
Leu Glu Lys Glu Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu
                   145               150               155
caa aag gaa cgc aga gca act cga aga tgg atc aaa gcc atg tgt ttg      650
Gln Lys Glu Lys Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu
                   160               165               170
gta aag aat tta gaa gca aat agt gta tta cct aaa ggt aca tca gaa      698
Val Lys Asn Leu Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu
                   175               180               185
cac atg tta cca act gcc tta agc agt ctt cct ttg gaa gat ttt aag      746
His Met Leu Pro Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys
                   190               195               200
atc ctt gaa caa gat caa caa gat aaa aca ctg cta agt cta aat cta      794
Ile Leu Glu Lys Gln Asp Gln Gln Asp Lys Thr Leu Ser Leu Asn Leu
                   205               210               215               220
aaa cag acc aag agt acc ttc att taaatttagc ttgcacagag cttgatgcct      848
Lys Gln Thr Lys Ser Thr Phe Ile
                   225
atccttcatt cttttcagaa gtaaagataa ttatggcact tatgccaaaa ttcattattt      908
aataaagttt tacttggaagt aacattactg aatttgtaga gacttgatta caaagaata      968

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aaaaacttca tatggaaatt ttatttgaaa atgagtgaaa gcgccttaca ttagaattac 1028
ggacttaaaa attttgctaa taaattgtgt gtttgaaagg tgaaaaaaa aaaaaa 1084

<210> 119
<211> 419
<212> DNA
<213> Homo sapiens

<220>
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<222> 33..290

<221> sig_peptide
<222> 33..92
<223> Von Heijne matrix
score 5.4
seq WFWHSSALGLVLA/PP

<400> 119
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Met Asn Leu His Phe Pro Gln
-20 -15
tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca cct ttc 101
Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro Pro Phe
-10 -5 1
tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt agg cta 149
Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys Arg Leu
5 10 15
tta aat atg atc atg acc gcg ctt gca ttt tca ttc atc acc tgt tta 197
Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr Cys Leu
20 25 30 35
tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa aat tgt 245
Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys Asn Cys
40 45 50
aat agt cgg cac gct gga ttt gta ggg cca gca aaa ttg cgg cag 290
Asn Ser Arg His Ala Gly Phe Val Gly Pro Ala Lys Leu Arg Gln
55 60 65
tgaaactagt ttcaacttcta aagcccttca ttcccccaca ggtaaagctc tcgaaccccc 350
atttgatcct tgggtccctat ttcgatccct ctttggaaac tgaaaatcgg tctccatggt 410
gtatgcaaa 419

<210> 120
<211> 682
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 485..616

<221> polyA_site
<222> 669..682

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tattttatttg atcacatctt taatcttttg ttctctatac gtggcctggt ttgattttatt 180
ttactattct tgctttctaa ggtaagtatt ttgttgtgta gtgctttatt tttttcatct 240
ttcttcttga ataataatga catttttagg ttataaattt tcctctggta ctgagtttgc 300
ctcatttaatt ttggcagtaa gcattctcct ttatttgctt tctatgtagt ctttaatttt 360
gcttttaact tcttctttga tctaaggatt acctacttgt taatttccaa atattatctt 420

Asn Lys Asp	Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu Glu	
75	80	85
gaa gaa gat gaa gat gaa gga gaa gct gca gat atg gaa gaa tat gaa	536	
Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr Glu		
90	95	100
gag agt gga ttg ttg gaa aca gat gag gct acc cta gat aca agg aaa	584	
Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg Lys		
105	110	115
ata gta gaa gct tgt aaa gcc aaa act gat gct gcc ggt gaa gat gct	632	
Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp Ala		
120	125	130
att ttg caa acc aga act tat gac ctt tac atc act tat gat aaa tat	680	
Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys Tyr		
140	145	150
tac cag act cca cga tta tgg ttg ttt gcc tat gat gag caa cgg cag	728	
Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg Gln		
155	160	165
cct tta aca gtt gag cac atg tat gaa gac atc agt cag gat cat gtg	776	
Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His Val		
170	175	180
aag aaa aca gtg acc att gaa aat cat cct cat ctg cca cca cct ccc	824	
Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro Pro		
185	190	195
atg tgt tca gtt cac cca tgc agg cat gct gag gtg atg aag aaa atc	872	
Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys Ile		
200	205	210
att gag act gtt gca gaa gga ggg gga gaa ctt gga gtt cat atg tat	920	
Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met Tyr		
220	225	230
ctt ctt att ttc ttg aaa ttt gta caa gct gtc att cca aca ata gaa	968	
Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile Glu		
235	240	245
tat gac tac aca aga cac ttc aca atg taatgaagag agcataaaat	1015	
Tyr Asp Tyr Thr Arg His Phe Thr Met		
250	255	
ctatcctaatt tattgtttct gatttttaaa gaattaaccc atagatgtga ccattgacca	1075	
tattcatcaa tatatacagt ttctctaata agggacttat atgtttatgc attaaataaa	1135	
aatatgttcc actaccagcc ttacttggtt aataaaaaatc agtgcaaaaa aaaaaa	1191	

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<210> 122
<211> 1008
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 657..923

<221> sig_peptide
<222> 657..896
<223> Von Heijne matrix
      score 3.5
      seq RGLLSACAPWGDG/ST

<221> polyA_signal
<222> 957..962

<221> polyA_site
<222> 974..1008

<400> 122

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ntcgnatgtg	gcacaaaaac	cctctgctgg	ctcatgtgtg	caactgagac	tgtcagagca	60
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gcacacagga	tgctctgcgt	caggtgggtg	cagaagtcag	tgcccaggcc	ccccacaca	180
gtccccaaag	gtccggcctc	cccagcgctg	ggctcctcgt	ttgaggggag	gtgacttccc	240
tcccagcagg	ctctttggaca	cagtaagctt	ccccagccct	gcctgagcag	cttttctctc	300
ttgcctcgtt	ccccactccc	cggctccagt	ccagggagct	cccaggggaag	tggtcgaccc	360
ctccagtggt	tggggccactc	tgctagagtc	catccgccaa	gctgggggca	tggcgaaggc	420
caagctgcgc	agcatgaagg	agcgaaagct	ggagaagaag	aagcagaagg	agcaggagca	480
agtgagagcc	acgagccaag	gtgggcactt	gatgtcggat	ctcttcaaca	agctgtgcat	540
gaggcgcaag	ggcatctctg	ggaaagaacc	tggggctggg	gaggggcccg	gaggagcctt	600
tgcccgctg	tcagactcca	tcctctctct	gcggccaccg	cagcagccac	aggtag atg	659

Met
-80

agg	aca	agg	acg	act	ggg	aat	cct	agg	ggg	ctc	cat	gac	acc	ttc	ccc	707
Arg	Thr	Arg	Thr	Thr	Gly	Asn	Pro	Arg	Gly	Leu	His	Asp	Thr	Phe	Pro	
				-75					-70					-65		
cgc	aga	ccc	aga	ctt	ggc	cgt	tgc	tct	gac	atg	gac	aca	gcc	agg	aca	755
Arg	Arg	Pro	Arg	Leu	Gly	Arg	Cys	Ser	Asp	Met	Asp	Thr	Ala	Arg	Thr	
			-60					-55						-50		
agc	tgc	tca	gac	ctg	ctt	ccc	tgg	gag	ggg	gtg	acg	gaa	cca	gca	ctg	803
Ser	Cys	Ser	Asp	Leu	Leu	Pro	Trp	Glu	Gly	Val	Thr	Glu	Pro	Ala	Leu	
			-45				-40						-35			
tgt	gga	gac	cag	ctt	caa	gga	acg	gaa	ggc	tgg	ctt	gag	gcc	aca	cag	851
Cys	Gly	Asp	Gln	Leu	Gln	Gly	Thr	Glu	Gly	Trp	Leu	Glu	Ala	Thr	Gln	
			-30				-25						-20			
ctg	ggg	cgg	gga	ctt	ctg	tct	gcc	tgt	gct	cca	tgg	ggg	gac	ggc	tcc	899
Leu	Gly	Arg	Gly	Leu	Leu	Ser	Ala	Cys	Ala	Pro	Trp	Gly	Asp	Gly	Ser	
			-15			-10				-5				1		
acc	cag	cct	gtg	cca	ctg	tgt	tct	taagaggctt	ccagagaaaa	cggcacacca						953
Thr	Gln	Pro	Val	Pro	Leu	Cys	Ser									
			5													
atcaataaag	aactgagcag	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaan											1008

<210> 123
 <211> 568
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 18..311

 <221> sig_peptide
 <222> 18..62
 <223> Von Heijne matrix
 score 8.4
 seq AMWLLCVALAVLA/WG

<400>	123																
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													Met	Glu	Ala	Met	
													-15				
gcg	gtc	ttg	gca	tgg	ggc	ttc	ctc	tgg	gtt	tgg	gac	tcc	tca	gaa	cga		98
Ala	Val	Leu	Ala	Trp	Gly	Phe	Leu	Trp	Val	Trp	Asp	Ser	Ser	Glu	Arg		
				1				5					10				
atg	aag	agt	cgg	gag	cag	gga	gga	cgg	ctg	gga	gcc	gaa	agc	cgg	acc		146
Met	Lys	Ser	Arg	Glu	Gln	Gly	Gly	Arg	Leu	Gly	Ala	Glu	Ser	Arg	Thr		
			15				20				25						
ctg	ctg	gtc	ata	gcg	cac	cct	gac	gat	gaa	gcc	atg	ttt	ttt	gct	ccc		194
Leu	Leu	Val	Ile	Ala	His	Pro	Asp	Asp	Glu	Ala	Met	Phe	Phe	Ala	Pro		
			30				35				40						

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aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      242
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45          50          55          60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa ggt ctt      290
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu
65          70          75
acc tct gaa ccc ctc aca gcc tagggacagg agcggccggc ttacctgggtg      341
Thr Ser Glu Pro Leu Thr Ala
80
ggtttggggga cgtcgggcagc tcgcgtacta cgccagcagg attgaggagc agagaaacag      401
ttgcagttgg ttgtattcag tacctgcatt tccgttggga actccacctg tacttgttat      461
tctgtggaac tttttttatt tgtagaagga gcaagaatat tgaccttact atatatgaca      521
cgaaacaatc tatgctgtat cgtgcctgct caatccttaa agttaac      568

<210> 124
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 151..426

<221> sig_peptide
<222> 151..258
<223> Von Heijne matrix
score 5.2
seq KVALAGLLGFGLG/KV

<221> polyA_signal
<222> 505..510

<221> polyA_site
<222> 527..538

<400> 124
cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac      60
catggcttca cgcctctgctc gtggaaacca agataaagat gcccatcttc caccaccaag      120
caagcagctc tgccttttttc tcttgtaagc atg ctt gtc acc cag gga cta gtc      174
Met Leu Val Thr Gln Gly Leu Val
-35
tac caa ggt tat ttg gca gct aat tct aga ttt gga tca ttg ccc aaa      222
Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys
-25          -20          -15
gtt gca ctt gct ggt ctc ttg gga ttt ggc ctt gga aag gta tca tac      270
Val Ala Leu Ala Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr
-10          -5          1
ata gga gta tgc cag agt aaa ttc cat ttt ttt gaa gat cag ctc cgt      318
Ile Gly Val Cys Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg
5          10          15          20
ggg gct ggt ttt ggt cca cag cat aac agg cac tgc ctc ctt acc tgt      366
Gly Ala Gly Phe Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys
25          30          35
gag gaa tgc aaa ata aag cat gga tta agt gag aag gga gac tct cag      414
Glu Glu Cys Lys Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln
40          45          50
cct tca gct tcc taaattctgt gtctgtgact ttcgaagttt tttaaacttc      466
Pro Ser Ala Ser
55
tgaatttgta cacatttaaa atttcaagtg tacttttaaaa taaaatactt ctaatggaac      526
aaaaaaaaaa aa      538

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09760-10750-1

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<221> sig_peptide
<222> 10..57
<223> Von Heijne matrix
      score 4.9
      seq FIYLOAHFTLCSG/WS
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<221> polyA_site
<222> 1735..1747
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[illegible]

175	180	185	190	
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc				675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Gln Lys Phe Pro Asp Gly Phe				
195	200	205		
tgg cta gga gag cag ctg gtg tgc tgg caa gca gcc acc acc cct tgg				723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp				
210	215	220		
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac				771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn				
225	230	235		
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg				819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val				
240	245	250		
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca				867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser				
255	260	265		
cag tca tcc acg gcc act gtt atg gga gct gtt atc atg gag gcc ttc				915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe				
275	280	285		
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc				963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser				
290	295	300		
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa gcc ccn				1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro				
305	310	315		
ttt tgt cac ctt gga cat gga aga ctg tgg cta caa cat tcc aca gac				1059
Phe Cys His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp				
320	325	330		
aga tgagtcaacc ctcatgacca tagcctatgt catggctgcc atctgcgcc				1112
Arg				
335				
tcttcatgct gccactctgc ctcatgggtg gtcagtggcg ctgcctcgcg tgccctgcgc				1172
agcagcatga tgactttgct gatgacatct cctgctgaa gtgaggagcg ccatgggag				1232
aagataggga ttccccctgga ccacacctcg gtggttccact ttggtcacaa gtaggagaca				1292
cagatggcac ctgtggccag agcacctcag gacctcccc acccaccaaa tgccctctgcc				1352
ttgatggaga aggaaaaggc tggcaagggtg ggttccaggg actgtacctg taggagacag				1412
aaaagagaag aaagaagcac tctgctggcg ggaatactct tggtcaccctc aaatttaagt				1472
cgggaaattc tgctgcttga aacttcagcc ctgaaaccttt gtcaccattc ctttaaattc				1532
tccaacccaa agtattcttc ttttcttagt ttcagaagta ctggcatcac acgcaggtta				1592
ccttggcggtg tgtccctgtg gtaccctggc agagaagaga ccaagcttgt ttcctctgtg				1652
gccaaagtca gtaggagagc atgcacagtt tgctatttgc tttagagaca gggactgtat				1712
aaacaagcct aacattgtgt caaaaaaaaa aaaaa				1747

<210> 126
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..491

 <221> sig_peptide
 <222> 78..218
 <223> Von Heijne matrix
 score 5.8
 seq LMCFLGIGLCAC/IC

<221> polyA_signal
 <222> 1652..1657

<221> polyA_site
<222> 1673..1686

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cactaactga gcagtttc atg gag aaa ttt gtt gat ccc gga aac cac aat 110
Met Glu Lys Phe Val Asp Pro Glu Asn His Asn
-45 -40
agc ggg att gat ctc ctt agg acc tat ctt tgg cgt tgc cag ttc ctt 158
Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu
-35 -30 -25
tta cct ttt gtg agt tta ggt ttg atg tgc ttt ggg gct ttg atc gga 206
Leu Pro Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly
-20 -15 -10 -5
ctt tgt gct tgc att tgc cga agc tta tat ccc acc att gcc acg ggc 254
Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly
1 5 10
att ctc cat ctc ctt gca ggt ctg tgt aca ctg ggc tca gta agt tgt 302
Ile Leu His Leu Leu Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys
15 20 25
tat gtt gct gga att gaa cta ctc cac cag aaa cta gag ctc cct gac 350
Tyr Val Ala Gly Ile Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp
30 35 40
aat gta tcc ggt gaa ttt gga tgg tcc ttc tgc ctt gct tgt gtc tct 398
Asn Val Ser Gly Glu Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser
45 50 55 60
gct ccc tta cag ttc atg gct tct gct ctc ttc atc tgg gct gct cac 446
Ala Pro Leu Gln Phe Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His
65 70 75
acc aac cgg aga gag tac acc tta atg aag gca tat cgt gtg gca 491
Thr Asn Arg Arg Glu Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
80 85 90
tgagcaagaa actgcctgct ttacaattgc cattttttatt ttttttaaaat aataactgata 551
ttttcccccac ctctcaattg tttttaattt ttatttgggt atataccatt ttattatgaa 611
aatctatttt atttatacac attcaccact aaatacacac ttaataccac taaaatttat 671
gtggtttact ttaagcgatg ccattctttca aataaactaa tctaggtcta gacagaagaa 731
aatggataga gacttgacac aaatttatga aagaaaattg ggagtaggaa tgtgaccgaa 791
aacaagttgt gctaatgtct gttagacttt tcagtaaaac caaagtaact gtatctgttc 851
aactaaaaac tctatatagg tttctttggg aaacctctca tcgtcaaaaac tttatgttca 911
ctttgtcgtt gtatagatgc agtcaaccac cagattatgt gctgttttca aagatttaag 971
ctctataaaa ttgggaaatt attcaagatc attttcccta agcattgaca catagcttca 1031
tctgaggtga gatattggcag ctgtttgtat ctgcactgtg tctgtctaca aagagtga 1091
aatacagttg ttacttgaaa ttttaacttt gtaactgcga gaattccagt tcggcggggc 1151
gaggattagt attattttta actctccgta agattttcag taaccacaaa ttgttttggg 1211
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aaagaacgtt tcaccataat gaccctccag agctgggaaa cctaccacaa gatctaaagt 1391
cttggctgtc cattaacctc caactatggt cttattttct tgtgtgaata tgaatgtcct 1451
ttccttgctc aaatcccttc ctgggtgtga tcaacattat ttaattgtct ctaattccag 1511
cattttttat aagtatgtct ataaacattg aacttttaaa aactatttta ttatttcac 1571
tactgtagca attgacagat taataaaatg taacttcata attttctacc ataacctcaa 1631
tgtctttttt aaaaaataaa attaaaaatg aaaagagacc caaaaaaaa aaaaa 1686

<210> 127
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..371


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<221> sig_peptide
<222> 69..287
<223> Von Heijne matrix
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      seq AVGFLFWIVLTS/WI

<221> polyA_signal
<222> 510..515

<221> polyA_site
<222> 530..542

<400> 127
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gcgcagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg      110
      Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
              -70              -65              -60
tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctg tgg      158
Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
              -55              -50              -45
ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc      206
Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
              -40              -35              -30
tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg      254
Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
              -25              -20              -15
ggc ttc ctg ttc tgg gtg ata gtg ctg acc tcc tgg atc acc atc ttc      302
Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
              -10              -5              1              5
cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctg tcc ttc      350
Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
              10              15              20
acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggccctgc      401
Thr Ile Pro Leu Gly Thr Pro
              25
ttattctccc aggacaggct ccttaaagca gaggagcctg tccctgggagc ccttctctcaa      461
actcctaaga cttgtttctca tgtccacagt tctctgctga catcccccaa taaaggacc      521
taactttcaa aaaaaaaaaa a      542

<210> 128
<211> 1174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..757

<221> sig_peptide
<222> 2..205
<223> Von Heijne matrix
      score 7.3
      seq LRILISPLPGAQP/QQ

<221> polyA_site
<222> 1160..1174

<400> 128
g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag      49
      Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu

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-65      -60      -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50      -45      -40
agc ggc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35      -30      -25
gct tca gcc ggc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20      -15      -10      -5
ggg gcc cag cct caa cag gag cca ctg gcc ctg gtc ttc cgc ttc gcc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
      1      5      10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat      289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15      20      25
gcc cac ctg cgc ttt tac acg gcc cgc cct ggc ccc cgg ctc gcc cta      337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30      35      40
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag      385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45      50      55      60
tgg cag cgc ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc      433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
      65      70      75
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc      481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
      80      85      90
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac      529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
      95      100      105
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag      577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
      110      115      120
aag gcc cgc tgc gtc ctg gag gcc ctg cag cag cac agg cgc agc cgc      625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
      125      130      135      140
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat tca aac      673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
      145      150      155
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggt      721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
      160      165      170
gag gcc aaa gat ggc agc aac ctc tgc agc aaa tgattgtgta      767
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
      175      180
acctgggggc acctgtcccc ctctggacct gattcaccga ttggaagtt tgtagcccta      827
gctgatactc aatggactag gcctcctcac ttgtcaatag tgtttccagg ctgggocgag      887
tggtctatgc ctgtggtccc ggcaactcgg gaggccagat ggggtgctc acctgaggtc      947
aggagttcga gaccatcctg gccaacatgg tgaaccccca tctccactaa aatgcaaaaa      1007
attagccagg tgtgtgtggcg ggcacctgta gtctcagcta ctccgggagga tgaggcagga      1067
aaatcgcttg aaacccaggag gtggaggttg cagttgagct gagatcgtgc cattgcactc      1127
cagcctgggc aacgagagca aaactccatc tcaaaaaaaa aaaaaaaa      1174

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<210> 129
 <211> 1285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

[illegible]

<222> 2...205

<221> polyA signal

<221> polyA site

<222> 1272..1285

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Met	Pro	Glu	Gly	Pro	Glu	Leu	His	Leu	Ala	Ser	Gln	Phe	Val	Asn	Glu	
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Ala	Cys	Arg	Ala	Leu	Val	Phe	Gly	Cys	Val	Glu	Lys	Ser	Ser	Val		
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Ser	Arg	Asn	Pro	Glu	Val	Pro	Phe	Glu	Ser	Ser	Ala	Tyr	Arg	Ile	Ser	
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Gly	Ala	Gln	Pro	Gln	Gln	Glu	Pro	Leu	Ala	Leu	Val	Phe	Arg	Phe	Gly	
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Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His	
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Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu	
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Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys	
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Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Tcg	Tyr	Gln	Gln	Phe	
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Pro	Lys	Glu	Val	Asp	Gln	Leu	Gly	Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser	
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Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe	Arg	Ala	Trp	Leu	Arg	Cys	Tyr	Gly	
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Met	Pro	Gly	Met	Ser	Ser	Leu	Gln	Asp	Arg	His	Gly	Arg	Thr	Ile	Gly	
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ttc	cag	ggg	gat	cct	gga	ccg	ttg	gca	ccc	aaa	ggg	cgc	aaq	tcc	cgc	766

Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
 175 180 185
 aaa aag aaa tcc aag gcc aca cag ctg agt cct gag gac aga gtg gag 817
 Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
 190 195 200
 gac gct ttg cct cca agc aag gcc cct tcc aag aca cga agg gca aag 865
 Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
 205 210 215 220
 aga gac ctt cct aag agg act gca acc cag cgg cct gag ggg acc agc 913
 Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
 225 230 235
 ctc cag cag gac cca gaa gct ccc aca gtg ccc aag aag ggg agg agg 961
 Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
 240 245 250
 aag ggg cga cag gca gcc tct ggc cac tgc aga ccc cgg aag gtc aag 1009
 Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
 255 260 265
 gct gac atc cca tcc ttg gaa cca gag ggg acc tca gcc tct 1051
 Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
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 score 7.3
 seq LRLILSLPGAQP/QQ

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 <221> polyA_site
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 gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc 97
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca 145
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct 193
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc 241
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly

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										1											5											10											
atg	tcc	ggc	tct	ttt	cag	ctg	gtg	ccc	cgc	gag	gag	ctg	cca	cgc	cat	289																											
Met	Ser	Gly	Leu	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His																												
15																20	25																										
gcc	cac	ctc	cgc	ttt	tac	acg	cgc	ccg	cct	ggc	ccc	cgg	ctc	gcc	cta	337																											
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu																												
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tgt	ttc	ptg	gac	atc	cgc	cgg	ttc	ggc	cgc	tgg	cag	ctt	ggg	gga	aag	385																											
Cys	Cys	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys																												
45																50	55																										
tgg	cag	ccg	ggc	cgc	ggg	ccc	tgt	gtc	ttg	cag	gag	tac	cag	cag	ttc	433																											
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe																												
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agg	gag	aat	gtg	cta	cga	aac	cta	cgc	gat	aag	gcc	ttt	gac	cgg	ccc	481																											
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro																												
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Ile	Cys	Glu	Gln	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn																											
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Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala	Leu	Gln	Gln	His	Arg	Pro	Ser	Pro																												
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Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	Arg	Thr	Lys	Leu	Gln	Asn	Pro	Asp																												
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Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser	Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe																												
175																180	185																										
cga	gcc	tgg	ctg	cgc	tgc	tat	cgc	atg	cca	ggc	atg	agc	tcc	ctg	cag	817																											
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Ala	Pro	Lys	Gly	Arg	Lys	Ser	Ser	Lys	Lys	Lys	Ser	Lys	Ala	Thr	Gln																												
225																230	235																										
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Leu	Ser	Pro	Glu	Asp	Arg	Val	Glu	Asp	Ala	Leu	Pro	Pro	Ser	Lys	Ala																												
240																245	250																										
cct	tcc	agg	aca	cga	agg	gca	aag	aga	gac	ctt	cct	aag	agg																														

cctttcttat tgtcttgccc tgcacatcggg ggtctgaatt ttggggagca ggcaatatct 1261
 gaaggtgcaa acaggcccta cggtctgtcc ctgcacaact ctcatggttt taattgtacc 1321
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 <222> 42..287
 <223> Von Heijne matrix
 score 4.4
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 787..792

<221> polyA_site
 <222> 808..821

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 Met Tyr Val Trp Pro
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tgt gct gtg gtc ctg gcc cag tac ctt tgg ttt cac aga aga tct ctg 104
 Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe His Arg Arg Ser Leu
 -75 -70 -65

cca ggc aag gcc atc tta gag att gga gca gga gtg agc ctt cca gga 152
 Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly Val Ser Leu Pro Gly
 -60 -55 -50

att ttg act gcc aaa tgt ggt gca gaa gta ata ctg tca gac agc tca 200
 Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser
 -45 -40 -35 -30

gaa ctg cct cac tgt ctg gaa gtc tgt cgg caa agc tgc caa atg aat 248
 Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn
 -25 -20 -15

aac ctg cca cat ctg cag gtg gta gga cta aca tgg ggt cat ata tct 296
 Asn Leu Pro His Leu Gln Val Val Gly Leu Thr Trp Gly His Ile Ser
 -10 -5 1

tgg gat ctt ctg gct cta cca cca caa gat att atc ctt gca tct gat 344
 Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile Ile Leu Ala Ser Asp
 5 10 15

gtg ttc ttt gaa cca gaa gat ttt gaa gac att ttg gct aca ata tat 392
 Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr
 20 25 30 35

ttt ttg atg cac aag aat ccc aag gtc caa ttg tgg tct act tat caa 440
 Phe Leu Met His Lys Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln
 40 45 50

gtt agg agt gct gac tgg tca ctt gaa gct tta ctc tac aaa tgg gat 488
 Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp
 55 60 65

atg aaa tgt gtc cac att cct ctt gag tct ttt gat gca gac aaa gaa 536
 Met Lys Cys Val His Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu
 70 75 80

gat ata gca gaa tct acc ctt cca gga aga cat aca gtt gaa atg ctg 584

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Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu
 85                      90                      95
gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg      631
Val Ile Ser Phe Ala Lys Asp Ser Leu
100                      105
ttctgggaca gtatcaatac tgaatgagcaa cctggcacac aaactatgag cagaccactt      691
cagcttgaga atgcagtgagg tctgaagatg gtcaagtcgt tctgccttag attttgatgt      751
cacctagaca acactttaac tcatatgaaa caaaaattaa aatacgtatt acaagtaaaa      811
aaaaaaaaaa
821

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<213> Homo sapiens

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<222> 62..916

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<222> 62..757
<223> Von Heijne matrix
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      seq LVTPAALRPLVLG/GN

<221> polyA_site
<222> 904..916

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g atg gga tgt gtt ttc cag agc aca gaa gac aaa cgt ata ttc aag ata      109
  Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
      -230                      -225                      -220
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta      157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
      -215                      -210                      -205
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc      205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
      -200                      -195                      -190                      -185
gta cac ttg atg ggg gac aac tta tgc aat gat ggc tct ctc ctg ctc      253
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
      -180                      -175                      -170
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc      301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
      -165                      -160                      -155
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg      349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
      -150                      -145                      -140
ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att      397
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
      -135                      -130                      -125
cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag      445
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
      -120                      -115                      -110                      -105
gta gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt      493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
      -100                      -95                      -90
cgt tac tac cac aaa ctc agg atg tct gcg gag tac tcc cag agc tgg      541
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
      -85                      -80                      -75
ggc cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat      589

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Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
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 Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
 -55 -50 -45
 tac acc tgc agt atc cac cta ggg aac ctg gtg ttc aag aaa acc att 685
 Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
 -40 -35 -30 -25
 gtg ctg cat gtc agc ccg gaa gag cct cga aca ctg gtg acc ccg gca 733
 Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
 -20 -15 -10
 gcc ctg agg cct ctg gtc ttg ggt ggt aat cag ttg gtg atc att gtg 781
 Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
 -5 1 5
 gga att gtc tgt gcc aca atc ctg ctg ctg cct gtc ctg ata ttg atc 829
 Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
 10 15 20
 gtg aag aag acc tgt gga aat aag agt tca gtg aat tct aca gtc ttg 877
 Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40
 gtg aag aac acg aag aag act aat cca aaa aaa aaa 916
 Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys Lys
 45 50

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 <222> 1124..1129

 <221> polyA_site
 <222> 1141..1153

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 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 gta cac ttg atg ggg gac atc tta tgc aat gat gcc tct ctc ctg ctc 253
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile

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gaatgttgaa tgtctttggc tcagtttcatt taataaaagat atctatttga aagttctcag 1277
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caccagagc caatatctag gcattttctt ggtagcaciaa attttcttat tgcttagaaaa 1397
attgtctctc ttgttatttc tgtttgtaag acttaagtga gttagggtct taaggaaagc 1457
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<211> 526
<212> DNA
<213> Homo sapiens

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<220>
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<222> 22..318

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<221> sig_peptide
<222> 22..93
<223> Von Heijne matrix
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<221> polyA_signal
<222> 497..502

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<221> polyA_site
<222> 516..526

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Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Gly Gly Val
                        -10
aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc tgc aaa 147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
                        5
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc 195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
                        20
tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt 243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
                        35
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc 291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
                        55
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg 338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
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aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat 398
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aaaaaaaaa 526

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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS

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<222> 8..292

<221> sig_peptide
<222> 8..118
<223> Von Heijne matrix
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      seq WLLLDALLRLGDT/KK

<221> polyA_signal
<222> 317..322

<221> polyA_site
<222> 339..352

<400> 136
ctgagat atg gca agt ccc gct gta aac agg tgg aaa agg cca agg ttg      49
      Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu
      -35                                -30                                -25
aag ccg gtg tgg cca cgg cgc ttg gaa tcc tgg ttg ttg ctg gat gct      97
Lys Pro Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala
      -20                                -15                                -10
ctt ttg cga tta gga gat acc aaa aag cga cag cct gaa gca gcc      145
Leu Leu Arg Leu Gly Asp Thr Lys Lys Arg Gln Pro Glu Ala Ala
      -5                                1                                5
aca aaa tcc tgt gtt aga agc agc tgt ggg ggt ccc agt gga gat ggg      193
Thr Lys Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly
10                                15                                20                                25
cct ccc cca tgc ctc cag cag cct gac cct cgt gcc ctg tct cag gcg      241
Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala
      30                                35                                40
ttc tct aga tcc ttt cct ctg ttt ccc tct ctc gct ggc aaa agt atg      289
Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met
      45                                50                                55
atc taattgaaac aagactgaag gatcaataaa cagccatctg ccccttcaaaa      342
Ile
aaaaaaaaa      352

<210> 137
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..378

<221> sig_peptide
<222> 16..84
<223> Von Heijne matrix
      score 9.8
      seq FLFFFLFLLTRG/SL

<221> polyA_signal
<222> 502..507

<221> polyA_site
<222> 522..542

<400> 137
cacgacctgt gggcc atg atg cta ccc caa tgg ctg ctg ctg ctg ttc ctt      51
      Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu

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                                -20                                -15
ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
-10                                -5                                1                                5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
10                                15                                20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tgc cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
25                                30                                35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
40                                45                                50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
55                                60                                65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
70                                75                                80                                85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
90                                95
tcctctcttgc tgctctctcc tcctccacct gctctctctcc ctaccagag ctctgtgttc      448
acctgtttcc ccagagcttc caccatgagt ggagggaagt ggggagtgat tgaataaag      508
agcttttttca atgaaaaaaaa aaaaaaaaaa aaaa                                542

<210> 138
<211> 233
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..233

<400> 138
gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
Met
1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
5                                10                                15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155
Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg Glu
20                                25                                30
gag aga aaa caa ata aat ggg aaa aaa gaa agg aca aaa tat gaa aca      203
Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu Thr
35                                40                                45
cca aga aaa aga gaa gga aaa aaa aaa aaa                                233
Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
50                                55

<210> 139
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..340

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<221> sig_peptide
<222> 83..124
<223> Von Heijne matrix
      score 7.5
      seq VALNLLILVPCCAA/WC

<221> polyA_signal
<222> 573..578

<221> polyA_site
<222> 607..660

<400> 139
gaatttgtaa aacttctgct cgtttacact gcacattgaa tacaggtaac taattggaag      60
gagagggggag atcactcttt tg atg gtg gcc ctg aac ctc att ctg gtt ccc      112
                               Met Val Ala Leu Asn Leu Ile Leu Val Pro
                               -10                               -5
tgc tgc gct gct tgg tgt gac cca cgg agg atc cac tcc cag gat gac      160
Cys Cys Ala Ala Trp Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp
                               1                               5                               10
gtg ccc cgt agc tct gct gct gat act ggg tct gcg atg cag cgg cgt      208
Val Pro Arg Ser Ser Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg
                               15                               20                               25
gag gcc tgg gct ggt tgg aga agg tca caa ccc ttc tct gtt ggt ctg      256
Glu Ala Trp Ala Gly Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu
                               30                               35                               40
cct tct gct gaa aga ctc gag aac caa cca ggg aag ctg tcc tgg agg      304
Pro Ser Ala Glu Arg Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg
                               45                               50                               55                               60
tcc ctg gtc gga gag gga tat aga atc tgt gac ctc tgacaactgt      350
Ser Leu Val Gly Glu Gly Tyr Arg Ile Cys Asp Leu
                               65                               70
gaagccaccc tgggctacag aaaccacagt ctccccagca attattacaa ttcttgaatt      410
ccttgggggat tttttactgc cctttcaaag cacttaagtg ttgatctaa cgtgtccag      470
tgtctgtctg aggtgactta aaaaatcaga acaaaacttc tattatccag agtcatggga      530
gagtagacccc tttccaggaa taatgttttg ggaacactcg aaatgaaatc ttcccagtat      590
tataaattgt gtatttataaa aaagaaaactt ttctgaatgc ctacctggcg gtgtatacca      650
ggcagtggtgc                                                    660

<210> 140
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..541

<221> sig_peptide
<222> 47..220
<223> Von Heijne matrix
      score 5.4
      seq QLLDSVLWLGLG/LT

<221> polyA_site
<222> 597..605

<400> 140
aaagtgggag gaggactagg tcttcccgtc acctccacct ctctcc atg acc cgg      55
                               Met Thr Arg
ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct      103

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Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
 -55 -50 -45 -40
 cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca 151
 Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
 -35 -30 -25
 cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc 199
 Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
 -20 -15 -10
 cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc 247
 Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
 -5 1 5
 act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc etc acc ttt gac 295
 Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
 10 15 20 25
 ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc 343
 Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
 30 35 40
 acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag 391
 Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
 45 50 55
 gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag 439
 Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
 60 65 70
 gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc 487
 Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
 75 80 85
 tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct 535
 Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
 90 95 100 105
 tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaatatac aatgaccacc 591
 Trp Ala
 cttcttcaaaa aaaa 605

 <210> 141
 <211> 396
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 46..285

 <221> sig_peptide
 <222> 46..150
 <223> Von Heijne matrix
 score 3.6
 seq LEFGLSSSAACNG/KE

 <221> polyA_signal
 <222> 364..369

 <221> polyA_site
 <222> 385..396

 <400> 141
 cctctacagg aatcagactc agcctctttt ggttttcagt gaagt atg cct ttt caa 57
 Met Pro Phe Gln
 -35
 ttt gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca 105
 Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser
 -30 -25 -20

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att gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag      153
Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys
-15                               -10                               -5                               1
gag atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc      201
Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys
5                               10                               15
ctg aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag      249
Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys
20                               25                               30
cca cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt      295
Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
35                               40                               45
aagtccttttg tcaaggctctg actagggtcaa gggtaaatgga ccagtatcat ctggtgatct      355
ggtaaacaaa taaagtggt ggcaccttca aaaaaaaaaa a      396

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<210> 142
<211> 432
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 22..240

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<221> sig_peptide
<222> 22..84
<223> Von Heijne matrix
score 12
seq VLVLCVLLLQAQG/GY

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<221> polyA_signal
<222> 397..402

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<221> polyA_site
<222> 421..432

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<400> 142
gctcagctc tgggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg      51
Met Ala Pro Gln Thr Leu Leu Pro Val Leu
-20                               -15
gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag      99
Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys
-10                               -5                               1                               5
atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat      147
Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp
10                               15                               20
cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag      195
Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Lys
25                               30                               35
ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta      240
Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu
40                               45                               50
tgagtgaggag agtgggtctgg gatgtgcatc ctgctccctg aacccttcca tccgagactg      300
tgccacatc cgaagcaciaa ggacatcaaa tcatcagcac aagaacatca acaggaatcg      360
caccctccc agtgtctgaa ctccctgtcc ctgtcaaatg aaccagaaca aatgcccatg      420
aaaaaaaaaa aa      432

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```

<210> 143
<211> 420
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 89..382

<221> polyA_site
<222> 408..420

<400> 143
gcttgccctga cccccatgtc gcctctgtag gtagaagaag tatgtcttcc tggacccccc 60
ggctggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag 112
                        Met Leu Gly Ala Glu Thr Glu Glu
                        1                    5

aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa 160
Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu
10                    15                    20

cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg 208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val
25                    30                    35                    40

cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc 256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala
45                    50                    55

aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct 304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser
60                    65                    70

gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc 352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala
75                    80                    85

gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc 402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr
90                    95

ccaccaaaaa aaaaaaaaaa 420

<210> 144
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..415

<221> sig_peptide
<222> 80..142
<223> Von Heijne matrix
score 5.4
seq TFCLIFGLGAVWG/LG

<221> polyA_signal
<222> 471..476

<221> polyA_site
<222> 488..501

<400> 144
cccgcttgat tccaagaacc tcttcgatat ttatttttat ttttaagag ggagacgatg 60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt 112
                        Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
                        -20                    -15

ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc 160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser

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-10	-5	1	5	
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc				208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr				
10	15	20		
gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc				256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu				
25	30	35		
ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa				304
Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu				
40	45	50		
cag ttt ttt cag aag ctg aga aat aaa cat gaa ttt act att ttg gtg				352
Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val				
55	60	65	70	
acc cta aaa cag acc cac tta aat tca gga gtt att ctc tca att cac				400
Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His				
75	80	85		
cac ttg gat cac agg taaatgtggt tgctggagtt tcctgtgttt tcattatatg				455
His Leu Asp His Arg				
90				
tggttaaagt aatatattaa agagaagtaa acaaaaaaaaa aaaaaa				501

<210> 145
 <211> 454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..361

 <221> sig_peptide
 <222> 152..283
 <223> Von Heijne matrix
 score 4.7
 seq FLLSLSLITYCFW/DP

<400> 145	
gacatttttac ttttttttgt taacgcttac cctagaaatt agaaatgaca ccacgtattc	60
ttagcgaagt ccagttttca gcattttgtc cttattggac aatagcaagg atattagaac	120
gtgttggttc cgcgtgcttc cgtcttgagt t atg tgc tgc tat tgt cgg ata	172
Met Cys Cys Tyr Cys Arg Ile	
-40	
ttt tgt ctt aga tgt acg tac ttt cct gtt cat tgt ggt atg tgt aat	220
Phe Cys Leu Arg Cys Thr Tyr Phe Pro Val His Cys Gly Met Cys Asn	
-35	-30
ttg cgt tac ttt gaa ttt tcc acg ttt tta ctt tct ttg tct ctc atc	268
Leu Arg Tyr Phe Glu Phe Ser Thr Phe Leu Leu Ser Leu Ser Leu Ile	
-20	-15
act tac tgc ttt tgg gac ccc ccc cat cgg ggt tca cat tcc ctc tcc	316
Thr Tyr Cys Phe Trp Asp Pro Pro His Arg Gly Ser His Ser Leu Ser	
-5	1
cta gag cac act ccc ttg gat ttc ctc gag tgg ggt ctg ctg cgg	361
Leu Glu His Thr Pro Leu Asp Phe Leu Glu Trp Gly Leu Leu Arg	
15	20
tgaagctttc ccatttttat tgcagattat ttccagaggg tatatagaat tcaggcagct	421
gttttggtt agcacattaa aaatattttc ccc	454

<210> 146
 <211> 1272
 <212> DNA
 <213> Homo sapiens

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<220>
<221> CDS
<222> 32..307

<221> sig_peptide
<222> 32..70
<223> Von Heijne matrix
score 4.2
seq MLFSLSLLSNLNQ/IG

<221> polyA_signal
<222> 1240..1245

<221> polyA_site
<222> 1261..1272

<400> 146
gtcagggtgc accgcccttt ggtccccgag c atg ctg ttt tct ctc agc ctt      52
Met Leu Phe Ser Leu Ser Leu
-10
ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac      100
Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His
-5 1 5 10
att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa      148
Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln
15 20 25
caa cta cag cag cag cct tgc gct aac aaa aaa gca gga aaa atc cac      196
Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His
30 35 40
aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa      244
Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys
45 50 55
cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca      292
Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser
60 65 70
cca ttt cta gct tgc tgaaccccaa aactaatctc caagaaggag aagcttctct      347
Pro Phe Leu Ala Cys
75
cgcagccgga gcaggtccct ttctagagat aggagaagag agagatcgct gtctcgggag      407
agaaatcaca agcgcgtccc atcctctctc aggtctcgta gtcgatttag gtcaaatgaa      467
aggaaataga agacagtttg caagagaagt ggtgtacagg aaattacttc atttgacagg      527
agtatgtaca gaaaattcaa gttttgtttg agacttcata agcttggtgc atttttaaga      587
tgttttagct gttcaaatct gtttgctctc tgaacacagt acacaaaagt gtaattctct      647
atggtttgaa atggatcata cgaggcatgt aataccaaga attgttaact tacaatgttc      707
ccttaagcaa aattgaattt gctttgaact tttagttatg cacagactga taataaacct      767
ctaaacctgc ccagcggaag tgtgtttttt tttaaattta aatacagaaa caactggcaa      827
aaattgaact aagatttact tttttttcca tagctgggat ataggctgca gctatagttg      887
aacaagcagt ctttaaaaac tgctgtgaaa cacaggccat cagggaaaaac gaaatgctgc      947
actattaagt tagaggtttt tgaaaaatcc aactctcacc ctgggcagag gttgcctagt      1007
tggtatagaa tgtttaagttt caagaaagt tacccttgc ttaggtcgta agttccttat      1067
ttgattgcgc tataatggata catggctggt cgtgacattc ttatgtgca aatttgtagt      1127
ttcaaaaaatg tctctgcagat ttaagggtac attgtagagc cgaactttga gttactgtgc      1187
aagatttttt ttcatgctgt cattttgtaat atgtttttgt agaactcctg ggattaaaag      1247
tttggttaca gattaaaaaa aaaaa
1272

<210> 147
<211> 804
<212> DNA
<213> Homo sapiens

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09972360.101501

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<220>
<221> CDS
<222> 114..734

<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
      score 5.2
      seq LLFDLVCFECQS/DD

<221> polyA_signal
<222> 768..773

<221> polyA_site
<222> 793..804

<400> 147
ccaacaccag gaagagctcg aagagcagcc agtggttcgg cttgtgccct gtatacttga      60
agctgccaaa caagtacggt agttctgaaa atccagaatg gcttgatgtt tac atg      116
                                Met
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att      164
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile
-40                                -35                                -30
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac      212
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp
-25                                -20                                -15                                -10
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt      260
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu
                                -5                                1                                5
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc      308
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala
10                                15                                20
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta      356
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val
25                                30                                35
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa      404
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu
40                                45                                50                                55
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa      452
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu
60                                65                                70
act aaa agg act gat tta acc caa gat gat ctc cac ttg aaa atc tta      500
Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu
75                                80                                85
aag gat att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca      548
Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr
90                                95                                100
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag      596
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln
105                                110
aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg      644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val
120                                125                                130                                135
gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct      692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala
140                                145                                150
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act      734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155                                160                                165
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgaaa      794
aaaaaaaaaa
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<213> Homo sapiens

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<222> 780..785

<221> polyA_site
<222> 791..802

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tgctgcaaga tctgttatcc gctctgtggt ttgtgtatcc ttgtgtcctg tgtgtgtggc 180
tgtgtgtggc ttggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc 231
Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala
1 5 10
ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc 279
Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe
15 20 25
caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa 327
Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln
30 35 40
ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata 375
Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile
45 50 55
aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg 423
Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val
60 65 70 75
aac cac ctc aaa gcc aat gtt aag tca gct gca gac ttg att agc ctg 471
Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu
80 85 90
cct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat 519
Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn
95 100 105
act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg 567
Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val
110 115 120
gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag 615
Asp Glu His Lys Lys Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln
125 130 135
cac ttc ttg aag gag act cct gga agc aac cag atc att ccg tca cct 663
His Phe Leu Lys Glu Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro
140 145 150
tca gcc aca tca gaa ctt gac aat aaa acc cac agt gag aat ttg aaa 711
Ser Ala Thr Ser Glu Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys
160 165 170
cag atg ggt gat aga tct gcc act ctg aaa aga cag tct ttg gac caa 759
Gln Met Gly Asp Arg Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln
175 180 185
gtc acc aac aga aca gat aca gta aaa atc caa aaa aaa aaa a 802
Val Thr Asn Arg Thr Asp Thr Val Lys Ile Gln Lys Lys Lys
190 195 200

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 <222> 38..148
 <223> Von Heijne matrix
 score 7.3
 seq LLSACLVTWGLG/EP

<221> polyA_signal
 <222> 1452..1457

<221> polyA_site
 <222> 1478..1490

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 Met Pro His Ser Ser Leu
 -35
 cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc cag aag gca gcc 103
 His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala
 -30 -25 -20
 ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg ggg cta gga gag 151
 Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu
 -15 -10 -5 1
 cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg 199
 Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu
 5 10 15
 cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg 247
 Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu
 20 25 30
 cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg 295
 Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr Val Arg
 35 40 45
 gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg ttg ctg ctg tcc 343
 Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu Ser
 50 55 60 65
 atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc ccg ccc ttc act 391
 Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro Phe Thr
 70 75 80
 tgg atg ctt gcc ctc ctg ggc ctc tgc cag gca ctg aac atc ctc ctg 439
 Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu
 85 90 95
 ggc ctc aag ggc ctg gcc cca gct gag atc tct gca gtg tgt gaa aaa 487
 Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys
 100 105 110
 ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca tat tac atc gga 535
 Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly
 115 120 125
 tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg att cga act tac 583
 Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr
 130 135 140 145
 aat cag cat tac aac aac ctg cta cgg ggt gca gtg agc cag cgg ctg 631
 Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu
 150 155 160
 tat att ctc ctc cca ttg gac tgt ggg gtg cct gat aac ctg agt atg 679

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Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met	
165 170 175	
gct gac ccc aac att cgc ttc ctg gat aaa ctg ccc cag cag acc ggt	727
Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly	
180 185 190	
gac cgt gct ggc atc aag gat cgg gtt tac agc aac agc atc tat gag	775
Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu	
195 200 205	
ctt ctg gag aac ggg cag cgg gcg ggc acc tgt gtc ctg gag tac gcc	823
Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala	
210 215 220 225	
acc ccc ttg cag act ttg ttt gcc atg tca caa tac agt caa gct ggc	871
Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly	
230 235 240	
ttt agc cgg gag gat agg ctt gag cag gcc aaa ctc ttc tgc cgg aca	919
Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr	
245 250 255	
ctt gag gac atc ctg gca gat gcc cct gag tct cag aac aac tgc cgc	967
Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Cys Arg	
260 265 270	
ctc att gcc tac cag gaa cct gca gat gac agc agc ttc tgc ctg tcc	1015
Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser	
275 280 285	
cag gag gtt ctc cgg cac ctg cgg cag gag gaa aag gaa gag gtt acc	1063
Gln Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val Thr	
290 295 300 305	
gtg ggc agc ttg aag acc tca gcg gtg ccc agt acc tcc acg atg tcc	1111
Val Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Met Ser	
310 315 320	
caa gag cct gag ctc ctc ctc agt gga atg gga aag ccc ctc cct ctc	1159
Gln Glu Pro Glu Leu Leu Leu Ser Gly Met Gly Lys Pro Leu Pro Leu	
325 330 335	
cgc acg gat ttc tct tgagaccag ggtcaccagg ccagagcctc cagtgggtctc	1214
Arg Thr Asp Phe Ser	
340	
caagcctctg gactgggggc tctcttcagt ggctgaatgt ccagcagagc tatttccttc	1274
cacagggggc cttgcaggga aggggtccagg acctgacatc ttaagatgcg tctgtgcccc	1334
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<221> polyA_site	
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Met Pro Ser Glu Gly Arg Cys Trp Glu	
1 5	
acc ttg aag gcc cta cgc agt tcc gac aaa ggt cgc ctt tgc tac tac	100
Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr Tyr	
10 15 20 25	
cgc gac tgg ctg ctg cgg cgc gag gat gtt tta gaa gaa tgt atg tct	148

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Arg	Asp	Trp	Leu	Leu	Arg	Arg	Glu	Asp	Val	Leu	Glu	Glu	Cys	Met	Ser		
				30						35				40			
ctt	ccc	aag	cta	tct	tct	tct	tct	gga	tgg	gtg	gta	gag	cac	gtc	cta		196
Leu	Pro	Lys	Leu	Ser	Ser	Tyr	Ser	Gly	Trp	Val	Val	Glu	His	Val	Leu		
			45					50					55				
ccc	cat	atg	cag	gag	aac	caa	cct	ctg	tct	gag	act	tcg	cca	tcc	tct		244
Pro	His	Met	Gln	Glu	Asn	Gln	Pro	Leu	Ser	Glu	Thr	Ser	Pro	Ser	Ser		
		60					65					70					
acg	tca	gct	tca	gcc	cta	gat	caa	ccc	tca	ttt	gtt	ccc	aaa	tct	cct		292
Thr	Ser	Ala	Ser	Ala	Leu	Asp	Gln	Pro	Ser	Phe	Val	Pro	Lys	Ser	Pro		
	75					80					85						
gac	gca	agc	tct	gcc	ttt	tcc	cca	gcc	tcc	cct	gca	aca	cca	aat	gga		340
Asp	Ala	Ser	Ser	Ala	Phe	Ser	Pro	Ala	Ser	Pro	Ala	Thr	Pro	Asn	Gly		
	90				95					100				105			
acc	aag	ggc	aaa	aaa	aaa	aaa											361
Thr	Lys	Gly	Lys	Lys	Lys	Lys											
				110													

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<221> polyA_site
 <222> 591..605

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Ser	Leu	Pro	Gln	Ala	Leu	Trp	Phe	Gln	Phe	Phe	Tyr	His	Ser	Gly			
	1				5				10					15			
agc	tcc	cta	gaa	tct	cct	gga	atg	ctt	aat	gga	cct	ttc	cag	cac	cga		95
Ser	Ser	Leu	Glu	Ser	Pro	Gly	Met	Leu	Asn	Gly	Pro	Phe	Gln	His	Arg		
				20					25					30			
aat	tca	aga	att	atg	act	cat	cgg	tca	gca	gaa	aag	tgaggatacc					141
Asn	Ser	Arg	Ile	Met	Thr	His	Arg	Ser	Ala	Glu	Lys						
				35					40								
ttttcttaac	ctaactgctt	ccctgcagt	ttctcaca	aa	tctactctt	tatatcttag											201
catatgtagc	ttctcaggat	gttaattctg	ttctctctgt		gttggtgtct	gagcaccag											261
aaggtagagc	caggggcact	tataaaccag	gagcattatt		tgacaggcac	ttaaagaaaga											321
cactggctac	gtaatccag	cactttggga	ggctgaggcg		gatggatcac	atgaggctcag											381
gagttcgaga	ccagcctggc	cagcatgggtg	aaaccctgtc		tctactaaaa	atacaaaaat											441
tagctgggtg	tggttgacaca	cgccgtgtaat	cccagctacc		tgaggaggctg	aggcaggaga											501
atcgcttgaa	cttggggaggc	ggaggttgca	gtgagcctag		attttgccat	tgcactccag											561
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<210> 152
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 <212> DNA
 <213> Homo sapiens

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 <222> 33..185

<221> sig_peptide
 <222> 33..80
 <223> Von Heijne matrix

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score 3.7
seq IALTLIPSMLSRA/AG

<221> polyA_signal
<222> 570..575

<221> polyA_site
<222> 586..591

<400> 152
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Met Leu Arg Ile Ala Leu Thr
-15
ctc atc cca tct atg ctg tca agg gct gct ggt tgg tgc tgg tac aag 101
Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys
-5 1 5
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg 149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp
10 15 20
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact 195
Asn Lys Lys Gly Asn Val Leu Gln Leu Pro Asn Phe
25 30 35
aatctcagat tggcagtgaa agtcaaaatg ttgccaaata tttatttcctt ttgcctaagt 255
ttggctacccc ggttcaattg ctttttattt ttaatgtctt gactcttcag agtctgtacc 315
tcaaaagaac aatgagaaca tttgctttgc tttctgtcga atccctaacc tcaacaatct 375
atactcggac tgtccagttc tctcctgtg ctatctttct tctatccaa gtagaatgta 435
tgccaggagc tccttccttc tagcaatttc tactaaaatg tccaagtaga atgtttcctt 495
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ctggctgtgc tatcaataaa aagatgaaag caaaaa 591

<210> 153
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<212> DNA
<213> Homo sapiens

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<222> 184..915

<221> sig_peptide
<222> 184..237
<223> Von Heijne matrix
score 3.5
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<221> polyA_signal
<222> 1119..1124

<221> polyA_site
<222> 1139..1150

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tttgaaacagg atagtaggta tccggagtcg attgagggcc agagcaggca ctgggggttcg 120
gatcctgggc aaagtgttccc acgttgaggg tctcgaggac gcctagatct ctttcccagg 180
gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag 228
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
-15 -10 -5
gcg atc ggt gct gat tgc gcg cga ttt gag gag ctg ctg ctg cag gcc 276
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
1 5 10

0397350.T01581

tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa	324
Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln	
15 20 25	
atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg	372
Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly	
30 35 40 45	
aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc	420
Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Ala	
50 55 60	
gac gtg acc gag gag gag ctg ctt cag atg cta gag gag gac caa gct	468
Asp Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala	
65 70 75	
ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat	516
Gly Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp	
80 85 90	
gca aaa ggc cag gga tgt acc gcc tac gac gta gct gtc aac agc gac	564
Ala Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asn	
95 100 105	
ttc tac cgg agg atg cag aac agc gat ttc ttg cgg gag ctc gtg atc	612
Phe Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile	
110 115 120 125	
acc atc gcc agg gag ggc ctt gag gac ata tac aac ttg cag ctg aat	660
Thr Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn	
130 135 140	
ccg gaa tgg cgc atg atg aag aac cgg cca ttc atg ggc tcc atc tcg	708
Pro Glu Tyr Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser	
145 150 155	
cag cag aac atc cgc tcg gag cag cgt cct cgg atc cag gag ctg ggg	756
Gln Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly	
160 165 170	
gac ctg tac acg ccc gcc ccc ggg aga gct gag tca ggg cct gaa aag	804
Asp Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys	
175 180 185	
cct cac ctg aac ctg tgg ctg gaa gcc ccc gac ctc ctc ttg gcc gaa	852
Pro His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu	
190 195 200 205	
gtt gac ctc ccc aaa ctg gat gga gcc ctg ggg ctg tcg ctg gag atc	900
Val Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile	
210 215 220	
ggg aga acc gcc tgg tgatgggggg cccccagcag ctgtatcatc tagacgctta	955
Gly Arg Thr Ala Trp	
225	
tatccccgcg cagatcaact ctcctgagag caaggcagcc ttccaccgga agaaaaagca	1015
attaatgggt gccatgcgcg ttcctgccgt gcctttctga tcagggtgtc tccttggtgc	1075
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tttaaaaaaa aaaaa	1150

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<211> 1513

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 58..1116

<221> sig_peptide

<222> 58..159

<223> Von Heijne matrix

score 4

seq IAVLYLHLYDVFG/DP

<221> polyA_signal

<222> 1486..1491

<221> polyA_site

<222> 1504..1513

<400> 154

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Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr	
-30 -25 -20	
act ggc tgg gca ggt att gct gtg ctt tac tta cat ctt tat gat gta	153
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val	
-15 -10 -5	
ttt ggg gac cct gcc tac cta cag tta gca cat ggc tat gta aag caa	201
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln	
1 5 10	
agt ctg aac tgc tta acc aag cgc tcc atc acc ttc ctt tgt ggg gat	249
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp	
15 20 25 30	
gca ggc ccc ctg gca gtg gcc gct gtg cta tat cat aag atg aac aat	297
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn	
35 40 45	
gag aag cag gca gaa gat tgc atc aca cgg cta att cac cta aat aag	345
Gly Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys	
50 55 60	
att gat cct cat gct cca aat gaa atg ctc tat ggg cga ata ggc tac	393
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr	
65 70 75	
atc tat gct ctt ctt ttt gtc aat aag aac ttt gga gtg gaa aag act	441
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr	
80 85 90	
cct caa agc cat att cag cag att tgt gaa aca att tta acc tct gga	489
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly	
95 100 105 110	
gaa aac cta gct agg aag aga aac ttc acg gca aag tct cca ctg atg	537
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met	
115 120 125	
tat gaa tgg tac cag gaa tat tat gta ggg gct gct cat ggc ctg gct	585
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala	
130 135 140	
gga att tat tac tac ctg atg cag ccc agc ctt caa gtg agc caa ggg	633
Gly Ile Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly	
145 150 155	
aag tta cat agt ttg gtc aag ccc agt gta gac tac gtc cag ctg	681
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu	
160 165 170	
aaa ttc cct tct ggc aat tac cct cca tgt ata ggt gat aat cga gat	729
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp	
175 180 185 190	
ctg ctt gtc cat tgg tgc cat ggc gcc cct ggg gta atc tac atg ctc	777
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu	
195 200 205	
atc cag gcc tat aag gta ttc aga gag gaa aag tat ctc tgt gat gcc	825
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala	
210 215 220	
tat cag tgt gct gat gtg atc tgg caa tat ggg ttg ctg aag aag gga	873
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly	
225 230 235	
tat ggg ctg tgc cac ggt tct gca ggg aat gcc tat gcc ttc ctg aca	921

Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
 240 245 250
 ctc tac aac ctc aca cag gac atg aag tac ctg tat agg gcc tgt aag 969
 Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
 255 260 265 270
 ttt gct gaa tgg tgc tta gag tat gga gaa cat gga tgc aga aca cca 1017
 Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
 275 280 285
 gac acc cct ttc tct ctc ttt gaa gga atg gct ggg aca ata tat ttc 1065
 Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
 290 295 300
 ctg gct gac ctg cta gtc ccc aca aaa gcc agg ttc cct gca ttt gaa 1113
 Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
 305 310 315
 ctc tgaaggata gcatgccacc tgcaactcac tgcatagcc tttctgtata 1166
 Leu
 ttcaaaacca agctaaagtgc ttccgttgct ttccaaggaa acaagagtc aaactgtgga 1226
 ctgtgatttt ttagcttttt tcagaattta tcttccattc agttcccttc cattatcatt 1286
 tacttttact tagaagatgc caaggaagtc tttaactttt aatttccatt tcttctctaaa 1346
 gggagagtga gtgatatgta cagtgttttg agattgtata catatatccc agaacttgga 1406
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 gaaactcaat acagataaag ataaatatgt gactattaaa aaaaaaa 1513

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 <212> DNA
 <213> Homo sapiens

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 <222> 327..416

 <221> polyA_site
 <222> 404..417

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 tgttgttatc cttggatgta caaaaaattc agaaaatgat ctctgtagat attctgtttt 180
 atttttggtca tctttagaag ttatcaggaa tgtgttttaa acaagaagag aacttttcta 240
 aggaatgata catagaaaag attttatttt aaaaatgagtt gtaaaagcttg tgtttctttg 300
 ttgctgcaag ctatctgccc aagtta atg caa atg gac aca ttt ttt atg tca 353
 Met Gln Met Asp Thr Phe Phe Met Ser
 1 5
 gaa aaa cac aca cac aca cac aca cat ata cac aca cac aca cga aaa 401
 Glu Lys His Thr His Thr His His Ile His Thr His Thr Arg Lys
 10 15 20 25
 aca aaa aaa aaa aaa a
 Thr Lys Lys Lys Lys
 30

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 <221> sig_peptide

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 score 4.9
 seq PSLAAGLLFGSLA/GL

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 aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt 107
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35
 ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa 155
 Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys
 -30 -25 -20
 gca ggc agc gtg cgc tcc ctg gct gca ggg ctg ctg ttt ggc agt cta 203
 Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
 -15 -10 -5
 gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg 251
 Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
 1 5 10 15
 gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg 299
 Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
 20 25 30
 ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc 347
 Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
 35 40 45
 agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc 395
 Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
 50 55 60
 cat tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca 448
 His
 tcttccacta ttttcaatat attaagagaa ataagtcgac catttttgca tctgacattt 508
 tacctaaaaa aaaagacacc aaacttgcca gagaggtgga aaatcagtcg tgattacaaa 568
 cctacagagg tggcgagtat gtaacacaag agctt 603

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 <212> DNA
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<220>
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 <222> 2..163

<221> polyA_signal
 <222> 488..493

<221> polyA_site
 <222> 511..522

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 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15
 ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat 97
 Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa 145
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 tcc tcc ggg cac ctt cct nntgaaggag tggctaagggt tggacaatac 193
 Ser Ser Gly His Leu Pro

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50

acgttctactg	cagctgctgt	cgggggccgtg	tttggcctca	ccacctgcat	cagcgcccat	253
gtccgcgaga	agcccgaaga	ccccctgaac	tacttccccg	gtggctgcgc	cnggagggct	313
gactctggga	gcacgcacgc	acaactacgg	gattggcgcc	gcccgctgcg	tgactcttgg	373
catagcgccc	tccctggta	agatgggccc	gctggagggc	tgggaggtgt	ttgcaaaacc	433
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ttctgtgtct	gtgtgtgaaa	aaaaaaaaa				522
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	Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr					
	-20 -15 -10					
gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg		99				
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu						
-5 1 5						
cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag		147				
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu						
10 15 20						
cgg ggc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct		195				
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser						
25 30 35 40						
ctc cct gca ttg cct cnt ggc cag ctg caa ccg cct cct att aca		243				
Leu Pro Ala Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr						
45 50 55						
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac		291				
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr						
60 65 70						
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc		339				
Phe Asp Val Lys Glu Tyr Asp Arg Ala His Phe Leu His Gly Cys						
75 80 85						
aat agc aag aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg		387				
Asn Ser Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val						
90 95 100						
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt		435				
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe						
105 110 115 120						
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact		485				
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys						
125 130						
gaatgaatgt actttataca tagcaataat aaaaaaaaga tatcataaat aaagttaaaa		545				
aggatggtag agaagaaaaat attcttagga atgactaaca ggataagtaa caacctgatt		605				
atttatttac tttaggttat ataaggttct tcatgcctgt gaattaatat tattgtgtaa		665				
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattata tcatgtttat		725				
agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca		785				
agnaaaccaa ctttaactg tattgaataa taagtacaat ttattatttt actttgaaac		845				
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[illegible]

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 Ser Val Met Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe
 180 185 190
 ggc aaa tac ggc aga aac gcc tac gtg tagcagctct ggcctgtggg 723
 Gly Lys Tyr Gly Arg Asn Ala Tyr Val
 195 200
 ccccgctgtc ttcccaatgc cccaaggaga ggggacctgg ccgggggcca ttcccctata 783
 gtaacctcag gggccggcca cgcccgctc ccgtagcccc gccccggcca cggcccgctg 843
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 ctctgaggct ggatccctca tcttctgacc ctgggttctg ggtgtgaa gggacggtgt 963
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 aaaaaaaaaa aaaaaaaaaa 1041

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 <222> 103..294

 <221> sig_peptide
 <222> 103..243
 <223> Von Heijne matrix
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 taacattaac ttccctaagt aataatcaat gaaagaaatt ct atg cat ggt ttt 114
 Met His Gly Phe
 -45
 gaa ata ata tcc ttg aaa gag gaa tca cca tta gga aag gtg agt cag 162
 Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly Lys Val Ser Gln
 -40 -35 -30
 ggt cct ttg ttt aat gtg act agt ggc tca tca tca cca gac acc tgg 210
 Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser Pro Val Thr Trp
 -25 -20 -15
 ttg ggc cta ctc tcc ttc cag aac ctg cat tgc ttc cca gac ctc ccc 258
 Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe Pro Asp Leu Pro
 -10 -5 1 5
 act gag atg cct cta aga gcc aaa gga gtc aac act tgagcctagg 304
 Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
 10 15
 gtgggctaca acaaaagatt ctaatttacc ttgcttcatc taggtccagg ccccaagtag 364
 cttgtctgag gaacttaaaa agtagctgtt atttattgta ttgtataagc taaaaacatt 424
 tatttttgtt gaatcgaaac aattccatgt agcaatcttt ttctgtgtca cggtgtttgt 484
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 taacaggcaa agtt 558

 <210> 161
 <211> 730
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 <213> Homo sapiens

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 <222> 81..518

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<221> sig_peptide
 <222> 81..173
 <223> Von Heijne matrix
 score 3.9
 seq ILFHGVFYAGGFA/IV

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 attttcaaga gagggtgtgct atg atg tgg caa aag tat gca gga agc agg cgg 113
 Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
 -30 -25
 tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc 161
 Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
 -20 -15 -10 -5
 ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg 209
 Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
 1 5 10
 gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag 257
 Ala Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu
 15 20 25
 gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc 305
 Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
 30 35 40
 atc gac agg gaa aac ttc gtg gac att gtt gat gcc aag ttg aag att 353
 Ile Asp Arg Glu Asn Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile
 45 50 55 60
 cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc 401
 Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
 65 70 75
 aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag 449
 Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
 80 85 90
 ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 497
 Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
 95 100 105
 ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 548
 Gly Asp Glu Val Lys Lys Glu
 110 115
 ctagtccatc cttccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg 608
 acagacactc ctgcaaccca gttttccagc caccagtggg atgatgggtat gtgccagcag 668
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 tg 730

<210> 162
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 66..326

<221> polyA_signal
 <222> 1066..1071

<221> polyA_site
 <222> 1087..1098

<400> 162
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1 5 10 15
ttg ccc cat ggt gtc ctg gga ccc aga gca aca gga tct gtc acc cac 158
Leu Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His
20 25 30
ctc tct ctt ctc ccc cag atc aag caa cgt gcc tca gag gct ttg ccc 206
Leu Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro
35 40 45
gaa ttg ctt cgt cct gtc acc ccc atc acc aat ttt gag ggc agc cag 254
Glu Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln
50 55 60
tct cag gac cac agt gga atc ttt ggc ctg gta aca aac ctg gaa gag 302
Ser Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu
65 70 75
ctg gag gtg gac gat tgg gag ttc tgagcctctg caaactgtgc gcattctcca 356
Leu Glu Val Asp Asp Trp Glu Phe
80 85
gccaggggatg cagagggccac ccagaggccc ttcttgaggg ccggccacat tcccgccttc 416
ctgggagcat tgggtagaaa ggacattctt ccaggaaagt tgactgtggt ctgattggga 476
aagaaaaatc tggagagata cttcactgct ccaaggcttt tgagacacaa gggaatctca 536
acaaccaggg atcaggaggg tccaaagccg acattcccag tcctgtgagc tcagggtgacc 596
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tcagagacgc aaaaaaaa aa 1098

<210> 163
<211> 346
<212> DNA
<213> Homo sapiens

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<222> 170..289

<221> sig_peptide
<222> 170..250
<223> Von Heijne matrix
score 3.6
seq LTLLLITPSPSPL/LF

<400> 163
ccatttgagc cccaccacgg aggttatgtg gtcccaaaag gaatgatggc caagcaatta 60
atttttcttc ctatgttctta gcttgcttct gcattgatgg gctttacaca actggcattt 120
agtctgcatt acacaaatag acactaattt atttgaaca agcagcaaaa atg aga act 178
Met Arg Thr
-25
tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act ctg ctt cta 226
Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Leu Leu Leu
-20 -15 -10
atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt ctg tcc ctc 274
Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly Leu Ser Leu
-5 1 5
aga tca gca atg tct tagccccctc cctctcttcc attccttctc gttggtaact 329
Arg Ser Ala Met Ser

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10
attttcttcta acttttta 346

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<211> 685
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 36..497

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 663..685

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Met Gly Ser Leu Ser Gly
1 5

ctg cgc ctg gca gca gga agc tgt ttt agg tta tgt gaa aga gat gtt 101
Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val
10 15 20

tcc tca tct cta agg ctt acc aga agc tct gat ttg aag aga ata aat 149
Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn
25 30 35

gga ttt tgc aca aaa cca cag gaa agt ccc gga gct cca tcc cgc act 197
Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr
40 45 50

tac aac aga gtg cct tta cac aaa cct acg gat tgg cag aaa aag atc 245
Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile
55 60 65 70

ctc ata tgg tca ggt cgc ttc aaa aag gaa gat gaa atc cca gag act 293
Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr
75 80 85

gtc tcg ttg gag atg ctt gat gct gca aag aac aag atg cga gtg aag 341
Val Ser Leu Glu Met Leu Asp Ala Ala Lys Asn Lys Met Arg Val Lys
90 95 100

agc agc tat cta atg att gcc ctg acg gtg gta gga tgc atc ttc atg 389
Ser Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met
105 110 115

gtt att gag ggc aag aag gct gcc caa aga cac gag act tta aca agc 437
Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser
120 125 130

ttg aac tta gaa aag aaa gct cgt ctg aaa gag gaa gca gct atg aag 485
Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu Ala Ala Met Lys
135 140 145 150

gcc aaa aca gag tagcagaggt atccgtgttg gctggatttt gaaaatccag 537
Ala Lys Thr Glu
gaattatggt ataacgtgcc tgtattaaaa aggatgtggt atgaggatcc atttcataaa 597
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<221> CDS
 <222> 18..320

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 <221> polyA_site
 <222> 542..554

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 Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
 15 20 25
 gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa 146
 Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
 30 35 40
 aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga 194
 Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
 45 50 55
 att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc 242
 Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly
 60 65 70 75
 tgt gcc tac aaa aaa ggc atc tgt gcg atg tgt ggn aaa aaa gtt ttg 290
 Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu
 80 85 90
 gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt 340
 Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val
 95 100
 ctggctttct aaatgatttt accttctgcc ttgaattttc aaggcataga tgtcaactta 400
 cagaataaca tgttttaaga taattaaagt taaaccagag aatttgattg ttactcattt 460
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 <212> DNA
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 <221> CDS
 <222> 71..1438

 <221> sig_peptide
 <222> 71..136
 <223> Von Heijne matrix
 score 3.5
 seq AAPVAAGLGPVIS/RP

 <221> polyA_signal
 <222> 1644..1649

 <221> polyA_site
 <222> 1665..1678

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 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val

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gac ttg gct tct ctg gac cct agg gtc act gtg tgt gac atg gcc cag      1117
Asp Leu Ala Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln
      315      320      325
gtt cct ttg gag gat gag tct gtg gat gtg gct ttt tgc ctt tca      1165
Val Pro Leu Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser
      330      335      340
ctg atg gga acc aac atc agg gac ttc cta gag gag gca aat aga gta      1213
Leu Met Gly Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val
      345      350      355
ctg aag cca ggg ggt ctc ctg aaa gtg gct gag gtc agc agc cgc ttt      1261
Leu Lys Pro Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe
      360      365      370
gag gat gtt cga acc ttt ctg cgg gct gtg acc aag cta ggc ttc aag      1309
Glu Asp Val Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys
      380      385      390
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc      1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe
      395      400      405
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc      1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly
      410      415      420
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgt atcttccttg      1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg
      425      430
agaggggagg agatctcaaa actccaggct cagaactgtg aagactgttt ccggcctggc      1518
tgtgagccaa gacctgggtc ctggtggacc ctgaggacaa agtgtgataa aacctctggc      1578
tcagacttgc tctactgaag gcttcttggt tataaatgac ataaagtac tggggctagc      1638
taaacataaa agagtattatt gtgaggaaaa aaaaaaaaaa      1678

<210> 167
<211> 494
<212> DNA
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<222> 25..318

<221> sig_peptide
<222> 25..75
<223> Von Heijne matrix
      score 7.4
      seq FFLLLQFFLRIDG/VI

<221> polyA_signal
<222> 452..457

<221> polyA_site
<222> 482..494

<400> 167
aggctgagtg tgaagattag agta atg cct tct agc ttt ttc ctg ctg ttg      51
      Met Pro Ser Ser Phe Phe Leu Leu Leu
      -15      -10
cag ttt ttc ttg aga att gat ggg gtg ctt atc aga atg aat gac acg      99
Gln Phe Phe Leu Arg Ile Asp Gly Val Leu Ile Arg Met Asn Asp Thr
      -5      1      5
aga ctt tac cat gag gct gac aag acc tac atg tta cga gaa tat acg      147
Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr Met Leu Arg Glu Tyr Thr
      10      15      20
tca cga gaa agc aaa att tct agt ttg atg cat gtt cca cct tcc ctc      195

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Ser Arg Glu Ser Lys Ile Ser Ser Leu Met His Val Pro Pro Ser Leu
 25 30 35 40
 ttc acg gaa cct aat gaa ata tcc cag tat tta cca ata aag gaa gca 243
 Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr Leu Pro Ile Lys Glu Ala
 45 50 55
 gtt tgt gag aag cta ata ttt cca gaa aga att gat cct aac cca gca 291
 Val Cys Glu Lys Leu Ile Phe Pro Glu Arg Ile Asp Pro Asn Pro Ala
 60 65 70
 gac tca caa aaa agt aca caa gtg gaa taaaatgtga tacaacatat 338
 Asp Ser Gln Lys Ser Thr Gln Val Glu
 75 80
 actcactatg gaatctgact ggacaccttg gctatttgta aggggttatt tttattatga 398
 gaattaattg cctgttttat gtacagattt tctgtagcct taaaggaaaa aaaaaataag 458
 atcgttacag gcaggtttca ctcaaaaaaa aaaaaa 494

<210> 168
 <211> 714
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 84..332

<221> sig_peptide
 <222> 84..170
 <223> Von Heijne matrix
 score 5.2
 seq PCYYLGLPQRALA/SV

<221> polyA_site
 <222> 702..714

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 cctatctctt ctgctggctg ggctcaatgc cgcgggtgag cgctcgccgc aggcgtctcc 60
 tacccttgag tgatgtgcct tga atg acg ctg ctt tca ttc gct gct ttc acg 113
 Met Thr Leu Leu Ser Phe Ala Ala Phe Thr
 -25 -20
 gct gct ttc tcc gtc ctc ccc tgt tac tac ctt ggg ctg ttt cag cgg 161
 Ala Ala Phe Ser Val Leu Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg
 -15 -10 -5
 gcg ctc gcg tcg gtc ttc gac cca ctt tgc gtt tgt tca cgt gtc ctc 209
 Ala Leu Ala Ser Val Phe Asp Pro Leu Cys Val Cys Ser Arg Val Leu
 1 5 10
 ccg aca cct gta tgt acc ttg gtc gca aca caa gcc gaa aaa ata tta 257
 Pro Thr Pro Val Cys Thr Leu Val Ala Thr Gln Ala Glu Lys Ile Leu
 15 20 25
 gag aat ggg ccc tgt cca acc aag gag gcg gcc cag ctt gtc ggg aag 305
 Glu Asn Gly Pro Cys Pro Thr Lys Glu Ala Ala Gln Leu Val Gly Lys
 30 35 40 45
 ggc agc gtt tcc gcc aga aat gct tcg tgaaaggcac ttgagggacc 352
 Gly Ser Val Ser Ala Arg Asn Ala Ser
 50
 ttgacgacat cctcaacagg ccttgtaggg aatgccagaa gaagcagtc ttggccgggc 412
 ggggtggctc atgcctgtgg tccagcact ttgggagccc ggggcgggc gatcacctga 472
 ggctcggagg tccagaccag cctgaccgac atggagaaac ccgcctnta ctagaataac 532
 aaaactagcc ggggtgtggt gcgcacgcct gtatgccag ctactcggga gggtagggca 592
 ggagacgttc ttgaaccagg gagcgaggat ttgtgtgag ccgagatcgc gccattgcac 652
 tccagcctgg gcacgccaaag agcgaaactc cgtctcaaaa aaaaaaaaga aaaaaaaa 712
 aa 714

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 <212> DNA
 <213> Homo sapiens

<220>
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<221> sig_peptide
 <222> 32..100
 <223> Von Heijne matrix
 score 7.4
 seq VLLLAALPPVLLP/GA

<221> polyA_signal
 <222> 770..775

<221> polyA_site
 <222> 793..805

<400> 169
 cctcttttcag cccgggagtcg ccccagcagg g atg ggc gac aag atc tgg ctg 52
 Met Gly Asp Lys Ile Trp Leu
 -20
 ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct 100
 Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Val Leu Leu Pro
 -15 -10 -5
 ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt acc 148
 Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Thr
 1 5 10 15
 ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag 196
 Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
 20 25 30
 gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta gat 244
 Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
 35 40 45
 att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa 292
 Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
 50 55 60
 caa aga aas tca gat gga gtt cac act gta gag act gaa gtt ggt gat 340
 Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
 65 70 75 80
 tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg 388
 Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
 85 90 95
 att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa 436
 Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
 100 105 110
 caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg 484
 Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
 115 120 125
 aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta 532
 Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
 130 135 140
 agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt 580
 Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg
 145 150 155 160
 gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct 628
 Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser
 165 170 175

atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat 676
 Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr
 180 185 190
 atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act 718
 Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr
 195 200 205
 taaaactcca aactagagta cgtaacattg aaaaatgagg cataaaaatg caataaactg 778
 ttacagtcac gaccaaaaaa aaaaaaa 805

 <210> 170
 <211> 787
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 26..481

 <221> sig_peptide
 <222> 26..88
 <223> Von Heijne matrix
 score 4.4
 seq AVASSFFCASCASF/AV

 <221> polyA_signal
 <222> 755..760

 <221> polyA_site
 <222> 775..787

 <400> 170
 gacagcctgg ataaaggctc acttg atg gct cag ttg gga gca gtt gtg gct 52
 Met Ala Gln Leu Gly Ala Val Val Ala
 -20 -15
 gtg gct tcc agt ttc ttt tgt gca tct ctg ttc tca gct gtg cac aag 100
 Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys
 -10 -5 1
 ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg 148
 Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu
 5 10 15 20
 act tcg acc agc ggc cct ggt ttc cat ctg atg ctg cct ttc atc aca 196
 Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr
 25 30 35
 tca tat aag tct gtg cag acc aca ctg cag aca gat gag gtg aag aat 244
 Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn
 40 45 50
 gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att 292
 Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile
 55 60 65
 gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag 340
 Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys
 70 75 80
 aac tat act gct gac tat gac aag gcc ctg atc ttc aac aag atc cac 388
 Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His
 85 90 95 100
 cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac 436
 His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr
 105 110 115
 att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca 481
 Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser
 120 125 130


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<211> 893
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..810

<221> sig_peptide
<222> 4..279
<223> Von Heijne matrix
      score 6.8
      seq AVMLYTWRSCSR/IP

<221> polyA_signal
<222> 858..863

<221> polyA_site
<222> 881..893

<400> 172
gcc atg atc acg cac gtc acc ctg gaa gat gcc ctg tcc aac gtg gac      48
      Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp
      -90 -85 -80
ctg ctt gaa gag ctt ccc ctc ccc gac cag cag cca tgc atc gag cct      96
Leu Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro
      -75 -70 -65
cca cct tcc tcc atc atg tac cag gct aac ttt gac aca aac ttt gag      144
Pro Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu
      -60 -55 -50
gac agg aat gca ttt gtc acg ggc att gca agg tac att gag cag gct      192
Asp Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala
      -45 -40 -35 -30
aca gtc cac tcc agc atg aat gag atg ctg gag gaa gga cat gag tat      240
Thr Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr
      -25 -20 -15
gcg gtc atg ctg tac acc tgg cgc agc tgt tcc cgg gcc att ccc cag      288
Ala Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln
      -10 -5 1
gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca      336
Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr
      5 10 15
gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat      384
Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr
      20 25 30 35
ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg      432
Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu
      40 45 50
tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg      480
Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu
      55 60 65
acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag      528
Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys
      70 75 80
aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca      576
Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala
      85 90 95
gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tgc      624
Ala Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser
      100 105 110 115
cag aac ctt tcc atg ttc ctg gcc aac cac aac agg atc acc cag tgt      672

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Gln Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys
120 125 130
ctc cac cag caa ctt gaa gtg atc cca ggc tat gag gag ctg ctg gct 720
Leu His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala
135 140 145
gac att gtc aac atc tgt gtg gat tac tac gag aac aag atg tac ctg 768
Asp Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu
150 155 160
act ccc agt gag aaa cat atg ctc ctc aag gta aaa ctc ccc 810
Thr Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
165 170 175
tgaggcgcga cccatggagc ctgggcttac cctctcacct tcttcttatt aaaaatccgt 870
tttaaaaaac aaaaaaaaaa aaa 893

<210> 173
<211> 1475
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 55..459

<221> sig_peptide
<222> 55..120
<223> Von Heijne matrix
score 7.2
seq GLWLALVDGLVRS/SP

<221> polyA_signal
<222> 1444..1449

<221> polyA_site
<222> 1462..1475

<400> 173
caggtccgcga gctacgtgtg ggaccgcgtg ctgacctgtg cgcagatcgt cctc atg 57
Met
cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg gcg ctg gtg gac 105
Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp
-20 -15 -10
ggg cta gtg cga agc agc ccc tcg ctg gac cag atg ttc gac gcc gag 153
Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala Glu
-5 1 5 10
atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc atg atg tcc ttc 201
Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe
15 20 25
atc ttc aac gcc ctc acc tgt gcc ctg ggc ttg ctg tac ttc atc cgg 249
Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg
30 35 40
cga gga aag cag tgt ctg gat ttc act gtc act gtc cat ttc ttt cac 297
Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His
45 50 55
ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc tcg gcg ctg acc 345
Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr
60 65 70 75
tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg gct gtc atc ggg 393
Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly
80 85 90
gag tac ctg tgc atg cgg acg gag ctc aag gag ata ccc ctc aac tca 441
Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn Ser

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95	100	105	
gcc cct aaa tcc aat gtc tagaatcagg ccctttggac atcccgtga			489
Ala Pro Lys Ser Asn Val			
110			
cacttgggcc ccttaacacc ttgggctgct cagaccctcc agatgaggtc cagcccagat			549
ctgagaggaa cccctggaat gtgaagtctc tgttgggtgtg ggagagatag tgagggcctg			609
tcaagaagag caggtagcag tcagcatgac agctgcaaga atgacctctg tctgttgaag			669
ccttgggtatc tgagagggtca ggaaggggac ctctttgagg gtaataacat aattggaacc			729
atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga gaaaaaaat			789
caaggatata tgattggagc aaaccacttc tttagtcatc tgtcttaacct cctcgggaca			849
gctgttacct ttgcagtgtt gccgaatcac agcagttacc tttgcaatgt tgcgaatca			909
cagcagttct gttggagaaa cgcttgggtt ccggatccag agccacagaa agaaatgtag			969
gtgtgaagta ttaggctgct gtcaggggaga ggatggcaga tggaggcatc aagcacaagg			1029
aaaatgcaca acctgtgccc tgttatcacac acgttcatgt gcgcccaga accatagact			1089
ttcttccagt tccttctacc aggtcccatc cctgctgccca gctctcaaca tagcaggcca			1149
taggaccagc agaagaatcc cagtgttgct caaagtctga ccatcataaa gacactgcct			1209
gtcttctagc aatgaccagg caccagctc ccaactggag ccaatttttt ttctgcctt			1269
atttagaatt ctttggcggg aagggtatga tgggttccca gagacaagaa gcccaacctt			1329
ctggcctggg ctgtgctgat agtgcctgagg gagataggaa ttgtctgcta agatttttct			1389
ttgggggtgga gtttctctg tgaggggctt gcagctatcc ttctgtgtga tacaataca			1449
gtattttcca tgaaaaaaa aaaaaa			1475
<210> 174			
<211> 321			
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<222> 48..248			
<221> sig_peptide			
<222> 48..161			
<223> Von Heijne matrix			
score 6.3			
seq LVFALVTVACCLA/DG			
<221> polyA_signal			
<222> 283..288			
<221> polyA_site			
<222> 308..321			
<400> 174			
gctgagaaga gttgagggaa agtgctgctg ctgggtctgc agacgcg atg aat aac			56
		Met Asn Asn	
gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc			104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly			
-35 -30 -25 -20			
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc			152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys			
-15 -10 -5			
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc			200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro			
1 5 10			
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg			248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu			
15 20 25			
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca			308
aaaaaaaaaaa aaa			321

0929260.10501

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<210> 175
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..399

<221> sig_peptide
<222> 25..186
<223> Von Heijne matrix
      score 3.5
      seq SILAQVLDQSARA/RL

<400> 175
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      Met Ala Asp Glu Glu Leu Glu Ala Leu
                                -50
agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt      99
Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly
-45                                -35                                -30
gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac      147
Asp Ala Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn
-25                                -20                                -15
agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt      195
Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser
-10                                -5                                1
aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac      243
Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr
5                                10                                15
ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa      291
Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu
20                                25                                30                                35
caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag      339
Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys
40                                45                                50
aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa      387
Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu
55                                60                                65
gat gac gat tat tgaactacaa gtgctcacag actagaactt aacggaacaa      439
Asp Asp Asp Tyr
70
gtctaggaca g      450

<210> 176
<211> 1173
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..1137

<221> sig_peptide
<222> 10..72
<223> Von Heijne matrix
      score 6.5
      seq LLTLLPPPPPLYT/RH

<221> polyA_signal

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<222> 1144..1149

<221> polyA_site

<222> 1162..1173

<400> 176

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	Met	Gly	His	Arg	Phe	Leu	Arg	Gly	Leu	Leu	Thr	Leu	Leu	Leu	
	-20						-15				-10				
ccg	ccg	cca	ccc	ctg	tat	acc	cgg	cac	cgc	atg	ctc	ggc	cca	gag	99
Pro	Pro	Pro	Pro	Leu	Tyr	Thr	Arg	His	Arg	Met	Leu	Gly	Pro	Glu	
	-5					1				5					
gtc	ccg	ccc	cca	aaa	cga	tcc	cgc	agc	aaa	ctc	atg	gca	ccg	ccc	147
Val	Pro	Pro	Pro	Lys	Arg	Ser	Arg	Ser	Lys	Leu	Met	Ala	Pro	Pro	
10				15						20				25	
atc	ggg	acg	cac	aat	ggc	acc	ttc	cac	tgc	gac	gag	gca	ctg	gca	195
Ile	Gly	Thr	His	Asn	Gly	Thr	Phe	His	Cys	Asp	Glu	Ala	Leu	Ala	
			30						35					40	
gca	ctg	ctt	cgc	ctc	ctg	ccg	gag	tac	cgg	gat	gca	gag	att	gtg	243
Ala	Leu	Leu	Arg	Leu	Leu	Pro	Glu	Tyr	Arg	Asp	Ala	Glu	Ile	Val	
			45						50				55		
acc	cgg	gat	ccc	gaa	aaa	ctc	gct	tcc	tgt	gac	atc	gtg	gtg	gac	291
Thr	Arg	Asp	Pro	Glu	Lys	Leu	Ala	Ser	Cys	Asp	Ile	Val	Val	Asp	
	60					65					70				
ggg	ggc	gag	tac	gac	cct	cgg	aga	cac	cga	tat	gac	cat	cac	cag	339
Gly	Gly	Glu	Tyr	Asp	Pro	Arg	Arg	His	Arg	Tyr	Asp	His	His	Gln	
	75					80					85				
tct	ttc	aca	gag	acc	atg	agc	tcc	ctg	tcc	cct	ggg	agg	ccg	tgg	387
Ser	Phe	Thr	Glu	Thr	Met	Ser	Ser	Leu	Ser	Pro	Gly	Arg	Pro	Trp	
90					95					100				105	
acc	aag	ctg	agc	agt	gcg	gga	ctc	atc	tat	ctg	cac	ttc	ggg	cac	435
Thr	Lys	Leu	Ser	Ser	Ala	Gly	Leu	Ile	Tyr	Leu	His	Phe	Gly	His	
					110				115					120	
ctg	ctg	gcc	cag	ttg	ctg	ggc	act	agt	gaa	gag	gac	agc	atg	gtg	483
Leu	Leu	Ala	Gln	Leu	Leu	Gly	Thr	Ser	Glu	Glu	Asp	Ser	Met	Val	
			125				130					135			
acc	ctc	tat	gac	aag	atg	tat	gag	aac	ttt	gtg	gag	gag	gtg	gat	531
Thr	Leu	Tyr	Asp	Lys	Met	Tyr	Glu	Asn	Phe	Val	Glu	Glu	Val	Asp	
		140					145					150			
gtg	gac	aat	ggg	atc	tcc	cag	tgg	gca	gag	ggg	gag	cct	cga	tat	579
Val	Asp	Asn	Gly	Ile	Ser	Gln	Trp	Ala	Glu	Gly	Glu	Pro	Arg	Tyr	
	155					160				165					
ctg	acc	act	acc	ctg	agt	gca	cga	gtt	gct	cga	ctt	aat	cct	acc	627
Leu	Thr	Thr	Thr	Leu	Ser	Ala	Arg	Val	Ala	Arg	Leu	Asn	Pro	Thr	
	170					175				180				185	
aac	cac	ccc	gac	caa	gac	act	gag	gca	ggg	ttc	aag	cgt	gca	atg	675
Asn	His	Pro	Asp	Gln	Asp	Thr	Glu	Ala	Gly	Phe	Lys	Arg	Ala	Met	
				190					195					200	
ctg	gtt	caa	gag	gag	ttt	ctg	cag	aga	tta	gat	ttc	tac	caa	cac	723
Leu	Val	Gln	Glu	Glu	Phe	Leu	Gln	Arg	Leu	Asp	Phe	Tyr	Gln	His	
			205					210					215		
tgg	ctg	cca	gcc	cgg	gcc	ttg	gtg	gaa	gag	gcc	ctt	gcc	cag	cga	771
Trp	Leu	Pro	Ala	Arg	Ala	Leu	Val	Glu	Glu	Ala	Val	Glu	Ala	Gln	
		220					225				230				
cag	gtg	gac	cca	agt	gga	gag	att	gtg	gaa	ctg	gcg	aaa	ggc	gca	819
Gln	Val	Asp	Pro	Ser	Gly	Glu	Ile	Val	Glu	Leu	Ala	Lys	Gly	Ala	
	235					240				245					
ccc	tgg	aag	gag	cat	ctc	tac	cac	ctg	gaa	tct	ggg	ctg	tcc	cct	867
Pro	Trp	Lys	Glu	His	Leu	Tyr	His	Leu	Glu	Ser	Gly	Leu	Ser	Pro	
	250					255				260				265	
gtg	gcc	atc	ttc	ttt	gtt	atc	tac	act	gac	cag	gct	gga	cag	tgg	915

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Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
80 85 90 95
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 494
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
100 105 110
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac 542
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
115 120 125
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc 590
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
130 135 140
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 638
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
145 150 155
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 686
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
160 165 170 175
agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 734
Arg Pro Ser Arg Gln Leu
180
tagcccccat cagaccctgc cccaagcacc atatggaaat aaagtctttt c 785

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<223> Von Heijne matrix
score 4
seq LVRRTLLVAALRA/WM

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Met Gly Ser Lys
-60
tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag agg cgg 103
Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln Arg Arg
-55 -50 -45
cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg aag gca 151
Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val Lys Ala
-40 -35 -30 -25
gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc agg acc 199
Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg Arg Thr
-20 -15 -10
ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg tgg agg 247
Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp Trp Arg
-5 1 5
acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg ttg agg 295
Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Gln Ala Leu Leu Arg
10 15 20
gtc tac gtc atc cag gag cag ggc acg gtc aag ctc cag tcc tgc atc 343
Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu Gln Ser Cys Ile
25 30 35 40
cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat gct ctc 391
Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn Ala Leu

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	45	50	55	
tgc ttg ttc cag gtc cca gag agc agc ctt gcc ttc cag act gat ggc				439
Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe Gln Thr Asp Gly				
	60	65	70	
ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag ttc cac				487
Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu Phe His				
	75	80	85	
att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg				535
Ile Glu Ile Leu Ser Ile				
	90			
cactacccta ataaatgtct gacc				559
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score 4.6				
seq LDPAVSLSAPAFSA				
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<222> 734..739				
<221> polyA_site				
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	Met Lys Gly Gly Ala Phe Ser Asn Leu			
	-40	-35		
aat gat tcc cag ctc tca gcc tcg ttt ctg caa ccc agc ctg caa gca				99
Asn Asp Ser Gln Leu Ser Ala Ser Phe Leu Gln Pro Ser Leu Gln Ala				
	-30	-25	-20	
aac tgt cct gct ttg gac cct gct gtg tca ctc tcc gca cca gcc ttt				147
Asn Cys Pro Ala Leu Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe				
	-15	-10	-5	
gcc tct gct ctt cgc tct atg aag tcc tcc cag gct gca cgg aag gac				195
Ala Ser Ala Leu Arg Ser Met Lys Ser Ser Gln Ala Ala Arg Lys Asp				
	1	5	10	15
gac ttt ctc agg tct ctt agt gat gga gac tca ggg aca tca gaa cac				243
Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His				
	20	25	30	
atc tca gcg gtg gtg act agc cct cgg att tcc tgc cat ggt gct gcc				291
Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala				
	35	40	45	
att ccc acc gcc cgt gcc ctc tgc cta ggc tgt tcc tgc tgc acc gaa				339
Ile Pro Thr Ala Arg Ala Leu Cys Leu Gly Cys Ser Cys Cys Thr Glu				
	50	55	60	
cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc				387
Arg Leu Leu Leu Pro Pro Ser Leu Ser Leu Glu Ala Pro Ala				
	65	70	75	
agc acc tgagctctct gctgattgct gttctccca gtctgtggaa gctttgccca				443
Ser Thr				
80				

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tatgcttttc	ttaaaagggt	tctgggcagg	gcaggcgccc	ccattttctca	gggatccccc	503
ccaggacaac	gccttttctc	tgtgtcttca	gctctcctta	ccagatatct	atatatttgt	563
atatattcag	tttcaccaac	aatgcataca	gtactttttt	ttttaagtaa	agaaccgcag	623
tcattcgaa	ggagcccat	tgattccctc	ccctcgcc	ccccaaatct	ggcacctgcc	683
caagggtatc	tcgaaccat	ttgggggtgc	ctttggcatt	ggataataga	aataaaattt	743
tacctcttc	tacaaaaaaa	aaaaaac				770

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 <213> Homo sapiens

<220>
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 <222> 58..1095

<221> sig_peptide
 <222> 58..114
 <223> Von Heijne matrix
 score 5.4
 seq LSHLLPSLRQVIQ/EP

<221> polyA_site
 <222> 1202..1213

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atg gcc atg gcc	cag aaa ctc agc cac ctc	ctg ccg agt ctg cgg cag
Met Ala Met Ala	Gln Lys Leu Ser His	Leu Leu Pro Ser Leu Arg Gln
	-15	-10
gtc atc cag gag	cct cag cta tct	ctg cag cca gag cct gtc ttc acg
Val Ile Gln Glu	Pro Gln Leu Ser	Leu Gln Pro Glu Pro Val Phe Thr
	1	5
gtg gat cga gct	gag gtg ccg ccg ctc	ttc tgg aag ccg tac atc tat
Val Asp Arg Ala	Glu Val Pro Pro	Leu Phe Trp Lys Pro Tyr Ile Tyr
	15	20
gcg ggc tac cgg	ccg ctg cat	cag acc tgg cgc ttc tat ttc cgc acg
Ala Gly Tyr Arg	Pro Leu His	Gln Thr Trp Arg Phe Tyr Phe Arg Thr
	30	35
ctg ttc cag cag	cac aac gag gcc	gtg aat gtc tgg acc cac ctg ctg
Leu Phe Gln Gln	His Asn Glu Ala	Val Asn Val Trp Thr His Leu Leu
	50	55
gcg gcc ctg gta	ctg ctg ctg ccg	ctg gcc ctc ttt gtc gag acc gtc
Ala Ala Leu Val	Leu Leu Leu Arg	Leu Ala Leu Phe Val Glu Thr Val
	65	70
gac ttc tgg gga	gac cca cac gcc	ctc ccc ctc ttc atc att gtc ctt
Asp Phe Trp Gly	Asp Pro His	Ala Leu Pro Leu Phe Ile Ile Val Leu
	80	85
gcc tct ttc acc	tac ctc tcc ctc	agt gcc ttg gct cac ctc ctg cag
Ala Ser Phe Thr	Tyr Leu Ser	Leu Ser Ala Leu Ala His Leu Leu Gln
	95	100
gcc aag tct gag	ttc tgg cat tac	agc ttc ttc ttc ctg gac tat gtc
Ala Lys Ser Glu	Phe Trp His	Tyr Ser Phe Phe Phe Leu Asp Tyr Val
	110	115
ggg gtg gcc gtg	tac cag ttt ggc	agt gcc ttg gca cac ttc tac tat
Gly Val Ala Val	Tyr Gln Phe	Gly Ser Ala Leu Ala His Phe Tyr Tyr
	130	135
gct atc gag ccc	gcc tgg cat gcc	cag gtg cag gct gtt ttt ctg ccc
Ala Ile Glu Pro	Ala Trp His	Ala Gln Val Gln Ala Val Phe Leu Pro
	145	150
atg gct gcc ttt	ctc gcc tgg ctt	tcc tgc att ggc tcc tgc tat aac
		155

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Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
 160 165 170
 aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg 681
 lys tyr ile gln lys pro gly leu leu gly arg thr cys gln glu val
 175 180 185
 ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt 729
 pro ser val leu ala tyr ala leu asp ile ser pro val val his arg
 190 195 200 205
 atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac 777
 ile phe val ser ser asp pro thr thr asp pro ala leu leu tyr
 210 215 220
 cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct 825
 his lys cys gln val val phe phe leu leu ala ala phe phe ser
 225 230 235
 acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg 873
 thr phe met pro glu arg trp phe pro gly ser cys his val phe gly
 240 245 250
 cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct 921
 gln gly his gln leu phe his ile phe leu val leu cys thr leu ala
 255 260 265
 cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat 969
 gln leu glu ala val ala leu asp tyr glu ala arg arg pro ile tyr
 270 275 280 285
 gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg 1017
 glu pro leu his thr his trp pro his asn phe ser gly leu phe leu
 290 295 300
 ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg 1065
 leu thr val gly ser ser ile leu thr ala phe leu leu ser gln leu
 305 310 315
 gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg 1115
 val gln arg lys leu asp gln lys thr lys
 320 325
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 cctggtaaaag ttgtttgtgt ctggccaaaa aaaaaaaa 1213

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 <213> Homo sapiens

 <220>
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 <222> 31..660

 <221> sig_peptide
 <222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

 <221> polyA_signal
 <222> 1288..1293

 <221> polyA_site
 <222> 1307..1318

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 Met Asp Asn Arg Phe Ala Thr Ala
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Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala	
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gct tcc att ggc aca gac ttc tgg tat gag tat cga agt cca gtt caa	150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln	
5 10 15 20	
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt	198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser	
25 30 35	
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat	246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn	
40 45 50	
ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg	294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met	
55 60 65	
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca	342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr	
70 75 80	
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt	390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val	
85 90 95 100	
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt	438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu	
105 110 115	
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc	486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys	
120 125 130	
ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat	534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr	
135 140 145	
ccc acc att gcc acg gcc att ctc cat ctc ctt gca gtg aca aag gag	582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Val Thr Lys Glu	
150 155 160	
agc atg ctt cca gct gga gct gag tcc aag cac aca gcc act cct gca	630
Ser Met Leu Pro Ala Gly Ala Glu Ser Lys His Thr Ala Thr Pro Ala	
165 170 175 180	
cac gca tgc gtg caa aca ggg aag ccc aag taggagaaga ggaagagggt	680
His Ala Cys Val Gln Thr Gly Lys Pro Lys	
185 190	
tgtagggatt tgggaagaac cttgattatt cctggaggga aaagacaaat ctactccct	740
gaaatcaccc tcgaatctac ttccaccctc agaacttaaa atgaactgca tccttttttt	800
catctttctt tcttctccag tgaatatgat ctccaaaccc ttatttttct ttgtgaactgt	860
aaaatttcca ctcattggagc atgcaaccaa cagatgcaat ctctgagaag atgaaaaattg	920
ggacctctta ttataaaatt gacctagctg gactcaggaa accaggggaag aagtcaatgc	980
aggcattttaa aatgtaaagt tttttctggt taaatctatt ttttttctt gtagggttgag	1040
tatttcttcc cagtttttct gctctgggtgt ataacaaca ggtcaaaatt tccactcttt	1100
ctctctgata gtagtgtaat cctaccttgc atacttaatg catagtgaaa tggcatctag	1160
cagaataaca caccocaaac acacacacac atttcattag gtgccccaaa aattctgtat	1220
ttagcttatt tatttattgt tatttttgc tttctttaac ccactatata ttgactgcga	1280
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<222> 31..90

<223> Von Heijne matrix
score 5.4
seq AFVIACVLSLIST/IY

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<222> 816..821

<221> polyA_site
<222> 840..853

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                               Met Asp Asn Arg Phe Ala Thr Ala
                               -20                               -15

ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
                               -10                               -5
gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
5                               10                               15                               20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
                               25                               30                               35
gat gaa gca gat gaa aag act tat aat gat gca cct ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Pro Phe Arg Tyr Asn
                               40                               45                               50
ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
55                               60                               65
cat tgg tat agc cca gaa agg aca gag tca ttt gat gtg gtc aca      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
70                               75                               80
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt      390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
85                               90                               95                               100
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt      438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
                               105                               110                               115
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc      486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
120                               125                               130
ttt ggg gct ttg atc gga ctt tgt agt tgc att tgc cga agc tta tat      534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
135                               140                               145
ccc acc att gcc acg ggc att ctc cat ctc ctt gca gat acc atg ctg      582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Asp Thr Met Leu
150                               155                               160
tgaagtcacg gccacatgga ggtgtcctgt gtagatgctc cagctgaaat cccaagctaa      642
gctcccaact gacagccaac atcatttcca gccatgtgtg ggagccatcc tggatgtcca      702
gctttaacaa gccttcagag gaacttcagcc acagctatta tcttactaca tcctgtgtgag      762
actctaataa agaaccaact agctgagccc aatcaacctt tggaactgat agaaataaaa      822
tgaattgttg ttttgcgaaa aaaaaaaaaa a      853

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<213> Homo sapiens

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<221> sig_peptide
 <222> 15..80
 <223> Von Heijne matrix
 score 8.5
 seq AALLLGLMMVVTG/DE

<221> polyA_signal
 <222> 795..800

<221> polyA_site
 <222> 814..826

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 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
 -20 -15
 tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc 98
 Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
 -10 -5 1 5
 ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag 146
 Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
 10 15 20
 ggc ctt gaa gtt ttc tac cca gag ttt ggg aac att ggc tgc aag gtt 194
 Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
 25 30 35
 gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag 242
 Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
 40 45 50
 ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg 290
 Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
 55 60 65 70
 gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga 338
 Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
 75 80 85
 ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag 386
 Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
 90 95 100
 aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc 434
 Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
 105 110 115
 cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt 482
 Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
 120 125 130
 cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga 530
 Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
 135 140 145 150
 ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa 578
 Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
 155 160 165
 cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca 626
 Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
 170 175 180
 acc ctg cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac 674
 Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
 185 190 195
 cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt 725
 Gln Ala Glu Ile Ala Ala Cys
 200 205
 ggccacaatg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccctt 785
 tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a 826

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<210> 184
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..295

<221> sig_peptide
 <222> 74..196
 <223> Von Heijne matrix
 score 5.4
 seq RLLYIGFLGYCSG/LI

<221> polyA_signal
 <222> 545..550

<221> polyA_site
 <222> 561..571

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<400> 184
cgggtagtgg tcgtcgtggg tttccttgta gttcgtgggc tgagaccagg cctcaagtgg      60
aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt      109
               Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe
               -40               -35               -30
ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg      157
Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro
               -25               -20               -15
cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat      205
Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp
               -10               -5               1
aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag      253
Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
               5               10               15
ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg      295
Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
20               25               30
taaaacgtga agactacctg tatgctgtga gggaccgtga aatgtttgga tatatgaaat      355
tacatccaga gggattttctt gaagaagata agaaaacata tgggtgaaatt ttgaaaaaat      415
tccatccaat acgttgaagt cttcaaaatg cttgctccag tttcactgat acctgctggt      475
ctggaatttg atggaacatg tttcttatga cagttgaagc ttatgctaata ctgtatgttg      535
acaccttgta attaaaatac gtacccaaaaa aaaaaa

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<210> 185
 <211> 659
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 440..658

<221> polyA_signal
 <222> 601..606

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<400> 185
cgccttacga gctgggaggt ggtgcctctc acccagctaa ttgctcteta gcccttggtc      60
ttcacagggt ttggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa      120
gactttgtgc ctatggttgg ggacagagtg aggtcggtgc cttgacgacg acagcatgcy      180

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gccccgtggc ctcctaagtg tgagcttgcg gcggaccgag gccacactgc ctccttgcct 240
gcttcgcca ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tggaattgct 300
agtttgc tagcagcatctt ttggacctgc gaaccatagt catttcacct caaatctgtt 360
tccaagtga aaacctttgg gtctttctat gcgaacggat tgaagaaacg caaaaagttt 420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga 472
               Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
               1         5         10
gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga 520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
               15         20         25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg 568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
               30         35         40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg 616
Val Lys Ser Ile Ala Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg
               45         50         55
cat gaa aac ttg gtg aat ctc ttg gaa gtg tgt aaa aaa aaa a 659
His Glu Asn Leu Val Asn Leu Leu Glu Val Cys Lys Lys Lys
60         65         70

<210> 186
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..283

<221> sig_peptide
<222> 38..85
<223> Von Heijne matrix
      score 4.1
      seq LLPATSLAGPVLS/TL

<221> polyA_signal
<222> 257..262

<400> 186
cacctgaatc ccaggaaccc tcaatgaggt ctccaag atg aag aga ctg ctg cca 55
               Met Lys Arg Leu Leu Pro
               -15
gct acc agc ctg gct ggc cct gtc ctg tcc acc ctc att gcc cca act 103
Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile Ala Pro Thr
-10         -5         1         5
ccc atg ttg ttt tgt gaa gat aaa agc tgg gat ctt ttt ctt ttt ttt 151
Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Leu Phe Leu Phe Phe
10         15         20
aag tct cac aag aca tgg ggc atc tcc aca aat tta agt tcc tgt cca 199
Lys Ser His Lys Thr Trp Gly Ile Ser Thr Asn Leu Ser Ser Cys Pro
25         30         35
ttt gga aat ttg ttt cta tgt gta cag ttt gtc aga gaa aaa caa agt 247
Phe Gly Asn Leu Phe Leu Cys Val Gln Phe Val Arg Glu Lys Gln Ser
40         45         50
ttt tgt atg aat aca gaa tgt gat tta cgc aag aat tgacaaaaaa 293
Phe Cys Met Asn Thr Glu Cys Asp Leu Arg Lys Asn
55         60         65
aaaaaaaaa 301

<210> 187
<211> 477

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<212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 121..477
 <221> sig_peptide
 <222> 121..288
 <223> Von Heijne matrix
 score 3.5
 seq SSCADSFVSSSSS/QP

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<400> 187
cctcggagca ggcggagtaa agggacttga gcgagccagt tgccggatta ttctatttcc      60
ctccctctc tcccgcccg tatctctttt caccctctc ccacctcgc tcgcgtagcc      120
atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg      168
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
   -55                -50                -45
tcc ttc gga gcc gag ccg tcc gcg ccc ggc gcc gcc ggg agc cca gga      216
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Ser Pro Gly
   -40                -35                -30                -25
gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat      264
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
               -20                -15                -10
tcc ttt gtt tct tcc tct tct cag cct gta tct cta ttt tcg acc      312
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
               -5                1                5
tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa      360
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
   10                15                20
att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc      408
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
   25                30                35                40
ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggg agc cag cct      456
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
               45                50                55
att tta gcc aaa aaa aaa aaa      477
Ile Leu Ala Lys Lys Lys
   60
  
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<210> 188
 <211> 323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 292..297

<221> polyA_site
 <222> 310..323

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<400> 188
a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca      49
  Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
   1                5                10                15
gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag      97
  
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Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
aac ccc cgc tgc act gtg gat gct ccc aca gca gca ggc cgg ggc cgt 145
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
ggc cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg 193
Gly Arg Gly Arg Pro His
50
ctggtgctgtg ggtgcactta cctccttggg ctgtgttact tcattttaca aggaaggggt 253
agtaattggc ccactctctt cttactggag gctattttaaa taaaatgtaa gacttcaaaa 313
aaaaaaaaa 323

<210> 189
<211> 1392
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..675

<221> sig_peptide
<222> 46..87
<223> Von Heijne matrix
score 5.3
seq LTLGLSFILAGL/IV

<221> polyA_signal
<222> 1364..1369

<221> polyA_site
<222> 1383..1392

<400> 189
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Met Leu Thr Leu
tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc 105
Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
-10 -5 1 5
att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg 153
Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
10 15 20
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag 201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly
25 30 35
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac 249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
40 45 50
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac 297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
55 60 65 70
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg 345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
75 80 85
gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att 393
Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
90 95 100
gtt atg cct cca aaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt 441
Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
105 110 115
ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct 489

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Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
 120 125 130
 gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa 537
 Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
 135 140 145 150
 ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg 585
 Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Asp Leu Leu
 155 160 165
 ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac 633
 Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His
 170 175 180
 ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag 675
 Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu
 185 190 195
 taagaggcaa cagatagagt gtccttggtg ataagaagtc agagatttac aatatgactt 735
 taacattaa gtttatggga tactcaagat atttactcat gcatttactc tattgctttat 795
 gctttaaaaa aaggaaaaaa aaaaaactac taaccactgc aagctcttgt caaatttttag 855
 ttttaattggc attgctgttt ttttgaacct gaatttacct gagtttctt tttttcttgc 915
 atttatagg tttagatttc tgaaagcagc atgaatatat cacctaacct cctgacaata 975
 atttccatcc gttgtttttt ttgtttgttt gttttttctt ttcttttaag taagctcttt 1035
 attcatctta tgggtggagca attttttaat ttgaaatatt tttaaattgtt ttggaacttt 1095
 ttgtgtaaaa tataatcagat ctcaacattg ttgggtttctt ttgtttttca ttttgtacaa 1155
 cttttcttgaa tttagaaatt acatcttttc agttctgtta ggtgctctgt aattaaacctg 1215
 acctatatgt gaacaatttt catgagacag ctatttttaa ctaatgacgt gattctttct 1275
 cactactact tgtattgtgg aatgcacaaa attgtgtagg tgctgaatgc tgtaaggagt 1335
 ttagggtgta tgaattctac aaccctataa taaattttac tctatacaaa aaaaaaaa 1392

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 <211> 999
 <212> DNA
 <213> Homo sapiens

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 <222> 62..385

 <221> polyA_signal
 <222> 974..979

 <221> polyA_site
 <222> 987..999

 <400> 190
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 g atg gga tgt gtt ttc cag agc aca gaa gac aaa tgt ata ttc aag ata 109
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc 253
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val

	85		90		95	
ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg						395
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr						
	100		105			
ccaaggggga agagctttca tgtgcaagag gcaaggaaac tgattatctt gagtaaatgc						455
cagcctttgg gctaagtact taccacagag tgaatcttca aaaaatgac ataattattt						515
cagtcataaa aaatagagtt attttattaa ataaaatatt gataattatt gtattattac						575
tttaaacaca cttccccctc aaaaagccc tgtgaaggat gttttgttca catatagtc						635
caaatatggt ttggcacatc atttattaaa tggaataaat agtacttgaa cctctggcacc						695
tctgacaaca aagtcacatg tctttttact atgccctaatt acccttcac acgttatccac						755
attgatgcta catctgtatt ttataggtac cctatgttag gtgttctggg ggatagaaaa						815
gaaataagca ggccaggctc agtgggtcat gcctgtaatc ctacgatttt gggaggctga						875
ggcagcagaa ctgcctgagc cccagggttc aagactgcag tgagctatga tggcaccact						935
gcattctagc ctgggtgaca gagcaagact ctgtctaaaa taaaaaaaga gaaaaaaaaa						995
aaaa						999

<210> 191
 <211> 725
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 422..550

 <221> sig_peptide
 <222> 422..475
 <223> Von Heijne matrix
 score 4.5
 seq LRWLMFVIPALWG/AE

 <221> polyA_site
 <222> 714..725

<400> 191						
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tagccagata ggtgagtaaa tatatttgca gtaacctatt tgctattcct tgcgtcaact						120
gtgttttaag ttctctccag aatcagagag agtatttgcca tccaagaaat cgtttttaga						180
tatgacattt gagctatcat cttgagacca atacctaaaa caatttcagt ttaagaaatg						240
tctaggtatg gtgaaaaaac agtttaaaac cagcaaaaaca gaattttatt ccctcagcga						300
ataccacaaa tgtacatata ccttgtattt ctgaaagcaa agcaagcatg ccaagtagtt						360
tttattttacc tgtacctata atacagcaag gtgaaacagg atatatattt gaagtttaaa						420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt						469
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu						
	-15		-10		-5	
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc						517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr						
	1		5		10	
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaaatac aaaattagct						570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr						
	15		20		25	
gggtgtggtg gggggcgctt gtagtccacg ctacttggga gactgaggca ggagaattgc						630
ttgaacacgg aaggcgaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg						690
gcaacagagt gagactccct ctcaaaaaaa aaaaa						725

<210> 192
 <211> 400
 <212> DNA
 <213> Homo sapiens

 <220>

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<221> CDS
<222> 124..231

<221> polyA_site
<222> 387..400

<400> 192
ctcgctctctc ctggcttctg gtatgcacca gcaattcctg gcgttccttg gctcctagaa      60
gcacactctc taccacatgg tcatcttcac cctgtgtgtc ttcacactac cctttctctg      120
tgc atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga      168
      Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
      1          5          10          15
tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag      216
Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
      20          25          30
acc ttt ttc caa ata tagtcactct ctgaggtact gatggttagg atctcaacat      271
Thr Phe Phe Gln Ile
      35
accttttttt ggaggacaca attgaaccca taacagggtg ttgtcaagga agaggttaaaa      331
tttgaaagaa aggtgggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa      391
aaaaaaaaa
      400

<210> 193
<211> 1053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..1051

<221> sig_peptide
<222> 131..169
<223> Von Heijne matrix
      score 4.2
      seq MLAVSLTVPLLGA/MM

<221> polyA_signal
<222> 1019..1024

<400> 193
gagcggggcg gacggggctgc gacagcgccg gcccttgccg ccgcagggtcgc tcacagacga      60
tgatggccag gccccggagg ctaaggacgg cagctccttt agcggcagag ttttcgcagt      120
gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc      169
      Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
      -10          -5
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa      217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
      1          5          10          15
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga      265
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
      20          25          30
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata      313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
      35          40          45
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc      361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
      50          55          60
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg      409
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser
      65          70          75          80

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<221> polyA_site	
<222> 1117..1128	
<400> 194	
cgctcttggtg agagcgtgag ctgctgagat ttggggagctt gcgcttaggcc cgcttggaagt	60
tctgagccga tggaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct	112
Met Phe Ala Pro Ala Val Met Arg Ala	
-30 -25	
ttt cgc aag aac aag act ctc gcc tat gga gtc ccc atg ttg ttg ctg	160
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu	
-20 -15 -10	
att gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat	208
Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr	
-5 1 5	
gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa	256
Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys	
10 15 20 25	
gag aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc	304
Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser	
30 35 40	
aag ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat	352
Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp	
45 50 55	
cct gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca	400
Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr	
60 65 70	
act tgacctgct gattctctttt tccnnntttt ttttttttta aataaaaaa	453
Thr	
ctattaactg gacttcttaa tatatacttc tatcaagtgg aaaggaatt ccaggcccat	513
ggaaacttgg atatgggtaa ttatgatgaca aataactctc actaaaggtc atgtacaggt	573
ttttatactt cccagctatt ccatctgtgg atgaaagtaa caatgttggc cactgatatt	633
ttacaccttg aaataaaaaa tgtgaatact gctccaaaaa aaaaaaacag taccgtgtgag	693
tctctcctgt ggcttggatt tacactgtggc aacgtggttg aaatgtatct gactcagaac	753
tatgatatac caaacctggc taaaaaaatt gaagaaattt aaaaggactt ggatgccaa	813
aagaaacccc ctagtgcagt agactgcttc cagcactgoc ttcaggatatt accgattcta	873
ctgcttcttga gggcctcgtt tactatctga accaaaagct ttgttttgc tctccagcct	933
cagcactctt cttcttctgt agacctgtg ttttttgcct taaagcaagc aaaatggggc	993
ccccatttga gaagactccg acgtttccaa catactacc tcttcccata atccccttcc	1053
aacatcatgg gaggttctaa gactggaatt atggtgctag attagtaaac atgactttta	1113
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<210> 195	
<211> 254	
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<213> Homo sapiens	
<220>	
<221> CDS	
<222> 37..162	
<221> sig_peptide	
<222> 37..93	
<223> Von Heijne matrix	
score 9.5	
seq LMCLSLCTAFALS/KP	
<221> polyA_signal	
<222> 224..229	
<221> polyA_site	
<222> 243..254	

400> 199																									
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ccgatcaagg	aggyttctctt	caactcccctc	ttcagtggct	actagtgtgc	attttctcccc	120																			
ctgtgttttg	tgaagagtac	ccagtactat	gac att cgc tgg tca tgt gag cac			174																			
Met Arg Trp Ser Cys Glu His																									
-115 -110																									
ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctg acc acg caa ctg						222																			
Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu																									
-105 -100 -95																									
ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg						270																			
Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu																									
-90 -85 -80																									
ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag						318																			
Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln																									
-75 -70 -65																									
cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg						366																			
His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg																									
-60 -55 -50 -45																									
cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg						414																			
His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val																									
-40 -35 -30																									
cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca						462																			
Pro Ser Asp Val Ser His Ala Ala Phe Tyr Phe Leu Phe His Arg Pro																									
-25 -20 -15																									
tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc						510																			
Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe																									
-10 -5 1																									
tat cag ctg tat tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt`						558																			
Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu																									
5 10 15 20																									
tcc atg gct ctc atc ctc ttc tgc aac tac tat gtt tta ttt aya ctt						606																			
Ser Met Ala Leu Ile Leu Phe Cys Asn Tac Tyr Val Leu Phe Lys Leu																									
25 30 35																									
ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac						654																			
Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn																									
40 45 50																									
agt tat gaa ctc aag gca aac taagctgct ctcaacaatg agggagaact						705																			
Ser Tyr Glu Leu Lys Ala Asn																									

55
 cagataaaaa tattttcata cgttctatatt tttctttgtg attttttataa atattttaaga 765
 tgtttttataat tttgtataact attatgtttt gaaagtcggg aagagtaagg gatatttaaat 825
 gtatccgtaa acaaaaaaaa aaaa 849

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 <213> Homo sapiens

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 <222> 18..173

<221> sig_peptide
 <222> 18..77
 <223> Von Heijne matrix
 score 6.5
 seq GLCVLQLTTAVTS/AF

<221> polyA_signal
 <222> 864..869

<221> polyA_site
 <222> 882..893

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 ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg 98
 Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
 -5 1 5
 aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc 146
 Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
 10 15 20
 cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcttgattca 193
 His His Phe Ile His Pro Cys Leu Asp
 25 30
 aagtggtacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgettcag 253
 agaggggcagc acctatacct ggtggtcttt ctgatggtca gttttattcc cctectgaat 313
 ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaaacca cttttagaac 373
 tatgatgact accttttgta aatgtgaaaa accctcacag aaagtcacg aggcaaaaag 433
 aggcaggcag tggagtcctc ctgtcgacag taaagttgaa atggtgacgt ccaactgctgg 493
 cttttattgaa cagctaataa agatttattt attgtaatac ctcacagacg ttgtaccata 553
 tccatgcaca tttagttgcc tgcctgtggc tggttaaggta atgtcatgat tcacctcttc 613
 tccagtgaga ctgagcctga tgtgttaaca aataggtgaa gaaagtcctg tgctgtattc 673
 ctaatcaaaa gacttaatat attgaagtaa cactttttta gtaagcaaga taccttttta 733
 tttoaatcca cagaatggaa tttttttgtt tcatgtctca gatttttttt gtatttcttt 793
 ttttaacact tacatttccc ttgtttttta acctatgcac atgtgctctt tgtacagttt 853
 taaaaagtgt aataaaatct gacatgtcaa aaaaaaaa mcv 896

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 <212> DNA
 <213> Homo sapiens

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 <222> 17..595

00973380.104501

<221> sig_peptide
 <222> 17..85
 <223> Von Heijne matrix
 score 3.70000004768372
 seq FLPLPLXRAFACRG/CQ

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 <222> 820..825

<221> polyA_site
 <222> 840..851

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 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
 -20 -15
 ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg 100
 Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
 -10 -5 1 5
 gag cgc gcc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga 148
 Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
 10 15 20
 ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat 196
 Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
 25 30 35
 aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa 244
 Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
 40 45 50
 tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa 292
 Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
 55 60 65
 tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa 340
 Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
 70 75 80 85
 aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg 388
 Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu
 90 95 100
 aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg 436
 Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala
 105 110 115
 gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat 484
 Asp Phe Tyr Lys Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr
 120 125 130
 tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg 532
 Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met
 135 140 145
 gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa 580
 Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln
 150 155 160 165
 aag aag agg agc aac taggagtcca ctctgaccga gccagagtcc aggtttccac 635
 Lys Lys Arg Ser Asn
 170
 aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga 695
 agccccacat ctctcctaagg ggccccatgg cctgtttggg gccagggttag gtcctggggc 755
 actgtggggc gctgtgctgc tgatgtgggc tctaggccag ctgtgtgtca cgtaactgtgt 815
 gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa 851
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 <212> DNA
 <213> Homo sapiens

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 <222> 89..334

<221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 3.59999990463257
 seq APTLXSLQLQAALL/CV

<221> polyA_signal
 <222> 462..467

<221> polyA_site
 <222> 484..495

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 ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg 112
 Met Ala Phe Thr Leu Xaa Ser Leu
 -10
 ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag 160
 Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
 -5 1 5 10
 gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt 208
 Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
 15 20 25
 gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att 256
 Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
 30 35 40
 cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca 304
 Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
 45 50 55
 att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaaat 354
 Ile Ala Ile Val Leu Leu Leu Leu Phe Gly
 60 65
 ggakactcag aaraggacat gccaktaraa kttattactt tggctattat tggaaatatt 414
 atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaaat aaaaccaggg 474
 tttctattta aaaaaaaaaa a 495

<210> 203
 <211> 884
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 21..614

<221> sig_peptide
 <222> 21..83
 <223> Von Heijne matrix
 score 10
 seq LWALAMVTRPASA/AP

<221> polyA_signal
 <222> 849..854

<221> polyA_site
 <222> 873..884

<400> 203
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 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
 -20 -15
 ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca 101
 Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
 -10 -5 1 5
 gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg 149
 Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
 10 15 20
 cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg 197
 Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg
 25 30 35
 ctg aca aag gcc agg aac agc ctg ggt ctc tat gcc cgc aca ata gaa 245
 Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
 40 45 50
 ctc ctg ggg cag gag gtc agc cgg gcc cgg gat gca gcc cag gaa ctt 293
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
 55 60 65 70
 cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg 341
 Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu
 75 80 85
 cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car 389
 Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
 90 95 100
 aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc 437
 Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Leu Xaa Xaa
 105 110 115
 gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc 485
 Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro
 120 125 130
 cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak 533
 Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa
 135 140 145 150
 cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc 581
 Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile
 155 160 165
 cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac 634
 Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala
 170 175
 tgaggaccaa tcatgtctga aggaacactt ccacgccccg tgaggccctt gtgcaggag 694
 gagctgctgt ttcactggga tcagccaggg cgccggggccc cactctctgag cacagagcar 754
 agacagacgc aggcggggac aaaggcagag gatgtagccc cattggggag ggggtggagga 814
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 aaaaaaaaaa 884

 <210> 204
 <211> 897
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 94..573

 <221> sig_peptide
 <222> 94..258
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IGILCSLLGTVLL/VV

09978260 101501

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<222> 862..867

<221> polyA_site
<222> 886..897

<400> 204
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tgaggagctg gagctggttg ggactgggcc gca atg gac aag ctg aag aag gtg      114
                               Met Asp Lys Lys Leu Lys Lys Val
                               -55                               -50

ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
                               -45                               -40                               -35

gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
                               -30                               -25                               -20

tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
                               -15                               -10                               -5

tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1                               5                               10                               15

ggt aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
20                               25                               30

aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
35                               40                               45

atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
50                               55                               60

cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                               70                               75                               80

ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
85                               90                               95

aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat      593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
100                               105

gaagcttttg aaggcactat ggacagaagc tgggtggacag tttttgtwact atcttcgaaa      653
cctctgtcct acagacatgt gcctttttatc ttgcagcaat gtgttgcttg tgattcgaac      713
atttgagggt tactttttgga agcaacaata cattctcgaa cctgaatgac agtagcacag      773
gatgagaagt ggggtctgtg tcttgtggag tgggaatcttc ctcattgtacc tgtttcctct      833
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aaaa
897

<210> 205
<211> 518
<212> DNA
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<220>
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<222> 74..397

<221> sig_peptide
<222> 74..127
<223> Von Heijne matrix

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score 7.69999980926514
seq LLLLPVLGLLVSS/KT

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<222> 472..477

<221> polyA_site
<222> 507..518

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aggcgctgc agg atg aaa gct ctc tgt ctc ctc ctc cct gtc ctg 109
Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
-15 -10
ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
-5 1 5 10
aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
15 20 25
agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
30 35 40
gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
45 50 55
gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
60 65 70
tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt gtg cag ccc 397
Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
75 80 85 90
tgaggtcgcg cgcagcgct gcacagcgcg ggcggagcgc gctccagctc cggaggggtt 457
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a 518

<210> 206
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..242

<221> sig_peptide
<222> 51..116
<223> Von Heijne matrix
score 6.5
seq SCLCPALFPGTSS/FI

<221> polyA_signal
<222> 319..324

<221> polyA_site
<222> 339..350

<400> 206
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Met Ile
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104

00073260.101501

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Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20 -15 -10 -5
ggt act tcc tcc ttt att gta gca ctc agc tcc cca gcc gat ctg tac 152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
1 5 10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa 200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
15 20 25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta 242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
30 35 40
tgattttgct gaatttttaaa taaaatgaaa accataaatt acatratgct tttattgach 302
cttgacmact ggcctaaata aaaaractct gacttcaaaa aaaaaaaa 350

<210> 207
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..191

<221> sig_peptide
<222> 111..155
<223> Von Heijne matrix
score 5.80000019073486
seq FLXLMTLTHVHS/SA

<221> polyA_signal
<222> 965..970

<221> polyA_site
<222> 986..996

<400> 207
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cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy 116
Met Gly
-15
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag 164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
-10 -5 1
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat 211
Pro Asn Glu Gln Pro Trp Leu Leu Asn
5 10
ggtacgcggt gctatacaga atctttggat atgtgcatca gtggtttatg ccaaattggt 271
ggctgcgatc accagctggg aagcaccgct aaggaarata actgtggggt ctgcaacrga 331
natgggtcca cctgccggct ggtccgaggg cartataaat cccakctctc cgcaacccaa 391
tcrgatgata ctgtggttgc aattccctat ggaagtakac atattcgctt tgtcttaaaa 451
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gacwdagaga tactgagaat ggctggacca ctacagcagc atttcattgt caawattcgt 631
aactcggggt ccgctgacag tacagtccag kkatctctct atcaaccccat catccaccga 691
tggaggggara cggatttctt tccttgtctc gcaacctgtg gaggaggtta tcagctgaca 751
ctgggtgagt gctacgatct gaggagcaac cgtgtggttg ctgaccaata ctgtcactat 811
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gccaggtcag tcaaatttgc tagtttcatt gtcataaaca taactcaagt tccaaatagg 931
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aaaaa 996

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FOR THE

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<221> polyA_signal
<222> 828..833
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<221> polyA_site
<222> 850..860
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						-20				
ggt	cgc	ctg	tgt	ctt	ctc	acc	atc	gtt	ggc	
Gly	Arg	Leu	Cys	Leu	Leu	Thr	Ile	Val	Gly	
		-15					-10			104
gga	cag	acg	ttg	aaa	gat	acc	acg	tcc	agt	
Gly	Gln	Thr	Leu	Lys	Asp	Thr	Thr	Ser	Ser	
1				5				10		152
atc	atg	gac	att	cag	gtc	ccg	aca	cg	gcc	
Ile	Met	Asp	Ile	Gln	Val	Pro	Thr	Arg	Ala	
				20				25		200
gaa	ctc	cag	ccc	acc	tct	cca	acc	cca	acc	
Glu	Leu	Gln	Pro	Thr	Ser	Pro	Thr	Pro	Thr	
			35					40		248
cca	caa	ccc	cag	acc	cag	acc	caa	ctg	gaa	
Pro	Gln	Pro	Gln	Thr	Gln	Thr	Gln	Leu	Gly	
		50				55		60		296
cta	gtg	aca	gat	cca	gag	aca	cac	wak	agc	
Leu	Val	Thr	Asp	Pro	Glu	Thr	His	Xaa	Ser	
		65				70		75		344
act	gat	gac	acc	acg	acg	ctc	tct	gag	aga	
Thr	Asp	Asp	Thr	Thr	Thr	Leu	Ser	Glu	Arg	
						85		90		392
gtc	cat	dac	aga	ccb	cba	kda	ccc	tca	akc	
Val	His	Xaa	Arg	Pro	Xaa	Xaa	Pro	Xaa	His	
				100				105		440
atg	acc	cct	tct	tct	atg	atg	aac	aca	ccc	
Met	Thr	Pro	Ser	Ser	Met	Met	Asn	Thr	Pro	
				115				120		488
tgg	tgc	cag	ctg	tgc	tgt	tca	tca	cag	gca	
Trp	Ser	Gln	Leu	Cys	Cys	Ser	Ser	Gln	Ala	
		130						135		536
gca	agt	gca	ggc	agc	tgt	ccc	ggt	tat	gcc	
Ala	Ser	Ala	Gly	Ser	Cys	Pro	Gly	Tyr	Ala	
		145				150		155		584
tcc	atc	aga	aac	agg	agc	tgc	aaac	ctg	ctgggc	
Ser	Ile	Arg	Asn	Arg	Ser				gaagaccaag	
160					165					632

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ccccctgccca gctcacccgtg cccagcctcc tgcattccct cgaagagcct ggccagagag 692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtctcc tacctcccc 752
aacctgccc gccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc 812
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<210> 209
<211> 593
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<213> Homo sapiens

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<221> CDS
<222> 24..560

<221> sig_peptide
<222> 24..101
<223> Von Heijne matrix
score 10.3999996185303
seq LLLLLCGPSQDQC/RP

<221> polyA_signal
<222> 563..568

<221> polyA_site
<222> 583..593

<400> 209
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Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
-25 -20
ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc 101
Leu Leu Pro Leu Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
-15 -10 -5
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc 149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
1 5 10 15
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga 197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly
20 25 30
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag 245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
35 40 45
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac 293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
50 55 60
aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc 341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65 70 75 80
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac 389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
85 90 95
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg 437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
100 105 110
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan 485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
115 120 125
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa 533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
130 135 140
acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct 580

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Thr His Phe Cys Leu Ser Ile Xaa Leu
 145 150
 gtaaaaaaaaaaaa

593

<210> 210
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 <213> Homo sapiens

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 <222> 109..558

<221> sig_peptide
 <222> 109..273
 <223> Von Heijne matrix
 score 3.70000004768372
 seq VAFMLTLPILVCK/VQ

<221> polyA_site
 <222> 1104..1114

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 ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca 117
 Met Ala Thr
 -55
 aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga 165
 Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
 -50 -45 -40
 ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc 213
 Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
 -35 -30 -25
 aca gcc ggg gtt gtg acc tgc gtg gcc ttc atg ctg act ctc ccg atc 261
 Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
 -20 -15 -10 -5
 ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act 309
 Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
 1 5 10
 cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc 357
 Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
 15 20 25
 gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc 405
 Ala Phe Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe
 30 35 40
 ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat 453
 Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
 45 50 55 60
 gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct 501
 Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
 65 70 75
 gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt 549
 Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
 80 85 90
 tat cgc tat tgaatatatt gtctgacca tgaataggac caacgtcaat 598
 Tyr Arg Tyr
 95
 gtctttcttg agctttccgc tccctcgtcgc aatgaaaact ttgtcctcct getcacctac 658
 ktccctctct tgatggcgt gaccttcctc wtgtcctcct tcaccttctg tggtkccttc 718
 accgggctgga avagacatgg ggcccacatc tacctcassa tgctskctc cattgccatc 778
 tgggtggcct ggatcaccct gctcatgctt cctgactttg accgcrvggt ggatgacacc 838

09070360.101601

Gly	Pro	Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asn	Gly	Leu	Glu	Gly	Leu	Phe	
		130					135					140				
gag	gat	att	gac	acc	tct	atg	tat	gac	aat	gaa	ctt	tgg	gca	cca	gcc	697
Glu	Asp	Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala	
		145					150				155					
tct	gag	ggc	ctc	aaa	cca	ggc	cct	gag	gat	ggg	ccg	ggc	aag	gag	gaa	745
Ser	Glu	Gly	Leu	Lys	Pro	Gly	Pro	Glu	Asp	Gly	Pro	Gly	Lys	Glu	Glu	
		160				165				170					175	
gct	ccg	gag	ctg	gac	gag	gcc	gaa	ttg	gac	tac	ctc	atg	gat	gtg	ctg	793
Ala	Pro	Glu	Leu	Asp	Glu	Ala	Glu	Leu	Asp	Tyr	Leu	Met	Asp	Val	Leu	
			180						185					190		
gtg	ggc	aca	cag	gca	ctg	gag	cga	ccg	ccg	ggg	cca	ggg	cgc			835
Val	Gly	Thr	Gln	Ala	Leu	Glu	Arg	Pro	Pro	Gly	Pro	Gly	Arg			
			195					200					205			
tgagccctcg	tgctggaatg	gttgctctggt	atctgaactg	agcctgtctgg	ctggaccaac											895
tgctctcgaa	aagacacagc	tggcttcctt	agtagacaga	acagggtctg	ggccactttg											955
gagagacaga	atctagtcct	gggcaacttc	acatccgtcc	tcctgtctca	gggctggcag											1015
ggggagcctg	gaattacccc	ctagtgatgg	aatgacaggg	tctggtgggg	actgaattcc											1075
ctggccctgg	ggcatagct	tgggtgtgtc	cttctctgat	acgggaagag	acccaatcag											1135
atttttcaaa	ttaaagccag	tcttgggaaa	tctcaaaaaa	aaaaaac												1182

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 <222> 59..505

<221> sig_peptide
 <222> 59..358
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LASSPLFTMGGLG/FI

<221> polyA_signal
 <222> 1042..1047

<221> polyA_site
 <222> 1062..1073

<400> 212																
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atg	gag	act	ttg	tac	cgt	gtc	ccg	ttc	tta	gtg	ctc	gaa	tgt	ccc	aac	106
Met	Glu	Thr	Leu	Tyr	Arg	Val	Pro	Phe	Leu	Val	Leu	Glu	Cys	Pro	Asn	
-100					-95					-90					-85	
ctg	aag	ctg	aag	aag	ccg	ccc	tgg	ttg	cac	atg	ccg	tcg	gcc	atg	act	154
Leu	Lys	Leu	Lys	Lys	Pro	Pro	Trp	Leu	His	Met	Pro	Ser	Ala	Met	Thr	
					-80				-75					-70		
gtg	tat	gct	ctg	gtg	gtg	gtg	tct	tac	ttc	ctc	atc	acc	gga	gga	ata	202
Val	Tyr	Ala	Leu	Val	Val	Val	Ser	Tyr	Phe	Leu	Ile	Thr	Gly	Gly	Ile	
			-65				-60						-55			
att	tat	gat	gtt	att	gtt	gaa	cct	cca	agt	gtc	ggt	tct	atg	act	gat	250
Ile	Tyr	Asp	Val	Ile	Val	Glu	Pro	Pro	Ser	Val	Gly	Ser	Met	Thr	Asp	
			-50				-45					-40				
gaa	cat	ggg	cat	cag	agg	cca	gta	gct	ttc	ttg	gcc	tac	aga	gta	aat	298
Glu	His	Gly	His	Gln	Arg	Pro	Val	Ala	Phe	Leu	Ala	Tyr	Arg	Val	Asn	
			-35				-30				-25					
gga	caa	tat	att	atg	gaa	gga	ctt	gca	tcc	agc	ttc	cta	ttt	aca	atg	346
Gly	Gln	Tyr	Ile	Met	Glu	Gly	Leu	Ala	Ser	Ser	Phe	Leu	Phe	Thr	Met	

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-20          -15          -10          -5
gga ggt tta ggt ttc ata atc ctg gac gga tgc aat gca cca aat atc      394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
          1          5          10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc      442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
          15          20          25
cta twr agt ttt ttc ayt gct aga gta ttc atg aga atg aaa ctg ccg      490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
          30          35          40
ggc tat ctg atg ggt tagagtcct ttgasaagaa atcagtggtat actggatttg      545
Gly Tyr Leu Met Gly
          45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa      605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga      665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttccgtctgg      725
ctatttgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata      785
ttccatatct accaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat      845
tttttggaaga tgacattttct gattttcaga aattaacata aaatccagaa gcaagattcc      905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc cttaactag      965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcttgc acaataagat      1025
gtatgaacgg agcagaataa aatacttttt ctaattaaaa aaaaaaaaaa      1073

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<212> DNA
<213> Homo sapiens

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<222> 1..207

<221> sig_peptide
<222> 1..147
<223> Von Heijne matrix
      score 7.59999990463257
      seq HLPFLLLLSCVGX/XP

<221> polyA_signal
<222> 784..789

<221> polyA_site
<222> 807..818

<400> 213
atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat      48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
          -45          -40          -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg      96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu
          -30          -25          -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg      144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Ser Cys Val Gly
          -15          -10          -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat      192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
          1          5          10          15
ttt ttt att cct gac tgagtcacca caccctctc cctgatcaa agggaatatK      247
Phe Phe Ile Pro Asp
          20
artttttaat ttgatcgac tgaggtgccg ggagaaactg cagkcccagg tatccmvaca      307

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gccaccaggga tgggtccctcg ccccccaccc accgcctctk cccacacctt tccaactgtg 367
tgcattgctgg gaaatggggg gtgtggggga aggggctgcc ggcttctttc aggangctga 427
rgtttggar gaaatcaac ctgggaracc accccggccg cgggcgctca gtggacaggt 487
gggargaaaa gaaaactctc taccttggar garggacatc ccgcttccct atccttagct 547
tttttgttgc tcctccccac tgccccctttt aatttatttg gttgttttgc gaaggagggg 607
ggaagggggg aagctggggc gggaactgtc cgaggtgctg agctggggcg ggaccggaat 667
cctcccggtg ggggtaccagg gactgagttg ggcctggggc cgtgtccaag gtgccaatga 727
tgccggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccgga aagaactata 787
aagcgctgga agcgctgca aaaaaaaaaa a 818

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<210> 214
<211> 971
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
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<221> sig_peptide
<222> 12..101
<223> Von Heijne matrix
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seq ILFCVGAVGACTL/SV

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<221> polyA_signal
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<221> polyA_site
<222> 961..971

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Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
-30 -25 -20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act 98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
-15 -10 -5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag 146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu
1 5 10 15
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag 194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
20 25 30
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac 242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu His Asn
35 40 45
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg 290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
50 55 60
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act 338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
65 70 75
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg 386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
80 85 90 95
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta 434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val
100 105 110
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct 482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala

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115      120      125
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc 530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe
130      135      140
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata 578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile
145      150      155
aaa gaa gac tca caa aag aag agt gct cgg cgt att ttt cag gaa 626
Lys Glu Asp Ser Gln Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu
160      165      170      175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa 674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln
180      185      190
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac 722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn
195      200      205
tat gaa agg cca tagaaacgtt ttaattttca atgaagtcac tgaaatcca 774
Tyr Glu Arg Pro
210
actccaggag ctatggcagt gttaaatgaac atatatcatc aggtctttaa aaaaaataaa 834
ggtaaaactga aaagacaact ggctacaaaag aaggatgccaa raatgtaagg aaactataac 894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa 954
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<212> DNA
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<222> 378..518

<221> sig_peptide
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score 5.5
seq SLMTCTTLINASA/IS

<221> polyA_signal
<222> 607..612

<221> polyA_site
<222> 628..640

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aatggcaggg aacctcttat ccggggcagg taggcgcctg tgggactggg tgcctctggc 180
gtgcagaagc ttctctcttg gtgtgcctag attgatcgtt ataaggctca ctctcccgcc 240
ccccaaagtg gttgatcgtt ggaacgagaa aagggccatg ttcggagtgt atgacaacat 300
cgggatcctg ggaaactttg aaaagcacc ccaagaactg atcagggggc ccatatggct 360
tcgagggttg aaaggga atg aat tgc aac gtt gta tcc gaa aga gga aaa 410
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys
-30 -25 -20
tgg ttg gaa gta gaa tgt tgg ctg atg acc tgc aca acc tta ata aac 458
Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn
-15 -10 -5
gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat 506
Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp
1 5 10

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aga aga gaa agc tgagaacttc ggaaaaaggct catctgtcac cctggaraag      558
Arg Arg Glu Ser
15
ggaaaactgta cttttccctg tgaggaacg gctttgtatt ttctctgtaa taaaaatgggg      618
ctcttttggg aaaaaaaaaa aa      640

<210> 216
<211> 745
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..304

<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
      score 4.59999990463257
      seq PLQWSLLVAVVAG/SV

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..743

<400> 216
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gtctgtcccg ggtggagcac gccgtggctg ccaagcaccg gccaccggc atg gcc ttt      118
                                     Met Ala Phe
ggc ttg cag atg ttc att cag agg aag ttt oca tac cct ttg cag tgg      166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
-25                                     -20                                     -15                                     -10
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg      214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
      -5                                     1                                     5
acg aga gtg gag tgc gag aaa tgc aac aac ctc tgg ctc ttc ctg gag      262
Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
      10                                     15                                     20
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc      304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser
      25                                     30                                     35
taggagagct ccagcagggg cacagargat tgggggcagg argartctgg aacacakcct      364
tcatgccccc tgaccccccag ccgaccctcc ccacacccta ggggtaccca gtctgtatcct      424
ctgtccgcat gtgtggccag gcctgacaaa cmcctgcaga tggctgtctg cccaactctg      484
gacctgccca ggaggtttgga gcagaaaaggc ctctccctgg ggtgtgtgtt ctctctatgg      544
gtattgggat gcatgtttctg cactgccagc agagaggggtg tgtctggggg ccaccaccta      604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc cctgtcatct      664
ccaacaagtc caaggtgaca gctgggtgcta ggggcgtggg gttaataaat ggcttatcct      724
tctctccaaa araaaaaaaaa c      745

<210> 217
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..419

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<221> sig_peptide
<222> 201..272
<223> Von Heijne matrix
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<222> 601..606

<221> polyA_site
<222> 627..637

<400> 217
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accccagaac tttggctccc tttcccttct ctctctggta gctccaggag gctgtgtgatc   180
cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc   233
      Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
      -20                               -15
ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc   281
Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
      -10                               -5                               1
tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg   329
Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
      5                               10                               15
ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar   377
Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
      20                               25                               30                               35
aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg   419
Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
      40                               45
targaaggtc tggcctgggg tcrggtgaag gagggcccag gtcagttctg gggtcccagt   479
gacctgcttt gccattctcc tgggtgcgct gctgctccct gtttctggag ctggatgttc   539
cccacctggc agttgagctg cctgagccaa tgtgtctgtc ttttgtaact gactgaacca   599
taataaaggg gaacatttgg ccctgtgaaa aaaaaaaaaa   637

<210> 218
<211> 1315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 123..302

<221> sig_peptide
<222> 123..176
<223> Von Heijne matrix
      score 4.30000019073486
      seq WTCLKSFPSPSTSS/HA

<221> polyA_signal
<222> 1279..1284

<221> polyA_site
<222> 1301..1312

<400> 218
aagagcatcc tgcgccccgg cgcgggggccc tgcggtagcc tcaggccccc cccttgagcc   60
cgcccgagag ccagtgccga atacagaaac tgcagccatg accacgcacg tcacctggga   120
ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg   167

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Met	Pro	Cys	Pro	Thr	Trp	Thr	Cys	Leu	Lys	Ser	Phe	Pro	Ser	Pro		
acc	agc	agc	cat	gca	tcg	agc	ctc	cac	ctt	cct	cca	tca	tgt	acc	agg	215
Thr	Ser	Ser	His	Ala	Ser	Ser	Leu	His	Leu	Pro	Pro	Ser	Cys	Thr	Arg	
cta	act	ttg	aca	caa	act	ttg	agg	aca	gga	atg	cat	ttg	tca	cgg	gca	263
Leu	Thr	Leu	Thr	Gln	Thr	Leu	Arg	Thr	Gly	Met	His	Leu	Ser	Arg	Ala	
ttg	caa	ggc	aca	ttg	acc	agg	cta	cag	tcc	act	cca	gca	tgaatgarat			312
Leu	Gln	Gly	Thr	Leu	Thr	Arg	Leu	Gln	Ser	Thr	Pro	Ala				
gctggaggaa	ggacatgakt	atgcggtcat	gctgtacacc	tggcgagcgt	gttccccggc											372
cattccccag	gtgaaatgca	acragcagcc	caaccgakta	raratctatg	araaracagt											432
araggtgctg	gagccggagg	tcaccaagct	catgaagtcc	atgtattttc	arcgcaaggc											492
catcgagcgg	ttctgcascg	agggtgaagcg	gctgtgccat	gccgagcgca	ggaaggactt											552
tgctctctgag	gcctacctcc	tgacccttgg	caagtctcatc	aacatgtttg	gtgtcctgga											612
gcagctaaag	aacatgaast	gcagcgtcaa	raatgaccac	tctgcctaca	agaggggcagc											672
acagttcctg	cggaagatgg	cagatcccca	gtctatccag	gagtcgcaga	acctttccat											732
gttctctggcc	aaccacaaca	ggatcaccca	gtgtctccac	cagcaacttg	aagtgatccc											792
aggctatgag	gagctgctgg	ctgacattgt	caacatctgt	gtggattact	acgagaacaa											852
gatgtacctg	actcccagtg	agaaacatat	gctcctcaag	gtaaaaactcc	cctgaggccg											912
caccatggga	gcctggggctt	acctctctac	ctctctctta	ttaaaaatcc	gttttaaaaa											972
acaagtgtttc	ttttttctta	aacattgata	cagatcttac	ggcacataat	ggtttgtaac											1032
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ttctacaatt	ttatgtgtaa	tgactgccaa	gtattctgtt	gtattggaa	attgtcatgt											1152
aacatatccc	ctgtgtgtgg	atatttgcta	aacttcatg	aacaccttg	tagcagtttt											1212
gtgtcacatc	tttttgcata	ggcaaacctc	ctagaagaga	aattgctggc	tcaaagggaa											1272
aaacagaata	aatcggtttt	tttatttcaa	aaaaaaaaaa	ccc												1315

<210> 219

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 98..673

<221> sig_peptide

<222> 98..376

<223> Von Heijne matrix

score 5.59999990463257

seq VLLLRQLFAQAEK/WY

<221> polyA_site

<222> 1025..1035

<400> 219

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ctcccggttcc tttaggtctg cgccgctgcc tgccgcc att gca gag ttg ggc cta 115

Met Ala Glu Leu Gly Leu

-90

aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163

Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg

-85

-80

-75

tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac 211

Ser Lys Arg Glu Lys Leu Lys Thr Val Asp Ser Cys Phe Gln Asp

-70

-65

-60

ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc 259

Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val

-55

-50

-45

-40

00978360.101501


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-60          -55          -50          -45
att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt      148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser

          -40          -35          -30
tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg      196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu

          -25          -20          -15
atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta      244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu

          -10          -5          1
cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga      292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5          10          15          20

atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg      340
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
          25          30          35

cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca      388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
          40          45          50

gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac      436
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
          55          60          65

caa aaa act ctt ttc tcc atg gtg ggg tgacagggtcc taaaaggaca      483
Gln Lys Thr Leu Phe Ser Met Val Gly
          70          75

atgtgcatat tacgacaaac acaaaaaaac tataccataa cccagggtgctg aaaataatgt      543
aaaaaaccttt atttttgttt ccagtcacaga gcaaaacaac acaaaaaaaa cataactatg      603
taaacacaaaa aataactgct gctaaatcaa aaactgtgtgc agcatctcct ttcaataaat      663
taaattggttg araacaatgc aaaaaaaaaa aaa      696

<210> 221
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 263..481

<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
score 11.1999998092651
seq ILVVLMLGLPLAQA/LD

<221> polyA_site
<222> 858..868

<400> 221
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ccaggcgccgg cggtaacctca cgggtggtgaa ggtcacaggg ttgcagcact ccagtagac      120
caggagctcc gggaggcagg gccgggccca cgtcctctgc gcaccacctt gaggttgagt      180
ctctgtgcgc cacccttgag ttggatccag ggctagctgc tgttgacctc cccactccca      240
cgctgccttc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg      292
Met Thr Pro Leu Leu Thr Leu Ile Leu Val
          -20          -15

gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt      340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10          -5          1          5

gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg      388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met

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	10		15		20		
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg							436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met							
	25		30		35		
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta							481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val							
	40		45		50		
tgatggctac tccaagcacg cgteccaccac ctectgtctgc cagtacgacc tctgcaacgg							541
caccggcctt gccaccccg ggcacccctggc cctggccccc atcctcctgg ccacccctctg							601
gggtctcttc taaagcccc gaggcagacc cactcaagaa caaagctctc gagacacact							661
gotayacct ckcacccakc tcacccctgcc tcacccctcca cactccctgc gacctctca							721
gcatgacca gggctcaggac tgtgggcaag aagacacccg acctccccc accaccacac							781
gacctcact cgaggccttg acctttcgat gctgtgtggg atcccaaaag tgtccggctt							841
tgatgggctg atcagcaaaa aaaaaaa							868

<210> 222
 <211> 775
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 42..299

<221> sig_peptide
 <222> 42..101
 <223> Von Heijne matrix
 score 5.40000009536743
 seq WFWHSSALGLVLA/PP

<221> polyA_site
 <222> 762..775

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					Met Asn Leu His Phe		
					-20		
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca							104
Pro Gln Tyr Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro							
	-15		-10		-5		1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt							152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys							
	5		10		15		
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc							200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr							
	20		25		30		
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa							248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys							
	35		40		45		
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg							296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg							
	50		55		60		65
cag tgaactwkk ttccwttcta aagcccttca ttcccccacaa gggttaagctc							349
Gln							
tcgaaacccc atttgatcct tggttcctat ttctgacctc ctttggaaac tgaatacgg							409
tctccatggt gtatgcaaat taaaakttgc ctgttttgtt actcttccaa cacagggtat							469
cagggaaaaa gaggccttat ctgttctctc atccccctgt ttttgacaga ctgctaagaa							529
ttcttcagga cttcctttgg ttggggattt tactttccca aaagtctgat ctgattttct							589
tcaggggtag acaagcttgt cctagtgtct tgcttcagggt ctatcagaa gaaacccagg							649
aatagaaaaa gtatgtgcct tgacttttgt cctgttgtgt gggactaaa gtgtttttgc							709
cagaattgtc aaaagctccg gttcaaaact tgtagagttt catggaaaaa caaaacaaaa							769

aaaaaa

775

<210> 223
<211> 1075
<212> DNA
<213> Homo sapiens

<220>
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<222> 198..431

<221> sig_peptide
<222> 198..260
<223> Von Heijne matrix
score 6.90000009536743
seq LLACGSLPLGLWQ/HL

<221> polyA_site
<222> 1064..1074

<400> 223
atataatttct gaggcagtag ccatctcact tgtaaaccta aaagacaccg cagagatttg 60
agggactcag aagtcacaata gagtaggtta aaaacacctt atttttcaaa ttaattgttt 120
taagaaacaa gcataacctgt gtaagtgaat tatcttaatt tgtgttgaaat caagtttagga 180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc 230
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
-20 -15
tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac 278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
-10 -5 1 5
tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca 326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
10 15 20
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt 374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
25 30 35
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac 422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
40 45 50
tct atc acc tagccattgt akccatacca agccgggctt cctacttccc 471
Ser Ile Thr
55
tctgctcccc ttggtttcct cctgtraart aaatctcact gacccttgat gcasctccaa 531
gcataataaa tatatatata ataaaacccat abtctaaaaa attcaaaacca ggawaaataa 591
asccaraaat ttgtatggga aaaatctgca caaatattatt tggccagcat gggtatcatg 651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca 711
actacttacc tctcaatacc aaaaargaaag caggaggcaa aatctctcaw taatttcata 771
aaaacaattc ttaktctggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc 831
saggtgggag gatcatggag tcgggagatc aamacctccc tgggtaacat ggtgaaaccc 891
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aaah 1075

<210> 224
<211> 981
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

09978360.101501

<222> 279..473

<221> sig_peptide

<222> 279..362

<223> Von Heijne matrix

score 4.40000009536743

seq SCFLVALIIWCYL/RE

<221> polyA_signal

<222> 944..949

<221> polyA_site

<222> 970..981

<400> 224

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gcgtgaggct catagcgctgg gcttcccga gacttctatc gttgcccggg tcccggggatc      180
gggccacacc tgccgccagg gaagaggacg accctgaccg ccccataggag ttttctccca      240
gcaaagccaa cctctaccgc tggtcgggtg gccatacc atg gga aag gga cat cag      296
                                     Met Gly Lys Gly His Gln
                                     -25
cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
                                     -20
atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
                                     -5
aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440
Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu
                                     15
cct gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg      493
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
                                     30
ctggcaggaa gggagccgac asccgcctt cggatttgat ktcacgtttg cccgtgactg      553
tcctggctat gctktgcgtc tcagcactra argacttgcc tgggtggatgg ggcacttggc      613
tatgctgatt cgcgtgaagg cggavcaaaa tctcagcaaa tcggaacctg ctctctscct      673
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cacttctggt gacactgttc atccagtgtt agtttgagg taatttgctt tctgagatag      853
aatacttggc agaagtgtga aactgtattg catgtgcggg cctgtgcaag gaacacttcc      913
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aaaaaaaaa
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<210> 225

<211> 1031

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..644

<221> sig_peptide

<222> 12..92

<223> Von Heijne matrix

score 4

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<222> 1002..1007

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<221> polyA_site
<222> 1020..1031

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          -25          -20          -15
gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca      98
Glu Leu Thr Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr
          -10          -5          1
aat aaa ttt gga gca gaa gag ara agc ctt att gga ctt tct ggc att      146
Asn Lys Phe Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile
          5          10          15
ttc atc ggc att gga gaa att tta ggt gga agc ctc ttc ggc ctg ctg      194
Phe Ile Gly Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu
          20          25          30
agc aag aac aat cgt ttt ggt aga aat cca gtt gtg ctg ttg ggc atc      242
Ser Lys Asn Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile
          35          40          45          50
ctg gtg cac ttc ata gct ttt tat cta ata ttt ctc aac atg cct gga      290
Leu Val His Phe Ile Ala Phe Tyr Ile Phe Leu Asn Met Pro Gly
          55          60          65
gat gcc ccg att gct cct gtt aaa gga act gac agc agt gct tac atc      338
Asp Ala Pro Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile
          70          75          80
aaa tcc agc aaa raa ttt gcc att ctc tgc akt ttt ctg tkg ggc ctt      386
Lys Ser Ser Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu
          85          90          95
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg      434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu
          100          105          110
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag      482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln
          115          120          125          130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt      530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu
          135          140          145
cac tgg caa ctc ctg gtc atg gtc atw ttt ggg ttt ttk gga aca att      578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile
          150          155          160
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc gcc      626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly
          165          170          175
tct gac tac cga agt atc tgcctggtg tccgtgaggg gacacgtatg      674
Ser Asp Tyr Arg Ser Ile
          180
acctcagaag cacagctgga cacagagctt ggtggaagaa gtgccttttg atcttcta      734
tatattgggt gatgttcagt atggaataac aagggaattaa gactgttaaa tcagccagag      794
tkgggtttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt      854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attctataa      914
tcagtgtata gaatgttaaa gttttcttct ctctctgtct cttgttgtaa gatcctgcct      974
tgatttagaa tactaggcca tatgtcatat aaatattttt tctggaataa aaaaaaa      1031

<210> 226
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS

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<222> 70..327

<221> sig_peptide

<222> 70..147

<223> Von Heijne matrix

score 9.60000038146973

seq WLIALASWSWALC/RI

<221> polyA_signal

<222> 1741..1746

<221> polyA_site

<222> 1763..1774

<400> 227

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agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg 111

Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp

-25

-20

-15

cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt 159

Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu

-10

-5

1

tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt 207

Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu

5

10

15

20

ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat 255

Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp

25

30

35

gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat 303

Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp

40

45

50

tcc cat gcc cac tgg cmt tgg rca taaaaaaatt ttcatcagaa ccaagatgg 357

Ser His Ala His Trp Xaa Ser Xaa

55

60

aatacgtctg aatcttattt tgatacgata cactggagac aattcacccct attccccaac 417

tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac 477

ttatgttggt taacctcaaa gttaaccttt tgctgggtga ttatcgagga ttgggaaaaa 537

gtgaaggaga agcaagtga gaaggactct acttagattc tgaagctgtg tttagactacg 597

tgtatgactag acctgacctt gataaaacaa aaatttttct ttttggccgt tccctgggtg 657

garcagtgcc tattcatttg gcttctgaaa attcacatag gatttcagcc attatggttg 717

agaacacatt tttaaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc 777

gttaccttcc tttatgggtc tacaaaaata aatttttctc ctacagaaaa attctctcagt 837

gtagaatgcc ttcacttttc atctctggac tctcagatca attaattcca ccagtaatga 897

tgaacaaact ttatgaaact tccccatctc ggactaagan attagccatt ttccagatg 957

gagactcaaa tgacacatgg cagtggccaa gctatttcac tgcacttgaa cagtctatca 1017

aagaagtcgt aaagagccat tctcctgaa aatggcmaa aacttcaact aatgtaacaa 1077

ttatataatg tttccctttt tgattattgc attgtatttt aatttggcca gaagtataaa 1137

gaatgttcc tttagaagtg tgttatgtct gtacctgtct gaagagtgc attaaacttt 1197

gaaggactt cactgtcact ttacgatatt ccaaatagtt ttttacctg gaaaaactaa 1257

ttcttgggat tctttccatc attttcatca aaactttcag tgtgattatg ttttcatatc 1317

ttcagtttaa tatgtcagta taatagatat tgttcaaaag tttcttgggt ctaaaagtgt 1377

gtaatctggt acacagatga atagctagat gtggaaagag atatgtaaac aagaaacctt 1437

tggttatgtt tctctaaagta aatatttgga caatcatggt aagcaaacct agtctctgaa 1497

ctgcatcttt cactctaaaa gttaaatgaa atgcatgatg gtattttatt ccttgaatta 1557

tgcaatgcaa cattttacat gtaaatagca ctggtcatat actgatgat atgggttatct 1617

gggttatatc tatttttatg taaactctat tttgttttt ggcaagaagt gaaattgaga 1677

cttatgtgca ggtgcccatt gaattttgct ctggtgtaag ctgagatcca gctttttctt 1737

acaaataaat gggaccctgt tttccaaaa aaaaaamcm 1777

<210> 228

<211> 970

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<212> DNA
 <213> Homo sapiens
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 <222> 12..497
 <221> sig_peptide
 <222> 12..104
 <223> Von Heijne matrix
 score 5.5
 seq LVGVLFVSVTTG/PW
 <221> polyA_signal
 <222> 935..940
 <221> polyA_site
 <222> 955..967

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<400> 228
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              -30              -25              -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
              -15              -10              -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg      146
Thr Gly Pro Trp Trp Gly Ala Val Ala Thr Ser Ala Gly Glu Glu Ser
              1              5              10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
15              20              25              30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
              35              40              45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
              50              55              60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
65              70              75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
80              85              90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
95              100              105              110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
115              120              125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact      597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt      657
gagcctccctt gattttaata gagaacttct atgtgtatgga ttttaaagatt tctctttttc      717
attcatatac cattttatga gttctgtata attttttgtg gttttttgtt tgttgagtta      777
aagtatatta ttgtgagatt tattttaatag gacttcccttt gaaagctgta taatagtggt      837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac      897
aaaggcaagt tgccacttgt catttttgggt tctgaaaaat aaaagtataa cttattcaca      957
aaaaaaaaaa mms
                                                    970

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<210> 229
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 90..383

<221> sig_peptide
 <222> 90..200
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFFNVHS/AV

<221> polyA_signal
 <222> 609..614

<221> polyA_site
 <222> 632..643

<400> 229
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 cacctcggcg atccccgact cccttcttt atg gcg tgc ctc ctg tgc tgt ggg 113
 Met Ala Ser Leu Leu Cys Cys Gly
 -35 -30
 ccg aag ctg gcc gcc tgc gcc atc gtc ctc agc gcc tgg gga gtg atc 161
 Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
 -25 -20 -15
 atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct ggt ttg 209
 Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
 -10 -5 1
 att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car 257
 Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Glu
 5 10 15
 aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct 305
 Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala
 20 25 30 35
 gca ggc ctt tac ctc ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg 353
 Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Xaa Arg
 40 45 50
 ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccc gcgcgtttcc 403
 Leu Asn Lys Arg Lys Glu Tyr Met Val Arg
 55 60
 ccgctccagc cctcctctta tttaaaract cctgcaccg tktcaccagg gtgcgctccc 463
 acccttgccg gcgcctctg tgggactggg ttcccgggc rararactga atcccttctc 523
 catctctg catccggccc ccgtggarar ggctgaggct ggggggctgt tccgtctctc 583
 cacccttcgc tgtgtcccg atctcaataa agagaatctg ctctcttcaa aaaaaaaaaa 643
 my 645

<210> 230
 <211> 773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..541

<221> sig_peptide

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<222> 332..376
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLPCCLLWSVFNP/ES

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 761..773

<400> 230
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 ttaggtaacc ttatatattac aataaatgaa gattaccctc aaatgctaga agctgtctag 120
 gtccgtccgg tgtgtcagat ttctctcaga ttagatgtgc caataaccaa gtttattoag 180
 taaacaactt gtacttggtt catctgggtt tattactctc acccataaac agtaatgact 240
 ctctgacct ctggaaaata gtaatgcttc caatcttgct ttgtgtatct catttaattt 300
 gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt 352
 Met Arg Phe Leu Pro Cys Cys
 -15 -10
 ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt 400
 Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe
 -5 1 5
 ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca 448
 Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser
 10 15 20
 ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac 496
 Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
 25 30 35 40
 ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act 541
 Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
 45 50 55
 tgaaaagaaa gtgtttttatt ttcaaatctg gtccatatatt acattctagt tcagagccaa 601
 gcctttaaact gtacagaatt tccactgtaa ttaaaactat ttagtgtag ttataaatag 661
 ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tgggtgaatgt 721
 atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa 773

<210> 231
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..222

<221> sig_peptide
 <222> 43..177
 <223> Von Heijne matrix
 score 4
 seq ENFLSLLSKSCSA/DP

<221> polyA_signal
 <222> 530..535

<221> polyA_site
 <222> 555..566

<400> 231
 aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt 54
 Met His Ser Leu

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                                     -45
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg      102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg
                                     -40      -35      -30
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt      150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu
-25      -20      -15      -10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc      198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
                                     -5      1      5
atg agg gac att gag aca aac aaa tgaatatgg gttaaagtac tctgagcagc      252
Met Arg Asp Ile Glu Thr Asn Lys
                                     10      15
tacaaaaaga araccagtct atcctgctgg agacagtggc cactggaara aagagctctt      312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcatcttggt      372
ttcgacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat      432
ctaactacat gagtggagacc agttgacaac acatggagca racatgagct gttctcagtg      492
artctacac aaattctcta ctcacaacac tgtgagcaat aaaatgggtg ttattttaag      552
ccaaaaaaa aaaa
                                     10      15
<210> 232
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..231

<221> sig_peptide
<222> 115..180
<223> Von Heijne matrix
score 5
seq HLFVTWSSQRALS/HP

<221> polyA_signal
<222> 419..424

<221> polyA_site
<222> 445..455

<400> 232
aacctgccag tkatgcaaat gccaaaatgt ggggtcatcat atagtattt tgaaaccttt      60
ctgaacatgt acaccacca atgctagagg ctgacttgga aaccggtggg tgca atg      117
Met
ccc gag gct gtg gaa caa tca gcc cat ctc ttt gtg acc tgg agc agt      165
Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser Ser
-20      -15      -10
cag agg gcc ctc agt cac ccc gcc cca ttc ctc acc ara raa aar aat      213
Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys Asn
-5      1      5      10
cca ttt cta tgg aag ctc tgacgtaact tcaagtgttt ctacaatact      261
Pro Phe Leu Trp Lys Leu
15
cctctctgcc cgccccatta aaacagttct tttgttaaaa aatavcctaa tgggtccaact      321
ttgctgtctg ttcttccaaa tgtttataat acacattatt tataaatatg tctgtttggg      381
aagctaagaa caagctagtt tttaacaac aaatggaaat aaatgcaatt attataaaaa      441
tycaaaaaaa aaaa
455

<210> 233
<211> 673

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..384

<221> sig_peptide
<222> 232..300
<223> Von Heijne matrix
score 3.70000004768372
seq FFLCAAFPLGAGV/KM

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 662..673

<400> 233
atttggcttg cagactgcct tctatcccag aacagctgag aaatctatga agctgagatt 60
ctgaaggacc cagcttaggt tcttccactt aggcctcaat tcccttcctt ttccaggggc 120
agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttctcttc ccagaagcca 180
ctggccccc atagcaccca gtgcctcctt ttacaagtg gaagaactag g atg gct 237
Met Ala
ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc 285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
-20 -15 -10
ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca 333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
-5 1 5 10
ctt cyg cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg 381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
15 20 25
cct tagcttctgg gcctatcscg tgccttccct cttyttccta ccacctcttc 434
Pro
tgcccttcct trawctctgt tgggcttggg gatcttagtt ttcttttggt tatttcccat 494
ctcatttttt tcttctgggc agttttttta aggggggggt ttgtgggttt ttgtttttgt 554
tttgctctcg aaaaarcatt tgcctttctt cctctcccaa cataacaatc gtggttaacag 614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa 673

<210> 234
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..427

<221> sig_peptide
<222> 143..286
<223> Von Heijne matrix
score 7.5
seq FVILLFIFTVVS/LV

<221> polyA_signal
<222> 606..611

<221> polyA_site
<222> 628..639

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atcgaagttt aaagaagggg aaacaggaga cagaaatata ctgaaccaa aagattccaa      120
agagcaagtg gaatctctaa ga atg gct tcc agc cac tgg aat gaa acc act      172
                               Met Ala Ser Ser His Trp Asn Glu Thr Thr
                               -45                               -40
acc tct gtt tat cag tac ctt ggt ttt caa gtt caa aaa att tac cct      220
Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro
-35                               -30                               -25
ttc cat gac aac tgg aac act gcc tgc ttt gtc atc ctg ctt tta ttt      268
Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile Leu Leu Leu Phe
-20                               -15                               -10
ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc ctt tat gaa gtg      316
Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe Leu Tyr Glu Val
-5                               1                               5                               10
ctt gam wgc tgc tgc tgt gta aaa aac aaa acc gtg aaa gac ttg aaa      364
Leu Xaa Xaa Cys Cys Val Lys Asn Lys Thr Val Lys Asp Leu Lys
15                               20                               25
agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt      412
Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg
30                               35                               40
gaa act gaa gtg gtc taacactcta taaaaatga acaaaatctc tgaaagcagc      467
Glu Thr Glu Val Val
45
tcaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc      527
tgactgaatg gttaaaacat ttctagtara aggggaaaaa aaakttaaac atgcactggt      587
tgtgtgtata scattttcat taaatatata gtaaaactyc aaaaaaaaaa aa      639

<210> 235
<211> 772
<212> DNA
<213> Homo sapiens

<220>
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<222> 284..463

<221> sig_peptide
<222> 284..379
<223> Von Heijne matrix
score 3.79999995231628
seq TFINITLWLGSLC/QR

<221> polyA_site
<222> 762..772

<400> 235
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aagctgctca gtaagtcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct      180
gttgaaatgaa ggtagacgca gcaggcagtt tgctcctacc agtgacctgg aagacggtgg      240
cacttctcga gtgagctcac ttaccttccc tgaatgggtga ggc atg gat gaa tat      295
                               Met Asp Glu Tyr
                               -30
tcc tgg tgg tgc cac gtg tta gag gtg gta aag ggt caa atg ttt act      343
Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr
-25                               -20                               -15
ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc      391
Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe
-10                               -5                               1

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tat gcc tgc ggt act tat ttc cta ata tat atc agc aca gta acg cct 439
Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro
5 10 15 20
agc tgg agg ctt tgt ctt gtt agt tgataaatta gtggtaacag gtatatttgg 493
Ser Trp Arg Leu Cys Leu Val Ser
25
ttacctccca aagtgcctggg attrcagacg tgagccaccg cgctctggccg aaacaattct 553
tttgaagag agaagctctc ctgtgttgcg caggctggtc tcagactcct ggggtcaagt 613
gagcctcctg ctttcgcctc ctaaagtgtc gggattacag cgctgagcca ccgaccgccg 673
acagatgtgt tgattttaaa gtgggtatga ggctgagccg ctggagtgtt agaccagcct 733
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<210> 236
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 162..671

<221> sig_peptide
<222> 162..398
<223> Von Heijne matrix
score 4.09999990463257
seq QGVLFICFTCARSP/FP

<221> polyA_signal
<222> 805..810

<221> polyA_site
<222> 830..840

<400> 236
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atgtttcccg ggaagaactg ggataaagggt gtcccagcac c atg gag gac ccg aac 176
Met Glu Asp Pro Asn
-75
cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc 224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
-70 -65 -60
cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc 272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
-55 -50 -45
cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg 320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met
-40 -35 -30
aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc 368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
-25 -20 -15
ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aya gcc 416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Lys Lys
-10 -5 1 5
ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg 464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu
10 15 20
ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt 512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
25 30 35
ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr 560

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[illegible]

30 35 40 45
 ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct 491
 Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala
 50 55
 tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct 539
 Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser
 65 70 75
 ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga 587
 Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg
 80 85 90
 cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc 632
 His Trp Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105
 tgaattatcac ctacaacctg tctctgggaca gtatcaatcac tgatgagcaa cctggcacac 692
 aaactatgag cagaccactt cagcttgaga atgcagtgagg tctgaagatg gtcaagtctg 752
 tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa 812
 aatacgctatt acaagcaaaa aaaaaaaa 840

<210> 238
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..362
 <221> sig_peptide
 <222> 21..200
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LVILSLKSTLDA/ET

<221> polyA_signal
 <222> 821..826
 <221> polyA_site
 <222> 838..849

<400> 238
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 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
 -60 -55 -50
 tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca 101
 Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
 -45 -40 -35
 gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att 149
 Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
 -30 -25 -20
 aaa gaa tgc cat ctc gtc ata ctg tgc ctg aag agc caa acc tta gat 197
 Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
 -15 -10 -5
 gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga 245
 Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
 1 5 10 15
 atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt 293
 Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
 20 25 30
 tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa cgc ctg 341
 Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu
 35 40 45

ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt 392
Phe Glu Leu Phe Ser Ser Lys

50
gggtgggctgg gaactcaatg tcttgtgacg kcccttwgga ttkctctakg ctygckgttg 452
gaatataacc aattataccw cagctgtaka aatwtgtttt taatgtgggg taccygggtg 512
ktgtggaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt 572
catggtagat tatattaaaa catcagtgagg ctgttattgt gcttaactac ctcaagtgtg 632
gcttaaaagca agtcttcaat tgaaaaactg tatagaaatg ctttatattt aaaaatgaaa 692
gtaaatgggar mttgcacata gctgaaaatg tgaagggctg cccaggaggg amatggaagc 752
tgtgtgcttc tcttgccata ccttgcccta tgcctctctt tgtttcaatc ctttgtcata 812
tcctttataa taaactggta aatgtaaaaa aaaaaaa 849

<210> 239
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..503

<221> sig_peptide
<222> 21..344
<223> Von Heijne matrix
score 5.30000019073486
seq ACMTLTASPGVFP/SL

<221> polyA_signal
<222> 1305..1310

<221> polyA_site
<222> 1330..1341

<400> 239
aaacaactcc ggaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag 53
Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln
-105 -100
tcc ccc cag gcc ctg gag gac tgg ggc ccg gtg aat atc tca gtc tca 101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
-95 -90 -85
atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc 149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
-80 -75 -70
aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt 197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
-65 -60 -55 -50
tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct 245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
-45 -40 -35
aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag 293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
-30 -25 -20
gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc 341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
-15 -10 -5
ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg 389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
1 5 10 15
cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa 437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
20 25 30

09978360.101501

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aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg      485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
      35          40          45
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag      533
Glu Lys Ser Ile Met Leu
      50
atgatgaccg ttcattaata aatttgcac tcatgcacac cagttacttc ctctttgtga      593
tggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga      653
gcaatcctga attttgtccc gagaaggtgg ctttggctga agcctaattc cacagctcct      713
tggtttttga gagagactga gagaaccata atccttgcct gctgaaccga gccctgggct      773
ggatgctctg tgaatacatt atcttgcgat gttgggttat tccagccaaa gacatttcaa      833
gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg      893
cacgtgcttt gccctgggta cagccagagc ccttcaacc caccctggac ttgaggacct      953
acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac     1013
gatgttttca ccaaggtcac aggagcattg cgctgctgat ggggttgaag ttgtgtttgg     1073
ttcttgtttc agcccaatat gttagaagaa ttgaaacag ctgcacacct tgatacggta     1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgctctgtg ctttaataatc     1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaacacata ccttaagttt     1253
ttttgttttt gttttgtttt ttgttttttt tgttttcctt tatgaagaaa aaataaata     1313
gtcacatttt aatacyaaaa aaaaaaaamc h      1344

<210> 240
<211> 671
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..201

<221> sig_peptide
<222> 1..63
<223> Von Heijne matrix
      score 5.09999990463257
      seq LLLKIWLQRPES/QE

<221> polyA_signal
<222> 637..642

<221> polyA_site
<222> 660..671

<400> 240
atg ctg gga ggt gac cat agg gct ctg ctt tta aag ata tgg ctg ctt      48
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
      -20          -15          -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg      96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
      -5          1          5          10
atg gag agg aga gtt aaa aat gac ctg atg tcc ttc ttg tcc acg gtt     144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
      15          20          25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca     192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
      30          35          40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg      241
Leu Arg Met
      45
ctcagttcat ttaaaaaaga tatctatttg aaagtcttca rarttgtaca tatgtttcac     301
agtacaggat ctgtacataa aagtttcttt cctaaccat tcaccaagag ccaatatcta     361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcttc ctgtgtattt     421

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09978360.103501


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ctgtttgttaa racttaagtg agttaggtct ttaaggaagg caacgctcct ctgaaatgct 481
tgtctttttt ctgttgccga aatarctggg ccttttttcgg gagttaratg tatarartgt 541
ttgtatgttaa acatttcttg taggcatcac catgaacaaa gatattttt ctattttattt 601
atttatgtg cacttcaaga agtcactgtc agagaaataa agaattgtct taaatgtcaa 661
aaaaaaaaaa

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<210> 241
<211> 1601
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 39..1034

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<221> sig_peptide
<222> 39..134
<223> Von Heijne matrix
score 6.09999990463257
seq LPLLTSAHLGLQ/QH

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<221> polyA_signal
<222> 1566..1571

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<221> polyA_site
<222> 1587..1597

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```

<400> 241
agccccagat cctgaaggag gtgcagagcc cagagggg atg atc kcg ctg agg gac 56
Met Ile Xaa Leu Arg Asp
-30
aca gct gcc tcc ctg cgc ctt gag aga gac aca agg cag ttg cca ctg 104
Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
-25 -20 -15
ctc acc agt gcc ctg cac gga ctg cag cag cag cac cca gcc ttc tct 152
Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser
-10 -5 1 5
ggg gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt 200
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
10 15 20
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc 248
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Ala Leu Phe
25 30 35
ctg cac cct gag ccc ttc acc cct cgg agt tcc ccc cag gtt ggc ttc 296
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
40 45 50
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc 344
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
55 60 65 70
ctc ttt gtc aac ctc aat aat gag ctc act gtg gag cag cag gtg gar 392
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
75 80 85
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc 440
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
90 95 100
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga 488
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
105 110 115
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc 536
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
120 125 130

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tgt	ccc	atg	tta	rar	aas	cag	ctc	atg	gat	ccc	cgg	gga	cct	ggg	gac		584
Leu	Pro	Met	Leu	Xaa	Xaa	Gln	Leu	Met	Asp	Pro	Arg	Gly	Pro	Gly	Asp		
135					140					145				150			
att	cgc	aca	gkg	ttc	cgg	cgc	ccc	ttg	gac	att	tac	gac	gtg	ctg	att		632
Ile	Arg	Thr	Xaa	Phe	Arg	Pro	Pro	Leu	Asp	Ile	Tyr	Asp	Val	Leu	Ile		
				155					160					165			
cgc	ctg	tct	cct	cgc	cat	atc	ccg	cgg	cac	cgc	cag	gct	gtg	cag	tcr		680
Arg	Leu	Ser	Pro	Arg	His	Ile	Pro	Arg	His	Arg	Gln	Ala	Val	Asp	Ser		
				170					175				180				
cca	gct	gcc	tcc	ttc	tgc	cgg	ggc	ctg	ctc	agc	cag	ccg	ggg	ccc	tca		728
Pro	Ala	Ala	Ser	Phe	Cys	Arg	Gly	Leu	Leu	Ser	Gln	Pro	Gly	Pro	Ser		
				185			190					195					
tcc	ctg	atg	ccc	gtg	ctg	ggc	tak	gat	cct	cct	cag	ctc	tat	ctg	acg		776
Ser	Leu	Met	Pro	Val	Leu	Gly	Xaa	Asp	Pro	Pro	Gln	Leu	Tyr	Leu	Thr		
	200					205					210						
cag	ctc	arg	gag	gcc	ttt	ggg	gap	ctg	gcc	ctt	ttc	tct	tat	gac	cag		824
Gln	Leu	Xaa	Glu	Ala	Phe	Gly	Asp	Leu	Ala	Leu	Phe	Phe	Tyr	Asp	Gln		
215				220					225					230			
cat	ggt	gga	cag	gtg	att	ggt	ctg	ctc	tgg	aag	ccc	acc	agc	ttc	cag		872
His	Gly	Gly	Glu	Val	Ile	Gly	Val	Leu	Trp	Lys	Pro	Thr	Ser	Phe	Gln		
				235					240					245			
ccg	cag	ccc	phe	aag	gcc	tcc	agc	aca	aag	ggg	cgc	atg	gtg	atg	tct		920
Pro	Gln	Pro	Phe	Lys	Ala	Ser	Ser	Thr	Lys	Gly	Arg	Met	Val	Met	Ser		
				250				255				260					
cga	ggt	ggg	cag	cta	gta	atg	gtg	ccc	aat	ggt	gaa	gca	ata	ctg	gag		968
Arg	Gly	Gly	Glu	Leu	Val	Met	Val	Pro	Asn	Val	Glu	Ala	Ile	Leu	Glu		
	265					270					275						
gac	ttt	gct	gtg	ctg	ggt	gaa	gcg	ctg	gtg	cag	act	gtg	cag	gcc	cga		1016
Asp	Phe	Ala	Val	Leu	Gly	Glu	Gly	Leu	Val	Gln	Thr	Val	Glu	Ala	Arg		
	280					285					290						
agt	gag	agg	tgg	act	gtg	tgatccccagc	tctggaggcaa	gctgtagacg									1064
Ser	Glu	Arg	Trp	Thr	Val												
	295				300												
gacacgagga	cattgtgacct				ctagacgaag	atgtcagtag			gatgacctcc	accctcctctg							1124
gcacatgaatc	ctccatggag	ggcctgtctg			ctgaacatgc	tgaactatct	ccaacaaaaa										1184
ccagcccocaa	ctttctctct	gatgtccag			ctatggggca	ggggctaggt	ggccctgtaa										1244
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<210> 242
<211> 1206
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 69..125
<223> Von Heijne matrix
      score 3.90000009536743
      seq ALSMSSSFSPHSSS/CS
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<221> polyA_site
<222> 1196..1205

<400> 242
acatttggtga ctttaccaat accctccag ttcttgatag acagctgtag gttgctgggt      60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt      110
      Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
      -15                      -10
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc      158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser
-5                      1                      5                      10
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
      15                      20                      25
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys
      30                      35                      40
att gtg ggc tgatttggtc ttctctctct cctccactg ttaactgccct      303
Ile Val Gly
      45
gcagcccttg ttcagggtga cagaccctta ttctggcctc tagtgtcctt gtctgtcatg      363
acacaccctt ccgcccaaat acctctgacc ccaaggctgg aatggggctg gtgggarata      423
agtttgctta ctcataatca tgcctcttct ctggcaccct gcttccctgc ggtgtcctca      483
aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt      543
gtattattat taagggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa      603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt      663
ctgaggcagc tgggtgccac cccttttcar atgttttagtc ctgcaaatag catctttctt      723
gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat      783
caakttgagt tttttccag cagggggttar gggagggtact cctgtgtgat atttgacact      843
araaaagtaa cttttttaca aaactgtttt tctaggtggg tggaaagtga aactgccaca      903
tcttgttggg ttattgtcaa raratcattt gcaacaacag taratgtccg ggttttgttt      963
ctgtcttttt attatgaaaa actatgttaa gggggaaaaa gtgggattat gtaaccarag      1023
gaatccctas ctttgttttc cttaraarac ttgttttagt ttttatcara cgtctgttgt      1083
agttgtarac aggaagagctt gtgaaaaaaa caccacatgg ascctgtaaa tgtttttgca      1143
caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gttttaccat ttaaaaaaaa      1203
aat
1206

<210> 243
<211> 536
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..285

<221> sig_peptide
<222> 115..204
<223> Von Heijne matrix
score 3.70000004768372
seq SMLLTIVYGYLC/SV

<221> polyA_signal
<222> 505..510

<221> polyA_site
<222> 525..536

<400> 243
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tgcctgagga ggctcgggtt ggatgcgaag gagctgcagc atccagggga caag atg      117

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Met
-30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc 165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
-25 -20 -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga 213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
-10 -5 1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa 261
Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
5 10 15
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcttgagcar 315
Glu Gln Lys Xaa Ser Gly Ile Met
20 25
asakgcccac ggcactgctgt ggagagactt caccctgccac catttccagg tcaacaggac 375
tagagcggttg atggtttttca aaccctgttg gaagaaagtg cccatgggtt ctctggttct 435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca 495
cctacagaca ttaataaatt tgctgtgtca aaaaaaaaaa a 536

<210> 244
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..344

<221> sig_peptide
<222> 90..140
<223> Von Heijne matrix
score 8.19999980926514
seq LLLITAILAVAVG/FP

<221> polyA_signal
<222> 500..505

<221> polyA_site
<222> 515..527

<400> 244
aataatrarac agctacaata ttccaggggcc artcacttgc catttctcat aacagcgtca 60
gagagaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc 113
Met Lys Lys Val Leu Leu Leu Ile
-15 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20
wtg ttt gtg ttc cct tac cca tat cca ttt cgc cca ett cca cca att 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile
40 45 50 55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccatttc cttgaaraat 414

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caaaattcct gttaataaaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc 529

<210> 245
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..311

<221> sig_peptide
 <222> 57..107
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

<221> polyA_signal
 <222> 467..472

<221> polyA_site
 <222> 482..493

<400> 245
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 Met
 aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt 107
 Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
 -15 -10 -5
 ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac 155
 Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
 1 5 10 15
 agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca 203
 Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
 20 25 30
 ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga 251
 Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
 35 40 45
 cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt 299
 Arg Asn Phe Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
 50 55 60
 ccg agc gaa aag taacaagaa ggaaaagtca cgataaacct ggtcacctga 351
 Pro Ser Glu Lys
 65
 aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaaa gaaaaacaaa 411
 tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 471
 atagcaaacg aaaaaaaaaa aa 493

<210> 246
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..302

<221> sig_peptide
 <222> 96..182
 <223> Von Heijne matrix

09073360..101501

score 5
seq ELSLLPSSLNVLA/TS

<221> polyA_site
<222> 501..514

<400> 246
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tctcatccag cggctgcgga actggggcgc cgggc atg acc tgc agg gga agc 113
Met Thr Cys Arg Gly Ser
-25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca 161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
-20 -15 -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca 209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
-5 1 5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt 257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10 15 20 25
crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg 302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
30 35 40
tagctgccac tgaaaaraag cgggtgactc cagctcctcc cataaaggag tgggagctgt 362
cctcgagcca gccttacctg tgacactgca cctccacggc caccgacta ctttgctccc 422
ttggattccc tccagggaga atgtgacctt atttatgaca aatacgtara gctcaggatg 482
cacttcctagt tttactttaa aaaataaaaa aatagagac 521

<210> 247
<211> 811
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..526

<221> sig_peptide
<222> 161..328
<223> Von Heijne matrix
score 4.19999980926514
seq XSPLLTLALLGQC/SL

<221> polyA_site
<222> 799..811

<400> 247
aaaaaattgc agtgctgaag acactggacc cgcaaaaggc tgtccctccc aaacctggga 60
ttctgggctc actgagttca cctgcgagtc agccctacct gcaactgctc ggtctagtag 120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc 175
Met Val Pro Trp Pro
-55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc 223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
-50 -45 -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct 271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35 -30 -25 -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg 319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
-15 -10 -5

09978360.101501

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ggg cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa      367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
1 5 10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg      415
Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
15 20 25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa      463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
30 35 40 45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt      511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
50 55 60
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaaa ccttcaaaara      566
Gln Phe Phe Leu Gly
65
caatgttatt acagcactct ccccttatcc aaakttttct tttcctgadt ttcagttagc      626
tatggtgcaac cgcttggaac atakttgaac acagtacaat aaratatttt gaggtggga      686
ktggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact      746
tgaaccagg aktttgarac caccctgggc aacatrgtra gacctcatct ctacaaaaaa      806
aaaaa      811

<210> 248
<211> 625
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..332

<221> sig_peptide
<222> 210..299
<223> Von Heijne matrix
score 8.10000038146973
seq ITCLLAFWVPASC/IQ

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 613..625

<400> 248
acaggtcscm ttaacatctc ttgatttgag ccactcccac tgtcatcagc ttacacctgg      60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccctaaaa      120
atgcatgtga tagttgatca agtcaactctc tggcctaaaa ccttccttgg ctccctgctg      180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc      233
Met Ala Cys Glu Thr His Gly Val
-30 -25
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc      281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
-20 -15 -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca      329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
-5 1 5 10
ctc tgattctctc tttcttttgg tcacagagaa aggggtacttt ctctgtcaaa      382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc      442
accctggcat actacacara tcaactctggg ctcaactgcc tgccctaatgg tcatctcccc      502
agtaaacctgt aagctccttg agggcaagga ttgtgttggg atttttgtat taacagtgcc      562
tggtcttggtg cctggcacct aaaagcact caataaatgt ttgtttaatg aaaaaaaaaa      622

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<210> 249
 <211> 684
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..361

<221> sig_peptide
 <222> 212..319
 <223> Von Heijne matrix
 score 4.09999990463257
 seq HWLFLASLSGIKT/YQ

<221> polyA_signal
 <222> 650..655

<221> polyA_site
 <222> 673..684

<400> 249
 atccccawns cactctctca cagagactgt tcttttctct ctgagaccct actccagctt 60
 gtatgttctaa atctgtgatt atgcactgtc tgtcttctct ttgaggtcag gggccatttc 120
 ttttgttctc tgctatgctc aggaccaga tcaaaggagc tcagtaacta tttacaggcg 180
 tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc 232
 Met Ala Pro His Thr Ala Ser
 -35
 ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag 280
 Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
 -25 -20 -15
 cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc 328
 His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
 -10 -5 1
 tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattacctt attcacaca 381
 Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile
 5 10
 aggtgttaat ggtggtaatg gcataktatt tattacccca ggggacccak aacgggtggt 441
 tcaaaacata tcattcccca gtgggtttaa actctggttag ctttccargg aatccaaaagt 501
 ggaatccagt ctcttagctg gawttcacag ggcccgtct gcacaacttg gcttctgtcg 561
 gcttccctan ccttgacttc ccaagcctta gtcacaccc tctctccacc ccagggtctca 621
 gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcat yaaaaaaaaa 681
 aaa 684

<210> 250
 <211> 628
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..482

<221> sig_peptide
 <222> 75..128
 <223> Von Heijne matrix
 score 3.59999990463257
 seq KMLISVAMLGAXA/GV

00973360.101501

<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

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<400> 250
aagtgcagacc gcgcggcaac agcttgccgc tgcggggagc tcccgctggc gctccgctgg      60
ctgtgcaggc gccc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca      110
               Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
               -15                               -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg      158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
               -5                               1                               5                               10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg      206
Thr Pro Gly Glu Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
               15                               20                               25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg      254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
               30                               35                               40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg      302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
               45                               50                               55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac      350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
               60                               65                               70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc      398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
               75                               80                               85                               90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg      446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
               95                               100                               105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg      492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
               110                               115
tcgggtgagc acgtgtcccc caaacccctgg actgactgct ttaaggtccg caaggcgggc      552
caggcccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaa catgttcctc      612
cammcacaaaa aaaaaa      628

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<210> 251
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..631

<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
score 8
seq LTLIGCLVTGVES/KI

<221> polyA_signal
<222> 777..782

<221> polyA_site
<222> 801..812

<400> 251

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aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                     Met Gln Asp
                                     -65
gct ccc ctg agc tgc ctg tca cgg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
-60                                     -55                                     -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
-45                                     -40                                     -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
-30                                     -25                                     -20                                     -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
-10                                     -5                                     1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Thr Tyr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
5                                     10                                     15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
20                                     25                                     30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
35                                     40                                     45                                     50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
55                                     60                                     65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
70                                     75                                     80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
85                                     90                                     95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
100                                     105                                     110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc      631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
115                                     120                                     125
taaactggaa ctggaccag gatgctttgc ascaacgccc tagggtttgc agtgaatgtc      691
caaatgcctg tgcctctctg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg      751
gaaaattaaag ctatactttt aagaaaataa atatttccat ttaaatgtca amaaaaaaaaa      811
ah                                                                                   813

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<210> 252

<211> 778

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..576

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix

score 4.80000019073486

seq MMVLSLGIILASA/SF

<221> polyA_signal

<222> 737..742

<221> polyA_site

<222> 763..775

<400> 252

agtaaaaaaa cactggaata aggaaggcgt gatgactttc agaagatgaa ggtaagtaga 60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag 120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc 174
Met Thr Ser Gln Pro Val Pro
-65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
-60 -55 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
-45 -40 -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
-30 -25 -20 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
-10 -5 1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
5 10 15
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg 462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
20 25 30
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct 510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
35 40 45 50
gcc agc tgc cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa 558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
55 60 65
tct tgt tct cct gtc ggg targataaca ggggttgctt ratttttagat 606
Ser Cys Ser Pro Val Gly
70
caatttttta tcagactcaa ataaacattt tttttgaaaa tcattcttatt cttcacatta 666
tcattcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaaatc 726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaah cc 778

<210> 253

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..897

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix

score 4.80000019073486

seq MMVLSLGIILASA/SF

<221> polyA_signal

<222> 1017..1022

<221> polyA_site

<222> 1044..1054

09970360.101501

<400> 253
agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga 60
aacggttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag 120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc 174
Met Thr Ser Gln Pro Val Pro
-65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
-60 -55 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
-45 -40 -35
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt 318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
-30 -25 -20 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
-10 -5 1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
5 10 15
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc 462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
20 25 30
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt 510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val
35 40 45 50
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg 558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu
55 60 65
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg 606
Ser Val Lys Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu
70 75 80
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat 654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His
85 90 95
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct 702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala
100 105 110
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa 750
Gly Thr Ser Val Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa
115 120 125 130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc 798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
135 140 145
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm 846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly
150 155 160
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act 894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
165 170 175
tct taagaaaaaa gggagaaaaa ttaatcagaa agttgattct tatgataata 947
Ser
tggaagaagt aaccattata gaaaagcaaa gcttgagttt cctaataatga agcttttaaa 1007
gtaatgaaca ttaaaaaaaa ccattatttc actgtcaaaa aaaaaamcc nkt 1060

<210> 254
<211> 444
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 146..292

<221> sig_peptide
<222> 146..253
<223> Von Heijne matrix
      score 5.5
      seq FTSMCILFHCLLS/FQ

<221> polyA_signal
<222> 395..400

<221> polyA_site
<222> 433..444

<400> 254
aacttgggac aagaratcaa actttaaaga tggctctaaag cccctcttaa aggtctgact   60
gtgtcgggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc   120
ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg   172
                               Met Gln Val Pro His Leu Arg Val Trp
                               -35                               -30
aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca   220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
      -25                               -20                               -15
agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa   268
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
      -10                               -5                               1                               5
aag aaa aga aaa ctt ara ctt ttc tgaatgtctt ttttacctaa ataaccattt   322
Lys Lys Arg Lys Leu Xaa Leu Phe
      10
tattgttgtt ttgctttttc tgccttcaaa ctactccac aggccaaata tavctggctg   382
ctctcttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa   442
aa                                                                                   444

<210> 255
<211> 754
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 126..383

<221> sig_peptide
<222> 126..167
<223> Von Heijne matrix
      score 7.5
      seq VALNLILVPCCAA/WC

<221> polyA_signal
<222> 726..731

<221> polyA_site
<222> 743..754

<400> 255
aattgatgt tacgatgttg tattgatatt taagaaagta attkratttg taaaacttct   60
gctcgtttac actgcacatt gaatacaggt aactaattgg wvaggagagg gaggtcactc   120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg   170

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Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
-10 -5 1

tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct 218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
5 10 15

gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt 266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
20 25 30

tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga 314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
35 40 45

ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag 362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu
50 55 60 65

gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar 413
Gly His Arg Ile Cys Asp Leu
70

aaaccacagt cttccagca attattacaa ttcttgaatt ctttggggat tttttactgc 473
cctttcaag cacttaaktg tkrratctaa cgtkttcag tgtctgtctg aggtgactta 533
aaaaatcaga acaaaacttc tattatccag agtcatggga gactacaccc ttccaggaa 593
taagtgtttt ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtattttaaa 653
aaaagaaact ttctgaatg cctacctggc ggtgtatacc aggcagtggt ccagttttaaa 713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaa a 754

<210> 256
<211> 629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..497

<221> sig_peptide
<222> 66..239
<223> Von Heijne matrix
score 5.40000009536743
seq QLDSVLWLGALG/LT

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 618..629

<400> 256
aactccagca atgctgacca aagtgggagg agcactaggt cttcccgta cctccacttc 60
tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat cgg 110
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
-55 -50 -45

atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt 158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
-40 -35 -30

cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc 206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu
-25 -20 -15

ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca 254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
-10 -5 1 5

gtc ttt tcc acc act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc 302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe

cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tgc 393
 Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
 85 90 95
 ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga 441
 Gly Glu His Pro Xaa Xaa
 100 105
 agtgtcacta ggaactgtca gcaggacaaa ggtctgtatg tcaactgaatt tacaaaraca 501
 gcaggaaacrs ackggtgggg atgggcagct gttrargcr atggggtkac tggccttcct 561
 ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggatcgat 621
 acagtgtatg acaatgtcat atagtataac acaacataat gaataaacg tgtatatgc 681
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 aatgcaacac aaaaaaaaaa aacc 765

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 <222> 593..598

 <221> polyA_site
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 Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
 -10 -5 1
 tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
 Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
 5 10 15
 gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
 Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
 20 25 30 35
 caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
 Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
 40 45 50
 cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
 Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
 55 60 65
 atg aak ttc gaa tgg tgc ccg gcc ccc atg gtg caa ggc gtg atc acc 345
 Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
 70 75 80
 agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
 Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
 85 90 95
 gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tgc 441
 Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser

100	105	110	115	
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc				489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys				
	120	125	130	
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga				534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly				
	135	140	145	
taaacactgtg ggtgccccca cctgtgcatt gggaccacra cttcacccctc ttggaracaa				594
taaacctctca tgcccccaaa aaaaaaaaaa				623

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<221> polyA_site
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agaagaaaaa bggccaanaag ccaaaa atg ara ctg atg gta ctt gtt ttc acc				112
	Met Xaa Leu Met Val Leu Val Phe Thr			
	-20	-15		
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc				160
Ile Gly Leu Thr Leu Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg				
	-10	-5	1	5
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt				208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu				
	10	15	20	
cgg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat				256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp				
	25	30	35	
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc				304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe				
	40	45	50	
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat				352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp				
	55	60	65	
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct				400
Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser				
	70	75	80	85
ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt				455
Gly Glu His His Ser				
	90			
tctagtttct atagtagtga atagagcata gattctataa attcttactt gtctaagaaa				515
gtaaatctgt gttaacaacag tagtaataaa agttaattca atccaaaaaa aaaaaa				571

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09978360.101501

<211> 612
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 score 4.59999990463257
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<221> polyA_site
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 aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg 106
 Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
 -10 -5 1
 tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc 154
 Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
 5 10 15
 cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg 202
 Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
 20 25 30
 gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag 250
 Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
 35 40 45 50
 gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct 298
 Val Pro Arg Arg Ala Gly
 55
 gaggaccatg caccacctgc tgctggaggt ggamtgaka gagggcaccg tgcagtgcc 358
 ggaatctgga cgtatgttcc ccacagccgc cgggatcccc aacatgtcgc tgagtgaa 418
 ggaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg 478
 ttgatctata cctctgttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac 538
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 ccaaaaaaaa aaaa 612

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 <212> DNA
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<221> sig_peptide
 <222> 32..103
 <223> Von Heijne matrix
 score 4.59999990463257
 seq FFIFCSLMTLLG/GV

03973360.101501

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<222> 508..513

<221> polyA_site
<222> 528..539

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                               -20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg      100
Phe Leu Leu Arg Phe Phe ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
-15                               -10                               -5
ggg ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctg aaa gat      148
Gly Gly Val Asn Lys ile Ala Glu Lys ile Cys Gly Asp Leu Lys Asp
1                               5                               10                               15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt      196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
20                               25                               30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc      244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
35                               40                               45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt      292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys ile Glu Arg
50                               55                               60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg      338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg
65                               70                               75
tgaactcatg aagtgtgtct ctgcaccatc cgaataaag acacaagaaa attcaractg      398
atttgaaat ctttgttwtta tttccmymak ggcgwtaag ctccatatg tttgtattt
458
tccctgacct agttttgtct ttcctggaaa ttaactgtat gakkattasa atgaaagagt      518
ctttctgtca aaaaaaaaaa a      539

<210> 262
<211> 964
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 21..527

<221> sig_peptide
<222> 21..95
<223> Von Heijne matrix
score 8.5
seq LKVLLEPLAPAAA/QD

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<222> 921..926

<221> polyA_site
<222> 953..963

<400> 262
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                               Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
                               -25                               -20                               -15
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat      101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
-10                               -5                               1

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tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac	149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr	
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caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc	197
Gln Arg Phe Phe Ala Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr	
20 25 30	
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag	245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln	
35 40 45 50	
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc	293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys	
55 60 65	
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act	341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr	
70 75 80	
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt	389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Leu Leu Cys	
85 90 95	
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa	437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu	
100 105 110	
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc	485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr	
115 120 125 130	
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc	527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala	
135 140	
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccctgtccc tggggaggcca	587
ggagcagcgc ccagagcacaca agcaggagcagc aggagtgtag cacaggcagg agccgacaca	647
agaacacaaag caggaagaggc ggcagaaaca ggaagagcaca gaagaggaaac aggaagaggga	707
gggaagcagc gaagaaggac aggggactaa ggaaggaggc gaggctgtgt ctcagctgca	767
gacagactca gagcccaagt ttactctga atctctatct tctaaccctt cctcttttgc	827
tcgccgggta cganaagtag agtctactcc tatgataatg gagaacatcc agggagctcat	887
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agcggcaaga tcgcatctcc cggtc atg gcc gac tat ctg ctg cgc ggt tac	173
Met Gly Asp Tyr Leu Leu Arg Gly Tyr	
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cgc atg ctg gcc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa	221

Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln
 -65 -60 -55
 gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca 269
 Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser
 -50 -45 -40
 gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc 317
 Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser
 -35 -30 -25 -20
 caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc 365
 Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly
 -15 -10 -5
 tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag 413
 Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu
 1 5 10
 gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct 461
 Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala
 15 20 25
 gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg 509
 Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu
 30 35 40 45
 caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg 557
 Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa
 50 55 60
 gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg 605
 Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg
 65 70 75
 ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc 647
 Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro
 80 85 90
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 <222> 262..471

 <221> sig_peptide
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 <223> Von Heijne matrix
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 <221> polyA_site
 <222> 682..693

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 aacacaaacg aaagaaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat 240
 cagtgacgtc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat 291
 Met Ile Leu Cys Phe Leu Leu Pro His His
 -15 -10
 cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg 339

Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg
 -5 1 5 10
 gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa 387
 Glu Lys Leu Arg Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys
 15 20 25
 raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga 435
 Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly
 30 35 40
 gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg 481
 Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp
 45 50 55
 ctgacccttt tgatttccaa vtctcascgtt ttggtgtgaag gcggcccaar aaggatgcgg 541
 ascccagcac tgtgaagcct acaaaaacat tgatgcgctg gcttggggat ttgaatttga 601
 acatctttca cactaagttc agactcatga aaaccaatctt cagatgtctt gtaaacacca 661
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 <222> 74..172
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 seq XLCLGMALCPRQA/TR

 <221> polyA_signal
 <222> 1627..1632

 <221> polyA_site
 <222> 1640..1652

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 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln
 -30 -25
 aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg 157
 Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu
 -20 -15 -10
 tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc 205
 Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe
 -5 1 5 10
 acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt 253
 Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg
 15 20 25
 ttc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga 301
 Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly
 30 35 40
 act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc 349
 Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly
 45 50 55
 ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag 397
 Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys
 60 65 70 75
 ggt gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca 445

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aat	att	gtt	tgt	agc	aaa	rat	tac	ttt	gtc	aca	gca	aac	tcc	aac	cta	493
Asn	Ile	Val	Cys	Ser	Lys	Xaa	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	
			95						100				105			
gtg	att	atc	aca	gca	ggg	gca	cgc	caa	raa	aag	gga	gaa	acg	cgc	ctt	541
Val	Ile	Ile	Thr	Ala	Gly	Ala	Arg	Gln	Xaa	Lys	Gly	Glu	Thr	Arg	Leu	
			110				115					120				
aat	tta	gtc	cag	cga	aat	gtg	gcc	atc	ttc	aag	tta	atg	att	tcc	agt	589
Asn	Leu	Xaa	Gln	Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	
			125				130					135				
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Ile	Val	Gln	Tyr	Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	
			140				145					150			155	
gtg	gat	atc	tta	act	tat	gta	gct	tgg	aag	ttg	agt	gca	ttt	ccc	aaa	685
Val	Asp	Ile	Leu	Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	
			160						165				170			
aac	cgt	att	att	gga	agc	ggc	tgt	aat	ctg	ata	mhg	gct	cgt	ttt	cgt	733
Asn	Arg	Ile	Ile	Gly	Ser	Gly	Cys	Asn	Leu	Ile	Xaa	Ala	Arg	Phe	Arg	
			175				180						185			
ttc	ttg	att	gga	caa	aag	ctt	ggg	atc	cat	tct	gaa	agc	tgc	cat	gga	781
Phe	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	
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tgg	atc	ctc	gga	gag	cat	gga	gac	tca	agt	gtt	cct	gtg	tgg	agt	gga	829
Trp	Ile	Leu	Gly	Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	
			205				210					215				
gtg	aac	ata	gct	ggg	gtc	cct	ttg	aag	gat	ctg	aac	tct	gat	ata	gga	877
Val	Asn	Ile	Ala	Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	
			220				225					230			235	
act	gat	aaa	gat	cct	gag	caa	tgg	aaa	aat	gtc	cac	aaa	gaa	gtg	act	925
Thr	Asp	Lys	Asp	Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	
			240						245				250			
gca	act	gcc	tat	gag	att	att	aaa	atg	aaa	ggg	tat	act	tct	tgg	gcc	973
Ala	Thr	Ala	Tyr	Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	
			255						260				265			
att	ggc	cta	tct	gtg	gcc	gat	tta	aca	gaa	agt	att	ttg	aag	aat	ctt	1021
Ile	Gly	Leu	Ser	Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	
			270				275					280				
agg	aga	ata	cat	cca	gtt	tcc	acc	ata	act	aag	ggc	ctc	tat	gga	ata	1069
Arg	Arg	Ile	His	Pro	Val	Ser	Thr	Ile	Thr	Lys	Gly	Leu	Tyr	Gly	Ile	
			285				290				295					
rat	gaa	gaa	gta	ttc	ctc	agt	att	cct	tgt	atc	ctg	gga	gag	aac	ggg	1117
Xaa	Glu	Glu	Val	Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	
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att	acc	aac	ctt	ata	aag	ata	aag	ctg	acc	cct	gaa	gaa	gag	gcc	cat	1165
Ile	Thr	Asn	Leu	Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His	
			320						325				330			
ctg	aaa	aaa	agt	gca	aaa	aca	ctc	tgg	gaa	att	cag	aat	aag	ctt	aag	1213
Leu	Lys	Lys	Ser	Ala	Lys	Thr	Leu	Trp	Glu	Ile	Gln	Asn	Lys	Leu	Lys	
			335						340				345			
ctt	taaa	gttgc	taaa	actacc	attcc	gaaat	tattga	agag	atcat	agata						1266
Leu																
caggattata	taacgaaatt	ttgaataaac	ttgaattcct	aaaagatgga	aacaggaaaag											1326
ctgttagagt	gattttccta	tttattttagt	cctccagctc	ttttattgag	catccacgtg											1386
ctggacgata	cttattttaca	attccckaagt	atttttggtta	cctctgatgt	agcagcactt											1446
gccaatgttat	atatatgtag	ttgmatattg	gttcccaaaa	agttaggatgt	aggtatttat											1506
tgtgtttctag	aaattccgac	tccttttoatt	agatatatgc	tattctcttc	attcttgcgt											1566
gtttatacct	atgttcattt	atatgtctga	aaaaagtagt	agctctctct	acaatgtaaa											1626
aataaatgta	catacaaaaa	aaaaaamcmc														1656

<211> 517
 <212> DNA
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<220>
 <221> CDS
 <222> 48..164

<221> sig_peptide
 <222> 48..89
 <223> Von Heijne matrix
 score 4
 seq YYMVCLFFRLIFS/EH

<221> polyA_signal
 <222> 482..487

<221> polyA_site
 <222> 505..517

<400> 266
 aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac 56
 Met Tyr Tyr
 atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att 104
 Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
 -10 -5 1 5
 ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca 152
 Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
 10 15 20
 aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt 204
 Thr Ser Ala Gly
 25
 taaaaatgggt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctgggtg 264
 atttatatgg ctcttcacaa ggtgttattt tggggatca aggtatggat gcttaaatca 324
 gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaa atcaaccttg 384
 gtctctccac caaaacccat taatttccat atcatcatct gcataaararg gaaaattcct 444
 acwtgaccag gttactgcaa ggatktkaat ttgaaatatt aaaatattat mcmcaattgg 504
 aaaaaaaaaaaa aaa 517

<210> 267
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..334

<221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSYASSALSPCLT/AP

<221> polyA_signal
 <222> 355..360

<221> polyA_site
 <222> 392..405

<400> 267

00973360.101501

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cccagcccaa gtcagccttc agcagcgctc tttctgcaca cagatattcc aggctacct 120
ggcattccag gacctccgma atgatgtccc agtcccttac aagcgttccc tggatgaggg 180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
-35 -30 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
-20 -15 -10
ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg 325
Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
-5 1 5 10
cct gac aac taaatatcct tatccaaatc aataaarwra raatcctccc 374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaa a 405

<210> 268
<211> 1087
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 195..347

<221> sig_peptide
<222> 195..272
<223> Von Heijne matrix
score 7.09999990463257
seq LASLQWSLTAWC/GS

<221> polyA_signal
<222> 1037..1042

<221> polyA_site
<222> 1071..1082

<400> 268
aaagtgtaga acacgggacct ctgagttatg ctcttgagag gtgccc aaagc tgggctgttt 60
acctacetta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg 120
gaattttatc tagaaaaagaa gactaagcag cttttgttct tctgtgaccc agttgtcgtgc 180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg 230
Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg
-25 -20 -15
cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc 278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser
-10 -5 1
ggc agc cac tgg aca gag aga cca akt cag akt tca cgg tgg akt tct 326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser
5 10 15
ctg tca gcg acc acc agg ggg tgatcacagc gaaggtgaac atccaggctg 377
Leu Ser Ala Thr Thr Arg Gly
20 25
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcattccctg 437
araatacacc agtgggggagc cccattctta tctgtaagtc cacagacccc gacttggggg 497
caggggggag cgtcctctac tcttccagc cccctcccca atttcttgcc attgacagc 557
cccgcggtat cktcacagtg atccgggagc tggactacga taccacrcmg gctaccagc 617
ctwcggctcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaaacttg 677
ccatcatcat cacagatgtc caggacatgg accccattct catcaacctg ccttacagca 737
ccaacatcta cgagcattct cctccgggca cgacggtgag catcatcacc gccatagacc 797
aggataaagg acgtccccgg ggcattggct acaccatcgt ttcaggggcat ctgtgtttac 857


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ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg      641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu
140 145 150
gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc      689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile
155 160 165 170
cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg      737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly
175 180 185
acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta      785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu
190 195 200
ctg tac atc ctc arg ccc tct cgg cag ctg targggtggg gaccggggar      835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu
205 210
macctgcctg tagcccccac caraccctgc cccaagcacc atatggaat aaagtctctt      895
cttaccatcca aaaaaaaaaa a
916

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<210> 270
<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..513

<221> sig_peptide
<222> 52..231
<223> Von Heijne matrix
      score 4
      seq LVRRTLLVAALRA/MM

<221> polyA_signal
<222> 553..558

<221> polyA_site
<222> 572..583

<400> 270
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Met Gly
-60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag      105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
-55 -50 -45
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg      153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
-40 -35 -30
aar gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtc cgc      201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
-25 -20 -15
agg acc ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg      249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
-10 -5 1 5
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg      297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu
10 15 20
ttt ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctc cag tcc      345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser
25 30 35

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09978360.101501

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tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat      393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn
  40                      45                      50
gct ctc tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act      441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr
  55                      60                      65                      70
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag      489
Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu
  75                      80                      85
ttc cac att gaa atc cta tca atc tgaagggcct ggggcatgga gaacaggctg      543
Phe His Ile Glu Ile Leu Ser Ile
  90
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa      583

<210> 271
<211> 697
<212> DNA
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<220>
<221> CDS
<222> 172..438

<221> sig_peptide
<222> 172..354
<223> Von Heijne matrix
score 4.69999980926514
seq LLPCNLHCSWLHS/SP

<221> polyA_signal
<222> 682..687

<221> polyA_site
<222> 685..697

<400> 271
agattggctg ggcagatggg ctgactggct gggcagatgg gtgggtgagt tccctctccc      60
cagagccatc ggccaggtac caaagctcag ctgtatggat tcccaacagg aggacctgag      120
cttccctggg acccattggt gtactggatt aacaagcgac ggcgctacgg c atg aat      177
Met Asn
-60
gca gcc atc aac acg ggc cct gcc cct gct gtc acc aag act gag act      225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr
-55                      -50                      -45
gag gtc cag aat cca gat gtt ctg tgg gat ttg gac atc ccc gaa gcc      273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala
-40                      -35                      -30
agg agc cat gct gac caa gac agc aac ccc aag gcg gaa gcc ctg ctc      321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala Leu Leu
-25                      -20                      -15
ccc tgc aac ctg cac tgc agc tgg etc cac agc agc ccc agg cca gat      369
Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg Pro Asp
-10                      -5                      1                      5
ccc cat tcc cac ttc cca tct ktc agg agg tgc cct ttg ccc cac cct      417
Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro His Pro
10                      15                      20
tgt gca acc tac ccc ccs kgc tgaaccactc tgtctcctat cetttgccca      468
Cys Ala Thr Tyr Pro Pro Xaa
25
cctgtcctga aaggaatggt ctcttcattt cctctctgaa tctggcccag gaagaccata      528
gttccaatgy caagcctttt ccttcaaaac tgtagcctcc tctcactgaa ggtgggagct      588

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gcaggaatca ggtgcagagt aggaatgga actaacctca ggaaggtggt attgacagag 648
gtaggagacc acctggatgt catgctatga aacattaaaa gaaaaaaaa 697

<210> 272
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..366

<221> sig_peptide
<222> 148..225
<223> Von Heijne matrix
score 5.5
seq LFTLLFLIMLVLK/LD

<221> polyA_signal
<222> 770..775

<221> polyA_site
<222> 792..803

<400> 272
aaatggggggg aaaagggcgg aaaaggacaa ggatcccaaac tggcgaattt gctgatcttc 60
gcgtccctct ccgctttccg gccggcagcg ctgccagggt atatttcctt ttttccgac 120
ctgcaacagc ctctttaaac tgttttaa atg aga atg tcc ttg gct cag aga gta 174
Met Arg Met Ser Leu Ala Gln Arg Val
-25 -20
cta ctc acc tgg ctt ttc aca cta ctc ttc ttg atc atg ttg gtg ttg 222
Leu Leu Thr Trp Leu Phe Thr Leu Leu Phe Leu Ile Met Leu Val Leu
-15 -10 -5
aaa ctg gat gag aaa gca cct tgg aac tgg ttc ctc ata ttc att cca 270
Lys Leu Asp Glu Lys Ala Pro Trp Asn Trp Phe Leu Ile Phe Ile Pro
1 5 10 15
gtc tgg ata ttt gat act atc ctt ctt gtc ctg att gtg aaa atg 318
Val Trp Ile Phe Asp Thr Ile Leu Leu Val Leu Leu Ile Val Lys Met
20 25 30
gct ggg cgg tgt aag tct gcc ttt gac ctc gac atg gat cac aca ata 366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile
35 40 45
taaaaaaaaa aacctggtac ctcattgcac tgtkacttaa attasccttc tgcctcgcac 426
ctctgtctaa actggaaacag ttactacca tgaatctatc ctatgtcttc attcctttat 486
gggctcttgt ggctggggct ttaacagaa ctcggatataa tgcctttttt gtgaaagact 546
gactctaaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc 606
tgaatctgtc aagcttcaag aataccagag aactgaggga aaataccaaa ttagtattta 666
tactacttc ataaaacagg attggtgaat caccgacttc tagtcaacct acagcttaat 726
tattcagcat ttgagttatt gaaatcotta ttatctctat gtaataaag tttgttttgg 786
acctcaaaaa aaaaaaa 803

<210> 273
<211> 823
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 175..336

<221> sig_peptide

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<222> 175..276
<223> Von Heijne matrix
      score 3.70000004768372
      seq SVLVNGHLLFSSA/CS

<221> polyA_site
<222> 812..823

<400> 273
aaggcgcgcg cgaccggcgg ctctttggcg cggattaggg ggtctcgggc agggagtcac 60
caagctttgg tgtatgtgtt ggccgggttct gaagctctga agaagctctg ctgaggaaga 120
ccaaagcagc actcgtgtcc aattagggaa tggacogttt gggttccttt agca atg 177
Met
atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg 225
Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp
-30 -25 -20
agc ctt ata tca agt gtg ctg aat gtg ggc cac ctg ctt ttt tcc tct 273
Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser
-15 -10 -5
gct tgc agt gtt tca ctg gag gct ttg agt aca aga aac atc aaa gcg 321
Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala
1 5 10 15
atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac 376
Ile Ile Leu Met Lys
20
tgctcaagaa raaatggccc ttttagaasc tgtgatggac tgtggctttg gaaattggca 436
ggatgtagcc aatcaaatgt gcaccaarac caaggaggag tgtgagaagc actatatgaa 496
gcattttcatc aataaaccyc tgtttgcatc trscctgctg aacctgaaac aascagrgga 556
agcaaaaaact gctgacacag ccattccatt tcactctaca ratgaccttc cccgacckac 616
ctttgactcc ttgctttctc gggacatggc cgggtacwtg ccmgctcgag cagattttac 676
tgaggaaatt gacaaatttc cagaatggga cttgagagac attgattttt ttgaagatga 736
ctcgagacatt ttacatgctc tgaagatggc tbtggtagat atctatcatt ccagggttaa 796
ggagagacaa agacgaaaaa aaaaaaaa 823

<210> 274
<211> 823
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 191..553

<221> sig_peptide
<222> 191..304
<223> Von Heijne matrix
      score 5.69999980926514
      seq LAFLSCLAFVLVD/TQ

<221> polyA_signal
<222> 766..771

<221> polyA_site
<222> 804..817

<400> 274
aactctgcag ggctctcaag gccaggcttc agggctggga ctacgtcctg aggcactggg 60
gagccatgag gggctgtggc agggaggggc aggggtgtgga aagactcccc tggggccatg 120
gtggagatgt gctgaggtct tctccctgat cgtcttctcc tcctgctgta ccgacggcta 180
ccagaackag atg gag tct ccg cag ctg cac tgc att ctg aac agc aac 229
Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn

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-35 -30
agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc etc 277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25 -20 -15 -10
agc tgc ctg gcc ttc ctg gtc ctg gac aca cag gag acc cgc att gcc 325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
-5 1 5
ggc acc cgc ttc aag aca gcc ttc cag ctg ctg gac ttc atc ctg gct 373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
10 15 20
gtt ctg tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac 421
Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
25 30 35
caa tgg cag cat tgc ccg ccc aaa gar kkc ctg ctg ggg agc agc agt 469
Gln Trp Gln His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
40 45 50 55
gcc cag gca gcc atc ggc stt cac ctt ctt ctt ctt cat cct tgt ctg gat 517
Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
60 65 70
att cca rgc cta cct ggc akk cca gga cct ccg aaa tga tgc tcca 563
Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
75 80
gtcccttaacm arcgcttctc ggatgaaggt ggcattggtgs kkaacaccct ccccttgccc 623
tctgccaaca gcctgtgaac atgcccacca ctggcccaca cagcctgagt tatgctagct 683
ctgcccctgtc cccctgtctg accgctcmaa agtccccccg gcttgctatg atgcctgaca 743
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aacaataaaa aaahncctt 823

<210> 275
<211> 1112
<212> DNA
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<220>
<221> CDS
<222> 106..603

<221> sig_peptide
<222> 106..216
<223> Von Heijne matrix
score 4.30000019073486
seq LWELKTLTLLSPGIA/VT

<221> polyA_site
<222> 1102..1112

<400> 275
agcgattgcg aatcctccgc tgagggtgatt tggatatccc tagaacgttg agggcacgag 60
tcgggtctctg agaccaggctc ctgagccagc agagccacgt tcctt atg agc acc gtg 117
Met Ser Thr Val
-35
ggg tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca 165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
-30 -25 -20
tgg gga ctg ccg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata 213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
-15 -10 -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg 261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
1 5 10 15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac 309

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-5      1      5
cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg      199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
10      15      20      25
cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc      247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
30      35      40
ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc      295
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
45      50      55
tac ctc tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act      343
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
60      65      70      75
cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag      391
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys
80      85      90      95
gtc tac ctg aag ggt gtg gac ccc aaa ttt cct gag gga ggg aar atg      439
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met
100      105      110      115
tct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg      487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa
120      125      130      135
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att      535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile
140      145      150      155
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg      583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp
160      165      170      175
gaa tgattgccgg cgggacagga atcaccoccaa tgctacagct gatccgggcc      636
Glu

atcctgaaag tccctgaaga tccaaaccag tgctttctgc tttttgccaa ccagacagaa      696
aaggataatca tcttgccggga ggactctagag gaactgcagg ccgcgtatcc caatcgcttt      756
aagctctgtgt tcactctgtga tcatcccccga aaagrtttggg cctacagcaa gggctttgtg      816
actgcgcagcw tgatcccgga acacctgcccc gctccagggg atgatgtgct ggtactgctt      876
tgtggggccmc ccccaatggt gcagctggcc tgccatccca acttggaaca actgggctac      936
tcacaaaaaa tgccgattcac ctactgagca tctctcagct tccctgggtgc tgttcgctgc      996
agttgtttccc catcagtaact caagcactak aagccttagr ktcctktctc cagagtttca      1056
ggtttttttca gttrsatacka gagctgaaat ctggatagta cctgcaggaa caatatctct      1116
gtagccatgg aagaggggcca aggcctcagtc actccttgga tggcctccta aatctccccg      1176
tggaacacagg tccaggagag gcccatggag cagtcctcttc catggagtaa gaaggaagg      1236
agcatgtacg cttgggtccaa gattggctag ttccttgata gcattctact ctcacctctt      1296
tgtgtctctg gatgaaagga acagctctgt caatggggtt tacttaaac tcaactgttca      1356
acctatgagc aaatctgtat gtgtgagatg aagttgagca tagcatactt ccagaggttg      1416
tcttatggag atggcaagaa aggaggaaat gatttcttca gatctcaaa gatcttgaaa      1476
tatcatattt ctgtgtgtgt cdctctcagc cctgcacac gctagaggga wacagctact      1536
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 <222> 99..371

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 <222> 99..290
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 score 3.79999995231628

seq LFIVVCVICVTLN/FP

<221> polyA_signal

<222> 491..496

<221> polyA_site

<222> 513..524

<400> 277

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ttactttttt ctgttaacgc ttaccctagr aattagaa atg aca cca cgt att ctt 116
Met Thr Pro Arg Ile Leu

-60

agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg 164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg

-55

-50

-45

ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct 212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala

-40

-35

-30

gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att 260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile

-25

-20

-15

gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt 308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe

-10

-5

1

5

ctt tgt ctg tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt 356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val

10

15

20

cac att ccc tct ccc tararcacac tccttggat ttctcradt ggggtctgct 411
His Ile Pro Ser Pro

25

gcggtgaagc tttccattt tatgtgcaga ttattttcag agggatatata gaattcaggc 471
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<210> 278

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<222> 44..112

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score 8.30000019073486

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<222> 978..989

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Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Xaa Leu Leu Leu Leu

-15

-10

-5

cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac 151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn

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<221> polyA_site

<222> 1006..1016

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ccc tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc      95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile
-45                               -40                               -35                               -30
cca cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc      143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val
-25                               -20                               -15
ctg tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac      191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp
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ccc tta gga tcc tgc gga tgg cyw tgc cac acg gcc car gtc cct gcg      239
Pro Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala
5                               10                               15
ccc ctg car ttg cct act gcc tgt cct ccc ctc cca cat ggc acc cgg      287
Pro Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg
20                               25                               30                               35
gct gta ggc ccc acg cca ggc ctc ctc cct gag gct gca gcc cca sgc      335
Ala Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa
40                               45                               50
acg tgc ggg gca ctg tcc tca cgc agc agg cac tgg tca tgt tcc att      383
Thr Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile
55                               60                               65
gtc arc tgc ctc cac ctg cac ara ctc ctg tct gtg gag acc aga arc      431
Val Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa
70                               75                               80
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt      479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val
85                               90                               95
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca      527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr
100                               105                               110                               115
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct      575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro
120                               125                               130
tgg gaa tgagcctgtc ctctgtgtga aggagggggt gggtctcaaa ccaactgactc      631
Trp Glu
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ccagcacttt ggagggccaa ggtggacaga tcatgaggtc aggagttcga gaccagcctg      811
gccaatacgg tgaaacccga tctctactaa rraatawcaw aaattagtcg ggcatggggt      871
atgtgtgctt gtagtccag ctactcatga ggyctgaggg agaagaatca cctgaattctg      931
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tgagactccg tctcaaaaaa aaaaam                                     1017
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<211> 529

<212> DNA

<213> Homo sapiens

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<222> 107..427

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<222> 107..190
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 seq RFLSLSAADGSDG/SH

 <221> polyA_signal
 <222> 499..504

 <221> polyA_site
 <222> 516..529

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 Met Val Leu
 acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt 163
 Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
 -25 -20 -15 -10
 ctg tcc gca gcc gac gcc agc gat gcc agc cac gac agc tgg gac gtg 211
 Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val
 -5 1 5
 gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt 259
 Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
 10 15 20
 tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt 307
 Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe
 25 30 35
 gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt 355
 Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu
 40 45 50 55
 cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga 403
 Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg
 60 65 70
 aag tca cct gaa att tct tgg ggt taaccatctt tagttaaatg gaattttaat 457
 Lys Ser Pro Glu Ile Ser Trp Gly
 75
 ttaaatgacg ctttgctaatt ttaagtgtt aagcattttg cattaataata ttcataata 517
 aaaaaaaaaa aa 529

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 <222> 45..407

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 <222> 45..83
 <223> Von Heijne matrix
 score 5.69999980926514
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 <221> polyA_site
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 <400> 281

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Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln
-5 1 5
atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc 152
Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe
10 15 20
tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc 200
Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe
25 30 35
ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa 248
Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu
40 45 50 55
ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg 296
Leu Val Gly Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val
60 65 70
ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag 344
Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln
75 80 85
aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca 392
Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro
90 95 100
aat ttg gct ctc aat tgataaacia gatagtgaga ttacttatct ggtaccatgg 447
Asn Leu Ala Leu Asn
105
tgcaaatag aaaaacctcc aaaagaagga gtctatgaac tggccacttt tcagatgaaa 507
cctgggtgggc cagctctctgt ggggtgatgca tttaaaaggg cagttcatgc tcactgtcaat 567
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<211> 880
<212> DNA
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<222> 201..332

<221> sig_peptide
<222> 201..251
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score 7.80000019073486
seq VLWLISFFTFDG/HG

<221> polyA_site
<222> 869..880

<400> 282
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yhcccwsvr tyctggwggt amgagataaa tcaccagtca cagactatgc acccgactgc 180
tgctgttcag tccagggaat atg aaa gtt gga gtg ctg tgg ctc att tct ttc 233

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Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe
-15 -10

ttc acc ttc act gac ggc cac ggt ggc ttc ctg ggg gtg agt tgg tgc	281
Phe Thr Phe Thr Asp Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys	
-5 1 5 10	
tat gtc tca tat ctc ttc tca act aac tct cct ctc tgc ttc cgg cgc	329
Tyr Val Ser Tyr Leu Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg	
15 20 25	
att tagaaccct cactctctag gggactgcaa ctgcataatt taatgtactt	382
Ile	
gagatcagaa gtctctgagt ctogtttcaa cattaccaac attcactgtg tggccttga	442
taagtragtc atttcacttc ttccggagcctt agatgatoma actgcaarag gaggatcttt	502
gattamacta tcttagagat cttttccagt tcaacacatg ctgtactatg gcttctcgga	562
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ctogcttgag tgatgckttc atctaggatc atgggttttaa tattctctac atgctgatga	682
ctcccagctg tatagctcca tctcagaacc tctccctctg ccacactcac atatocatta	742
cctacgtgtt atttccagct gggaaatcca gcggaaacct ggnaacttca ttgnnttcaa	802
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<212> DNA

<213> Homo sapiens

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<222> 217..543

<221> sig_peptide

<222> 217..255

<223> Von Heijne matrix

score 6.40000009536743

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<221> polyA_site

<222> 1206..1217

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graagrwgga aaactgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca	180
gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg	234
Met Cys Leu Leu Thr Ala	
-10	
tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt	282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys	
-5 1 5	
tta tgc aag agg aga tgg ccc tgg ngc ccc tgc ccc cgg atc tac tgc	330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys	
10 15 20 25	
tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc	378
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala	
30 35 40	
cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg	426
Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro	
45 50 55	
ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc	474
Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu	
60 65 70	
cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt	522

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Gln	Pro	Ala	Ser	Leu	Xaa	Thr	His	Leu	Ser	Lys	Pro	Lys	Arg	His	Phe		
75						80					85						
ara	aar	aar	rra	tgt	caa	gcc	tgatgaarac	atgagtgaggc	aaaacattgc							573	
Xaa	Lys	Lys	Xaa	Cys	Gln	Ala											
90						95											
aatgtacara	aatgagggtt	tctatgctga	tccttacctt	tatcacgagg	gacggatgag											633	
catascctca	tcccattggt	gacaccact	ggatgtcccc	gaccacatca	ttgcatatca											693	
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gagcgctgca	ggattatcca	gccttgtaga	cctcgccctt	cctctaattg	agaagcaagt											1053	
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catggagaaa	cagattgccca	gtttaactgg	ccttgcttcag	tctgcctttt	ttaaagggcc											1173	
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<222> 18..140

<223> Von Heijne matrix

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<221> polyA_site

<222> 948..959

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			-40				-35										
gag	atg	gta	cag	gcg	ctt	tac	gag	gct	cct	gct	tac	cat	ctt	att	ttg		98
Glu	Met	Val	Gln	Ala	Leu	Tyr	Glu	Ala	Pro	Ala	Tyr	His	Leu	Ile	Leu		
	-30		-25				-20						-15				
gaa	ggg	att	ctg	atc	ctc	ttg	ata	atc	aga	ctt	ctt	ttc	tct	aag	act		146
Glu	Gly	Ile	Leu	Ile	Leu	Trp	Ile	Ile	Arg	Leu	Leu	Phe	Ser	Lys	Thr		
	-10		-5				-5					1					
tac	aaa	tta	caa	gaa	cga	tct	gat	ctt	aca	gtc	aag	gaa	aaa	gaa	gaa		194
Tyr	Lys	Leu	Gln	Glu	Arg	Ser	Asp	Leu	Thr	Val	Lys	Glu	Lys	Glu	Glu		
	5					10					15						
ctg	att	gaa	gag	tgg	caa	cca	gaa	cct	ctt	gtt	cct	cct	gtc	cca	act		242
Leu	Ile	Glu	Glu	Trp	Gln	Pro	Glu	Pro	Leu	Val	Pro	Pro	Val	Pro	Lys		
	20					25					30						
gac	cat	cct	gct	ctc	aac	tac	aac	atc	gtt	tca	ggc	cct	cca	agc	cac		290
Asp	His	Pro	Ala	Leu	Asn	Tyr	Asn	Ile	Val	Ser	Gly	Pro	Pro	Ser	His		
	35				40				45					50			
aaa	act	gtg	gtg	aat	gga	aaa	gaa	tgt	ata	aac	ttc	gcc	tca	ttt	aat		338
Lys	Thr	Val	Val	Asn	Gly	Lys	Glu	Cys	Ile	Asn	Phe	Ala	Ser	Phe	Asn		
			55					60				65					
ttt	ctt	gga	ttg	ttg	gat	aac	cct	agg	gtt	aag	gca	gca	gct	tta	gca		386

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 Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr
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 ggc aca ttt gaa tgaaratgaa ggatcattga tttccttgtg tatggataat 486
 Gly Thr Phe Glu
 100
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 <223> Von Heijne matrix
 score 3.90000009536743
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 <221> polyA_site
 <222> 910..920

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 Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu
 -20 -15 -10
 cca gca gag tgc tat ggy aac grt yct gac att gag atg gct tgg gcc 148
 Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala
 -5 1 5 10
 atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca 196
 Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser
 15 20 25
 gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac 244
 Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr
 30 35 40
 tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc 292
 Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa
 45 50 55
 cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat 340
 Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn
 60 65 70
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      1          5          10          15
cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg      559
Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
      20          25          30
tat gat aga aaa tcc aca atc aaa tct tgaaccaaata aacatatata      606
Tyr Asp Arg Lys Ser Thr Ile Lys Ser
      35          40
attactaata ttttaagtgt ggaagacaca caaaaaaactt aaaagcacga acaacctaac      666
ttgaaaaara attttaaaat atgattaacc tgaaraaaar araactcctaa ragccaaagc      726
tcctttttat ttagctctgga attttcctat tggttcctaa caaactgtcc caatgtcata      786
taagggaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt      846
aagtagtaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt      906
attatctgta taaaaattgg cagggggaag ctaaaaggaa aggagattgg agatctcaat      966
tctatcatgg tgtatttcat acgcaaatca ragcatgcat tgttttttgt ttttggaar      1026
avaarggaag tgtgtctgcg cccatgtttc ctcccggtgt tatagttcaa actctatata      1086
tatttcaggt tatttttgtt tagcccttca ttataaatgg gcaggaaatt gtttatcaac      1146
ctagccagtt tattactagt gaccttgact tcagtatctt gcgacttctt ttatatTTTT      1206
cttttattat cctgagctcg taactaaca attttgtctt caaatTTTTa tccaatatcc      1266
attgcaccac accaaatcaa gcttcttgat ttccaaaaat aaaaaggggg aaatacttac      1326
aactgttaaa aaaaaaaaaa
<210> 287
<211> 585
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 331..432
<221> sig_peptide
<222> 331..387
<223> Von Heijne matrix
score 7
seq AGLSSCLLPICWL/ER
<221> polyA_signal
<222> 548..553
<221> polyA_site
<222> 573..585
<400> 287
aagcctaggt gtggcgcccc gaccggaact tcactcttgg ccagcccttt cccacctgg      60
gcgcgggass ggtgccagtc tttaaacaac ctctcgatgg gtcccacgaa gatgtttcca      120
gacccttgga atgccaaagt caagtcttag tatgtctcgc ggagaggccg gtggaagaag      180
caacgagaa gaagcaccoc agttctctgc tgagcacatg ggcattctga ataaagatt      240
aattcccgag ctctctctga agctcggtat ggccacaaca cttaattctg ccgaggagga      300
ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc      354
Met Phe Leu Lys Ser Gly Ala Gly
-15
ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat      402
Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
-10          -5          1          5
ggc agg agg cca agc asc cat cct gga agg tgaagcctc atactaagga      452
Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
10          15
cgtcaracag cgaataara rectgggtcc ttgacctgt aaasatctcc ctccccatcc      512

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tggctctgtct gccttgactc ctttcatatg aaaaaataa acttttaact tgcgtwaacc 572
 aaaaaaaaaaaa aaa 585

<210> 288
 <211> 914
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..703

<221> sig_peptide
 <222> 59..220
 <223> Von Heijne matrix
 score 5.09999990463257
 seq FLLSQMSQH/VQA/VQ

<221> polyA_signal
 <222> 886..891

<221> polyA_site
 <222> 903..914

<400> 288
 acaaatatca atgatgttta tgaatctagt gtgaaagtkt taatcacatc acaaggct 58
 atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak 106
 Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
 -50 -45 -40
 ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg 154
 Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
 -35 -30 -25
 tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca 202
 Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
 -20 -15 -10
 cag cac cag gta cat gca gtt cag caa ctg gcc aag gtt atg ggc tgg 250
 Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
 -5 1 5 10
 caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc 298
 Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
 15 20 25
 abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg 346
 Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
 30 35 40
 cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc 394
 Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
 45 50 55
 agt ttc ctg gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac 442
 Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
 60 65 70
 aar ata aca aat gga gtc atc ttc gtg ggc cat tca aar aag ttc agt 490
 Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
 75 80 85 90
 gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta 538
 Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
 95 100 105
 tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct 586
 Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
 110 115 120
 aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat 634
 Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr

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      125              130              135
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata      682
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
      140              145              150
ata att agg aaa tgt ttt att tagcactttc aaacttttca cttataaat      733
Ile Ile Arg Lys Lys Cys Phe Ile
      155              160
gacaagtgtc ttgaaatgca gaagtttatg tacagttgta tatacagtat gacaagatgt      793
aaaaataaat gtttttcatg cagtttataaa tattactaac ttaagggttt ctatgtgctt      853
tttaaaatat tccttctttg atgttgacat caataaaagt atgtgggtta aaaaaaaaaa      913
a
      914

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<210> 289
<211> 1161
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 672..752

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<221> sig_peptide
<222> 672..722
<223> Von Heijne matrix
score 4.30000019073486
seq LLYAHLSTSKRA/VV

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<221> polyA_site
<222> 1150..1161

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<400> 289
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ataaagcctt cctttaaagc tttataataa tcataattat taataatgct gttgtgcata      120
cttatagtat gcatatatcc agcatatggt gcatgtsttc agaattacat aagatgaaat      180
ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctgggt gaagaaatag      240
tattttctct tctcagggtg tctccctgcc ttggcccctc ccagaagccc cggctttaaa      300
agtgaaaatg tttgaaacat gaaacatgtc ttaggaagag atcagcatgg ccataagttg      360
artgattttc atatatgcct ctgcccatgt caaatatatt tttgacatga ataaatctaa      420
cagtatacar aataatctat gtaaracct aacgtgtaca tgtgaaaaag catttctata      480
taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaat      540
tcaaaataga gcsstgcaag ataaactgcaa tcataccaaa aactatttga gtaaatggat      600
ttttaaagta atttttgttt aaaaaaattt atatttcaga agsagaaaaat gtcaaatgat      660
agtctttgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca      710
Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr
      -15              -10              -5
tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt      752
Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
      1              5              10
tgaatgactt gggtcaagctg tgtgtaaaaa atttaacat aagtcaagta cagtgtacta      812
tgtttaataa agttacattt aatgcattta ttgcataat gaatatatac atgaagaggc      872
tttatgtctt ctggtatttg attttgaatg ttttttaagt cagtggtgccc tttaggcaag      932
aactttcgaa ataatcatct ctttgtgttt tctgtatttt caggtaacat gtacacattt      992
tagaaaccca catagttttt tcaccttaaa aaattgattg tattatttaa atatatcaat      1052
tagatggggc tttcctataa ttaggatatt ccaaatagtt gctgaaatca atbtgtgccat      1112
tgaccaatgg atgcacttgg ttagccttaa ttttttyaaa aaaaaaaaaa      1161

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<210> 290
<211> 363
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 57..311

<221> sig_peptide
<222> 57..128
<223> Von Heijne matrix
      score 5.30000019073486
      seq LPHLLFLPHYIET/PK

<221> polyA_signal
<222> 332..337

<221> polyA_site
<222> 351..363

<400> 290
acatttcttta ctgccttacg ctcatcctga ggtccacctt ggtctctaaa aacacc atg      59
                                     Met
tgt tct cat gcc tcc atg tct ttt cac aca ctg ttc cat ttg ctc ttc      107
Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu Phe
      -20                               -15                -10
ctc cca cat tac att gaa act ttc aag cct cag tcg aaa cat tgc ttc      155
Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys Phe
      -5                               1                   5
ttc tgg ata gca gcc ttc ttg aca tcc ctc ctc act ccc cag tcc cta      203
Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser Leu
      10                               15                20                25
cag ggc ttc cat agc tct tta tgt gca ctt cga tcc cag cat ttt cca      251
Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe Pro
      30                               35                40
tcg act tgt aat tgt ttc tgc tac ctg aca atc atc gcc ttg drd tac      299
Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa Tyr
      45                               50                55
tgg gac aac ctt tgattactca ttatatactc aataaatatt tgttgaacca      351
Trp Asp Asn Leu
      60
aaaaaaaaaa aa      363

<210> 291
<211> 645
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..232

<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.70000004768372
      seq IALTLIPSMLSRA/AG

<221> polyA_signal
<222> 617..622

<221> polyA_site
<222> 634..645

<400> 291

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accttctgtg tatttatgct attctctttg tggtccatt cttctttcaa tcttctcagc      60
ttataaccgt ctttccctt atg cta agg ata gcc ctt aca ctc atc cca tct      112
Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser
-15 -10

atg ctg tca agg gct gct ggt tgg tgc tgg tac aag gag ccc act cag      160
Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln
-5 1 5 10
cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg aat aar aaa ggc      208
Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly
15 20 25
aac gtt ttg cag ctt cca aat ttc tgaaraaact aatctcarat tggcagttaa      262
Asn Val Leu Gln Leu Pro Asn Phe
30 35

agtcaaaatg ttgccaaata tttattcctt ttgcctaakt ttggtaccc ggttcaaattg      322
cttttttatt ttaatgtctt gactcttcar agttcgtacc tcaaaaaraac aatgaraaca      382
tttctgttgc tttctgtcga atccctaacc tcaacaatct atacctggac tgtccagttc      442
tctctctgtg ctatctttct tttctatcaa gtaraatgta ygccaggarc tctttccctc      502
tarcaatttc tactaaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat      562
ttattaattt gctaraatcc aktaaatcat ttggtagct ctggctgtgc tatcaataaa      622
aagatgaaag caaaaaaaaa aaa      645

<210> 292
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..291

<221> sig_peptide
<222> 91..219
<223> Von Heijne matrix
score 3.79999995231628
seq LISVLYLIPKTLT/TN

<221> polyA_signal
<222> 367..372

<221> polyA_site
<222> 389..400

<400> 292
aacaagaagg gagtttttata attcacttta aaaggagatt tgatggtaaa gtttaaagat      60
taaaatatatt tgttcttcaa ttacagagcgt atg acc cca cag tat ctg cct cac      114
Met Thr Pro Gln Tyr Leu Pro His
-40

ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc      162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe
-35 -30 -25 -20
ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa      210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys
-15 -10 -5

aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt      258
Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys
1 5 10

atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga      311
Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln
15 20
ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa      371
aattttattt cctaagyaaa aaaaaaaaaa      400

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<400> 294
 atatttgccc cttactttat cttgtgcctt gagaaattgc tggggagaga ggt atg 56
 Met
 tcc act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc 104
 Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser
 -55 -50 -45
 cag cag cca ggt tcc ctc acc cca agc tca ccc act gtt ggg gag att 152
 Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile
 -40 -35 -30
 atc tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt 200
 Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu
 -25 -20 -15 -10
 atg ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc 248
 Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr
 -5 1 5
 tcc att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct 296
 Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Ser Gly Ala
 10 15 20
 ggg ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag gwg atc tac 344
 Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
 25 30 35
 acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna 392
 Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
 40 45 50 55
 dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat 440
 Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
 60 65 70
 gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc 488
 Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
 75 80 85
 cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc 536
 Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
 90 95 100
 cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa 584
 Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
 105 110 115
 gtc aat taacaattta tgcacaggta ctagttttat tgtattaccg ttccagggtgta 640
 Val Asn
 120
 gctttgaaaa aagtatctca aaaaggcaac atgggcccag cgcagtggtt caegcctgta 700
 atccccgacac ttgtgggagc caaggtgggg agatcgccgt aggtctggag ttcaagacca 760
 gctgtgccaa cagggtgaaa cccgtctctc aaaaaaatar gaaaaattgc caggtgtggt 820
 ggcagacgtc tgtrgtccca gctattcagg agactgaggg acgagaattc catgaacca 880
 ggatgcggag gttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag 940
 tggattctctg tttcaaaaaa aaaaamcm 968

 <210> 295
 <211> 901
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 133..846

 <221> sig_peptide
 <222> 133..345
 <223> Von Heijne matrix
 score 9.39999961853027
 seq VVSFLLLAGLIA/TY

<222> 890..901

<400> 295

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tactgatcta	tnnatggcag	agaaaaaaa	attgtgacca	gagacgtga	gcaatgaaca	120
aggaacrtca	ta atg rwn nnk ttc	aca gac ccc	tct tca gtt	aat gaa aag		171
	Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys					
	-70		-65		-60	
aag agg arg	agg gag cgg	gaa gaa	agg cag	aat atg gtc	ctg tgg aga	219
Lys Arg Arg	Glu Arg Glu Glu Glu	Glu Glu Glu	Gln Asn Ile Val	Leu Trp Trp Arg	Gln Gln	
	-55		-50		-45	
cgg ctc att	acc ttg	cag tat	ttt tct	ctg gaa atc	ctt gta atc	267
Pro Leu Ile	Thr Leu Gln Tyr	Phe Ser Leu Glu Ile	Leu Val Ile Leu			
	-40		-35		-30	
aag gaa tgg	acc tca	aaa tta	tgg cat	cgt caa	agc att	315
Lys Glu Trp	Thr Ser Lys Leu	Trp Trp His Arg	Gln Ser Ile	Val Val Val	Val Ser	
	-25		-20		-15	
ttt tta ctg	ctg ctt	gct ggg	ctt ala	gct acg	tat tat	363
Phe Leu Leu	Leu Glu Ala	Gly Leu Ile Ala	Thr Thr Tyr	Tyr Val	Glu Glu Gly	
	-10		-5		1	5
gtg cat caa	cag tat	gtg caa	cgt ata	gag aaa	cag ttt	411
Val His Gln	Gln Tyr Val	Gln Arg Ile Glu	Lys Gln Phe	Leu Leu Tyr		
	10		15		20	
gcc tac tgg	ata ggc	tta gga	att ttg	tct tct	tct ggg	459
Ala Tyr Trp	Ile Gly Leu	Gly Ile Leu	Ser Ser Val	Gly Gln	Leu Gly Thr	
	25		30		35	
ggg ctg cac	acc ttt	ctg ctt	tat ctg	ggt cca	cat ata	507
Gly Leu His	Thr Phe Leu	Leu Tyr Leu	Gly Pro His	Val Ile Ala	gcc tca	
	40		45		50	
aca tta gct	gct tat	gaa tgc	aat tca	ggt aat	ttt ccc	555
Thr Leu Ala	Ala Tyr Glu	Cys Asn Ser	Val Asn Phe	Pro Glu Pro	Pro Pro	
	55		60		65	70
tat cct gat	cag att	att tgt	cca gat	gaa gag	ggc act	603
Tyr Pro Asp	Gln Ile Ile	Cys Pro Asp	Glu Glu Gly	Thr Thr Glu	Gly Thr	
	75		80		85	
att tct ttg	tgg agt	atc atc	tca aaa	gtt agg	att gaa	651
Ile Ser Leu	Trp Trp Ser	Ile Ile Ser	Lys Val Arg	Ile Glu Ala	Cys Met	
	90		95		100	
tgg ggt atc	ggg aca	gca atc	gga gag	ctg cct	cca tat	699
Trp Gly Ile	Gly Thr Ala	Ile Gly Glu	Leu Leu Pro	Pro Tyr Phe	Met Ala	
	105		110		115	
aga gca gct	cgc ctc	tca ggt	gct gaa	cca gat	gat gaa	747
Arg Ala Ala	Arg Leu Ser	Gly Ala Glu	Pro Asp Asp	Glu Glu Tyr	Gln Gln	
	120		125		130	
gaa ttt gaa	gag atg	ctg gaa	cat gca	gag tct	gca caa	795
Glu Phe Glu	Glu Met Leu	Glu His Ala	Glu Ser Ala	Gln Val Arg	Arg Thr	
	135		140		145	150
gtg ggg ata	gaa aat	aga aca	ctt tac	tct ttc	cta aag	843
Val Gly Ile	Glu Asn Arg	Thr Leu Tyr	Phe Phe	Leu Lys	Arg Leu	
	155		160		165	
agg taaaattg	tt agtagt	tta ctg	gaagaaga	aaactg	ctaa agta	901
Arg					aaaaa	

<210> 296

<211> 1347

<212> DNA

<213> Homo sapiens

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<221> CDS

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<222> 138..671

<221> sig_peptide
<222> 138..248
<223> Von Heijne matrix
      score 3.5
      seq LVFNFLILITILT/IW

<221> polyA_signal
<222> 1319..1324

<221> polyA_site
<222> 1338..1347

<400> 296
aagaatgctt gtgaagtagc aactaaagtg gcagtggttc ttctgaaatt ctcaggcagt      60
cagactgtct taggcaaact ttgataaaat agcccttatac caggttttta tctaaggaat      120
cccaagaaga ctgggga atg gag aga cag tca agg gtt atg tca gaa aag      170
          Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys
          -35                               -30

gat gag tat cag ttt caa cat cag gga gcg gta ggt gag ctg ctt gtc ttc      218
Asp Glu Tyr Gln Phe Gln His Gln Gly Ala Val Glu Leu Leu Val Phe
          -25                               -20                               -15

aat ttt ttg ctc atc ctt acc att ttg aca atc tgg tta ttt aaa aat      266
Asn Phe Leu Leu Ile Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn
          -10                               -5                               1                               5

cat cga ttc cgc ttc ttg cat gaa act gga gga gca atg gtg tat ggc      314
His Arg Phe Arg Phe Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly
          10                               15                               20

ctt aya att gga cta att tta csa tat gct aca gca cca act gat att      362
Leu Xaa Met Gly Leu Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile
          25                               30                               35

gaa agt ggr rct gtc tat gac tgt gta aaa cta act ttc agt cca tca      410
Glu Ser Gly Xaa Val Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser
          40                               45                               50

act ctg ctg gtt aat atc act gac caa gtt tat gar tat aaa tac aar      458
Thr Leu Leu Val Asn Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys
          55                               60                               65                               70

aga gaa ata agt cag cac amc atc aat cct cat cam gga aat gct ata      506
Arg Glu Ile Ser Gln His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile
          75                               80                               85

ctt gaa aag atg aca ttt gat cca raa atc ttc ttc aat gtt tta ctg      554
Leu Glu Lys Met Thr Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu
          90                               95                               100

cca cca att ata ttt cat gca gga tat agt cta aag aag aga cac ttt      602
Pro Pro Ile Phe Phe His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe
          105                               110                               115

ttt caa aac tta gga tct att tta acg tat gcc ttc ttg gga act gcc      650
Phe Gln Asn Leu Gly Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala
          120                               125                               130

atc tcc tgc atc gtc ata ggg taagtgcacat tcggagctca agttgcaggt      701
Ile Ser Cys Ile Val Ile Gly
          135                               140

ggctgtgggg tcygtgatct gtgtgagggg tctaacactt ccaggattct tgctggckgg      761
gaaaattgct ttttttttar tawatcacaw atttgtatgt tttttcgwac ttaattccac      821
ggctctckgam aaatacaagg cttcaaatca aagcaaaacta waggattgct ggactttctc      881
tgtgagttct ggactttctga cttagggaat gtggatcact tgcccttgagt tatgtgaagc      941
gcattgcaatt ctcttttttag tttagagtaat sccgatattgc tcactgcatc cttttttgtc      1001
ttgtatttag agaccttacc tgtattttggc aggagtgcaa aagtaactat atgccaagag      1061
ttttctttctt aaaggaaaagt ttacaagaca gcagttctgaa acagatatgt ccaaatatca      1121
acagagttgc ttaatacagg gatagctttt cagttaatac cctgtagaat gcagactctt      1181

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tttttcattg tattttcttg attatgctac tgagccctaa gtcacacggt atatactctg 1241
gcttgcagct catcataaag taaaatgtgg taccaaatgg tgaaggcaat ccagcctctg 1301
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<211> 987
<212> DNA
<213> Homo sapiens

<220>
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<222> 124..411

<221> sig_peptide
<222> 124..186
<223> Von Heijne matrix
score 6.30000019073486
seq MVALCCCLWKISG/CE

<221> polyA_signal
<222> 948..953

<221> polyA_site
<222> 971..983

<400> 297
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tcagttctta ctgaagtgc gtatgaaact gaaatttcca aggaactgaa tttgtgagc 120
caa atg agc atg caa ttc ttg ttt aag atg gtg gcc tta tgc tgt tgt 168
Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys
-20 -15 -10
ctc tgg aag atc tcc ggc tgt gag gaa gtc cct cta act tac aac ctg 216
Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu
-5 1 5 10
ctc aag tgc ctc cta gat aaa gcg cac tgt gta ctc ctg aca cct tgt 264
Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys
15 20 25
ggg tac atc ttt tcc ttg atc agt cca gaa att ctc aaa ctc act tta 312
Gly Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu
30 35 40
atc act ttg cav atc ctc tta ata ctc aaa aat cta cac tta ctg tgg 360
Ile Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp
45 50 55
ctg aca gtt tca agc awa tgt gtt cat cgc agt agt gca aga aaa gaa 408
Leu Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu
60 65 70
aag tagaagaacc ctgcagagat ttgatggaac ccagcttcta ttcattaaaa 461
Lys
75

ccaatggcaa aatataaagc aaataggagg tgacgaaggt tacaaaaata cgtattgttt 521
atgttttccc tgggggtgtgc tgattgtcag gcatcagttc cctgtgccat tcattcccca 581
acacagcatg catcagaaat tttatcaata aatgctttct ctctcaatgt tcaacctatg 641
ctgatagacc attaaatata gtttttgggt tcacagcttg tcatcatcat ttgtctatac 701
ctgtggcaaa gaatatctaa taagatactc tcagcatttt gcacacttaa actaatatgc 761
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tgtgaacatt caacattagg tttaaatttt atttttaaaa gttaataata aaaggatata 881
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<212> DNA
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<222> 372..494

<221> sig_peptide
<222> 372..443
<223> Von Heijne matrix
score 5.30000019073486
seq RILLLFHYCCLRS/SE

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..745

<400> 298
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aaccgaagcg agatgagctc aagatcatgc ctggggaagc atggtgctct aggggtgcct 180
ttttattcct ttcatgtgat tatagactgt ttccaagtgt atgggttagaa atggtaaagt 240
gggtctgggtg ttttgaggta gaacccagcc tagggcaaga tatgaactgt tcttgaggta 300
gaaatgtcta cagtcagttg ttcatcttag ctgcatctt aaaacacaaa ccttcagtt 360
gctttcactt a atg cac aca ttt gcc aat gac aga ggg tta tac agg atc 410
Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile
-20 -15
ctt ctt tta cat ttc tat tgt ctg cta cgc tca gag tat att ttg 458
Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu
-10 -5 1 5
ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt 504
Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu
10 15
attgaaaadt aaktgccctt ccattccagg cctcctcata ttgtacttgt ttctgtccaa 564
atctggggga tcatttggat ttaactttg taatctatgg ctctgtactg ttgaaagstc 624
tcaattctgt ggggtctcct tagtatgtat gtgacttttc atgttgcaat atcacacgat 684
gggatggccc gacttttgcct cttaataaat aatctgaatg agtaagaraa aaaaaaaaaa 744
acc 748

<210> 299
<211> 1106
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 112..450

<221> sig_peptide
<222> 112..192
<223> Von Heijne matrix
score 7.19999980926514
seq SLLEFLLLEGGXT/EQ

<221> polyA_signal
<222> 1053..1058

<221> polyA_site
<222> 1095..1106

<400> 299
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 gaaggcgvakk rcnnnnrctt gaaggttctg tcaccttttg cagtgggtcca a atg aga 117
 Met Arg
 raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tgc ttg ttg ttc 165
 Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
 -25 -20 -15 -10
 ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag 213
 Phe Leu Leu Leu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
 -5 1 5
 aca tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg 261
 Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
 10 15 20
 cat cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc 309
 His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
 25 30 35
 tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat 357
 Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn
 40 45 50 55
 gtt cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc 405
 Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg
 60 65 70
 tgc cca gaa gac tcc tta ccc cca gtg aac aat rwg gtg acc agc 450
 Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr Ser
 75 80 85
 tagtcttgck agtacaattg gacaacttac caacatggas agctgttctg agctgrrggg 510
 ctctttcaga atcggaaccc cmatcaatgc acccagtgca gctgttcgga rggaaacktg 570
 tatttgtgttc tcaagacttg ccccaaatga acctgtgcct tccacgtctc tgttccarat 630
 tcctgtctgcc ggggtwtgcag argagatgga caactgtcat ggggaacmttc tgatgggtgat 690
 atcttccggc aacctgcgca cagagaagca agacattctt accaccgctc tcaactgat 750
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 tggcacccaa acctccgggc atttggcatt gtggagtgtg tgctatgtac ttgtaatgtc 990
 accaagcaag agtctaagaa aatccactgc cccaatcgat acccctgcaa gtatccctcaa 1050
 aaaaatagacg gaaaatgtct caaggtgtgt ccaggtataaa aagcaaaaaa aaaaaa 1106

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 <211> 1191
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 117..866

 <221> sig_peptide
 <222> 117..170
 <223> Von Heijne matrix
 score 10.6999998092651
 seq LILLALATGLVGG/ET

 <221> polyA_signal
 <222> 1159..1164

 <221> polyA_site
 <222> 1178..1190

 <400> 300
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agagcbtnmag cccccagacc taggaacctg gggcccgtc cccccccctc caggcc atg 119
Met
agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 167
Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly
-15 -10 -5
gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag 215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
1 5 10 15
ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg 263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
20 25 30
acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag 311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
35 40 45
ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag 359
Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
50 55 60
ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc 407
Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
65 70 75
ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg 455
Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
80 85 90 95
gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc 503
Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
100 105 110
acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc 551
Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
115 120 125
ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cag acc ttg 599
Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
130 135 140
cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc 647
Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
145 150 155
tac ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa 695
Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
160 165 170 175
ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt 743
Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
180 185 190
aac cag tot ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg 791
Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
195 200 205
atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac 839
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
210 215 220
tgg atc cag gag acg atg aag aac aat tagactggac ccacccacca 886
Trp Ile Gln Glu Thr Met Lys Asn Asn
225 230
cagccccatca cccctccattt ccacttggtg tttggttcct gtctactctg ttaataagaa 946
accctaaagcc aagaccctct acgaacattc ttggggcctc ctggactaca ggagatgctg 1006
tcacttaata atcaacctgg ggttcgaaat cagtgagacc tggattcaaa ttctgccttg 1066
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aaaac 1191

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<211> 1070
<212> DNA
<213> Homo sapiens

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<222> 13..465

<221> sig_peptide
<222> 13..75
<223> Von Heijne matrix
score 3.90000009536743
seq PVAVTAAPVLS/IN

<221> polyA_signal
<222> 1035..1040

<221> polyA_site
<222> 1060..1070

<400> 301
agagtcgagaa aa atg gct gcg agt acc tcc atg gtc ccg gtg gct gtg acg      51
Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
-20 -15 -10
gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg      99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
-5 1 5
cgg gaa att aaa aag caa ctg ctg ctt att gcg gcc ctt acc cgg gag      147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
10 15 20
cgg gcc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct      195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
25 30 35 40
ctc cct gca ttg cct ctg gcc gag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
45 50 55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
60 65 70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
75 80 85
aat gca aga aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ala Arg Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
90 95 100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
105 110 115 120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
125 130
gaatgaatgt actttataca tagcaataat aaaaaaaaga tatcataaat aaagttaaaa      545
aggatgggtaa aaaaaaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atttattttac ttaggtgttat ataagggttct tcatgcctgt gaattaatat tattgtgttaa      665
gaattaagttt aaaaagccgtg ggctgacttct taaatttata aattcattta tcatgtttat      725
agtatatttta ttgtttttct ttcattggcta ttaaaagta tgaactgaaa ggacaatgca      785
agtaaaccmaa cttaactact tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acttctcatt tcttagtaca ggttgagtat ccttattttg aagtgtcttg      965
gaccaaaagt gtttcagatt tcagattttt ttcagatttt ggatatattg cattatactt      1025
actgggttgaa ataaaaaatg ctgcagttag tgcataaaaa aaaaa      1070

<210> 302
<211> 1213

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0392350.101501

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..718

<221> sig_peptide
<222> 2..76
<223> Von Heijne matrix
score 3.90000009536743
seq RVGLLLGGGGVYG/SR

<221> polyA_signal
<222> 1170..1175

<221> polyA_site
<222> 1203..1213

<400> 302
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Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
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tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt 97
Leu Leu Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
-5 1 5
cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga vtg cag aga cga 145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
10 15 20
agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt 193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
25 30 35
atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg 241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
40 45 50 55
gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg gaa aaa 289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
60 65 70
cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag tca gct 337
Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
75 80 85
ggg cga caa cag aaa aar aaa ata gag aga odd kaa kas amc ctg arg 385
Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
90 95 100
aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg ttt gct 433
Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
105 110 115
att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc ata ttt 481
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120 125 130 135
gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct tas rtc 529
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
140 145 150
sra gga ctg tct cat cga aat ctg ctg gga gat gac acc aca gac tgt 577
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
155 160 165
tcc ttc att ttc ctg taw att ctc tgt act atg tgc att cga cag aac 625
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
170 175 180
att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc aag cag 673
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln

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185          190          195
gca ggt gga ttt ctt ggc cca cca cct cct tct ggg aag ttc tct      718
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
200          205          210
tgaactcaag aactctttat ttctctacat tctttctaga cacacacaca tcagactggc      778
aactgttttg tascagagc cataggtagc cttackactt gggcctcttt ctagttttga      838
attatttcta agccttttgg gtatkattag agtgaataat gcagccagca aacttgatag      898
tgcttttggg cctagatgat tttatcaaa taagtggatt gattagttaa gttcaggtaa      958
tgtttatgta atgaaaaaca aatagcatcc ttcttggttc attacataa gtattttctg      1018
tggggaccgc tctcaaggca ctgtgtatgc cctgcaagtt ggctgtctat gagcatttag      1078
agatttagaa gaaaaattta gtttgtttaa cctgtgtaac tggttgtttt gttgtgttt      1138
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<222> 86..709
<221> sig_peptide
<222> 86..361
<223> Von Heijne matrix
score 6.30000019073486
seq LLMSILALIFIMG/NS
<221> polyA_signal
<222> 943..948
<221> polyA_site
<222> 963..973
<400> 303
aaagcatcct tccctaggac tgctgtaagc ttgagcctc tagcaggaga catgcctcgg      60
ggacgaaaga gtcggcgccg ccgta atg cga gag cgg cag aag aga acc gca      112
Met Arg Glu Pro Gln Lys Arg Thr Ala
-90 -85
aca atc gca aaa tyc rrg gcs tva gag ggc ctc ega gac ccc tat ggc      160
Thr Ile Ala Lys Xaa Xaa Ala Xaa Glu Gly Leu Arg Asp Pro Tyr Gly
-80 -75 -70
cgc ctc tgt ggt agc gag cac ccc cga aga cca cct gag cgg ccc gag      208
Arg Leu Cys Gly Ser Glu His Pro Arg Arg Pro Pro Glu Arg Pro Glu
-65 -60 -55
gaa gac cgg agc act cca gag gag gcc tct acc acc cct gaa gaa gcc      256
Glu Asp Pro Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala
-50 -45 -40
tcg agc act gcc caa gca caa aag cct tca gtg ccc cgg agc aat ttt      304
Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe
-35 -30 -25
cag ggc acc aag aaa agt ctc ctg atg tct ata tta gcg ctc atc ttc      352
Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe
-15 -10 -5
atc atg ggc aac agc gcc aag gaa gct ctg gtc tgg aaa gtg ctg ggg      400
Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly
1 5 10
aag tta gga atg cag cct gga cgt cas cac agc atc ttt gga gat ccg      448
Lys Leu Gly Met Gln Pro Gly Arg Xaa His Ser Ile Phe Gly Asp Pro
15 20 25

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aag aar atc gtc aca gaa ran ttt gtg cgc aga ggg tac ctg att tat 496
Lys Lys Ile Val Thr Glu Xaa Phe Val Arg Arg Gly Tyr Leu Ile Tyr
30 35 40 45
ara ccg gtg ccc cgt abc agt ccg gtg gag tat gas ttc ttc tgg ggg 544
Xaa Pro Val Pro Arg Xaa Ser Pro Val Glu Tyr Xaa Phe Phe Trp Gly
50 55 60
ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg 592
Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val
65 70 75
gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac 640
Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp
80 85 90
tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt 688
Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly
95 100 105
gct arg ggt tat tcc gcc cct taagtatarct tgaggcagac ccttgggggt 739
Ala Xaa Gly Tyr Ser Ala Pro
110 115
gtaaaagaga gtcacaggta ccccaaggag tagatgccag ggtcctaagt tgaataatgmt 799
gtcgaattggg gggcgggggac actgtatttg atatttgtga tcagtgtatca ttgttcaact 859
gcgaatataga gtgtttgctt ttgataatgg aaaattgtat tcgttttaaa attccgtttg 919
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<210> 304
<211> 810
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..320

<221> sig_peptide
<222> 63..179
<223> Von Heijne matrix
score 3.90000009536743
seq VLAIGLLHIVLS/IP

<221> polyA_signal
<222> 771..776

<221> polyA_site
<222> 799..810

<400> 304
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gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg 107
Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
-35 -30 -25
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt 155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
-20 -15 -10
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc 203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
-5 1 5
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc 251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
10 15 20
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag 299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
25 30 35 40

00973360.101501

gcg agg ctg cta acc cac tgg tgagcagatg gattatgggg tccagttcac 350
Ala Arg Leu Leu Thr His Trp

45

ggcctctcgg aaktctctga ccatcacacc catcgtgctg tacttctctca ccagcttcta 410
cactaaktac raccaaatcc attttgtgct caacaccgtg tccctgatra gcgtgcttat 470
ccccaagctc cccagctctc acggaktccg gatttttgga atcaataakt actgaaaktg 530
casccccctc cccgtcccg ggtggcaggg gaggggtagg gtaaaaggca tktgctgcaa 590
chctgaaaaa araaaraara rsctctgga cactgccara ratgggggtt gagcctctggt 650
cctaatttcc cccctcgtct cccccagtag ccaacttgga gtgacttgta ytggggttgg 710
ggtaggcccc ctgggctctg accttttctg aattttttga tcttttctt ttgctttttg 770
aatararact ccatggagtt ggtcatggaa aaaaaaaaaa 810

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<211> 771

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 299..418

<221> sig_peptide

<222> 299..379

<223> Von Heijne matrix

score 3.59999990463257

seq LTLLLITPSPSPL/LF

<221> polyA_signal

<222> 739..744

<221> polyA_site

<222> 762..771

<400> 305

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taagaaaaaga gcaagctgtc cagagagtga gaagtttgaa aagagaggtg cataagagag 120
aaatgatgtc catttgagcc ccaccacgga ggttatgtgg tcccaaaagg aatgatggcc 180
aagcaatttaa ttttctctcc tagttcttag ctgtctctg cattgattgg ctttacacaa 240
ctggcattta gtctgcatta cacaatataga cactaattta ttggaacaa gcagcaaa 298
atg aga act tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act 346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
-25 -20 -15

ctg ctt cta atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt 394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
-10 -5 1 5

ctg tcc ctc aga tca gca atg tct tggccctct cctctcttcc attccttcc 448
Leu Ser Leu Arg Ser Ala Met Ser

10

gttggtactc atttcttcta acctttaata aacatttagg tataatacat tacagtaagt 508
gctatttaga tactaaactta aaacatacta tatattttaa ggatctaaga atcctttara 568
rrrggcacat gactgaagta cctcagctgc gcagcctgta accagttttt ttaagttaaa 628
agtaaraatg ccagcccttaa cctabccctg carataaaag ctacttttta ttaataccag 688
ccctgaataa tggcactaat ccacactctt ccttaragtg atgctggaaa aataaaatca 748
ggggcttcag attaaaaaaa aaa 771

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<211> 409

<212> DNA

<213> Homo sapiens

<220>

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<221> CDS
<222> 186..380

<221> sig_peptide
<222> 186..233
<223> Von Heijne matrix
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      seq FFLFLSFVLMYDG/LR

<221> polyA_signal
<222> 383..388

<221> polyA_site
<222> 396..409

<400> 306
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acctagtttt ttaaagggtt gaatataata atgcagtatt tgcagtataa aaaggaagga      120
atttgtagag aatcattttg gtgctcaagt ctcttagcag tgccttattg cctcatagca      180
agaag atg ctg ggg ttt ttt ttg ttt ttg tcc ttt gta tta atg tat gat      230
      Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
      -15                      -10                      -5

ggt ttg cgc ctt ttt ggc att ctt tca aca tgt cgt gta cat cac acc      278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
      1                      5                      10                      15

atg aat cag ttc cta att gat ata tct agc ttt acc tcc cga gtt aaa      326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys
      20                      25                      30

aaa aaa atc ttt tta ttt tat gcc ttc awa ggt tgc ycg ttt car agt      374
Lys Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser
      35                      40                      45

gcc aca taaataaaat gtttaacaaa aaaaaaaaaa      409
Ala Thr

<210> 307
<211> 613
<212> DNA
<213> Homo sapiens

<220>
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<222> 69..458

<221> sig_peptide
<222> 69..233
<223> Von Heijne matrix
      score 4
      seq AALCGISLSQLFP/EP

<221> polyA_signal
<222> 564..569

<221> polyA_site
<222> 602..613

<400> 307
aagaacctga gcagcctgtc ttcagacaga gagaggccca cggctgtttc ttgaaaytgg      60
cgctggga atg gcc atg tgg aac agg cca tgb bag ang ctg cct cag cag      110
      Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
      -55                      -50                      -45

cct cts sta gct gag ccc act gca gag ggg gag cca cac ctg ccc acg      158

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Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
-40 -35 -30
ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt 206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25 -20 -15 -10
ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc 254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
-5 1 5
tgc aca gag ttc atg gca ggc ctg gtg ckm tgg ctg gag ttg tct gaa 302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
10 15 20
gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa 350
Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
25 30 35
gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa 398
Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
40 45 50 55
gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa 446
Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
60 65 70
gga tgg gca cta tgacccccgg gccagagtcc tcgtttgccca catgacctcc 498
Gly Trp Ala Leu
75
ctgctccaag tgcccttgga ggagctggat gtccttgaaa agatgttctt ggagagcctg 558
aaggaaatca aagaagagga atctgaaatg gccgaggcat cccraaaaaa aaaaa 613

<210> 308
<211> 986
<212> DNA
<213> Homo sapiens

<220>
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<222> 12..638

<221> sig_peptide
<222> 12..263
<223> Von Heijne matrix
score 4.19999980926514
seq ITMLQMLALLGYG/LF

<221> polyA_signal
<222> 951..956

<221> polyA_site
<222> 975..985

<400> 308
accctatcaa g atg gtc aac ttc ccc cag aaa att gca ggt gaa ctc tat 50
Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr
-80 -75
gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg 98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
-70 -65 -60
atg aag acg tct gac act att atc cgg gag gcc acc ctg atg ggc aca 146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
-55 -50 -45 -40
gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att 194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
-35 -30 -25
tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg 242

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Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
-20 -15 -10
ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc 290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
-5 1 5
atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg 338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
10 15 20 25
ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct 386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
30 35 40
cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct 434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
45 50 55
gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa 482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
60 65 70
dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc 530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
75 80 85
atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg 578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
90 95 100 105
ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc 626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
110 115 120
ctg cag tca cac tgacccccacc tgaattcttt ggccagtcct ctttcccgca 678
Leu Gln Ser His
125
gctgcagaga ggargaasac tattaagga cagtcctgat gacatgtttc gtagatgggg 738
tttgacgctg ccactgagct gtactgtcgt aagtacctcc ttgatgcctg tcggcacttc 798
tgaaagggcac aaggccaaga actcctggcc aggactgcga ggctctgcag ccaatgcaga 858
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<222> 282..389
<221> sig_peptide
<222> 282..332
<223> Von Heijne matrix
score 3.5
seq RWWCFHLQAEASA/HP
<221> polyA_signal
<222> 1413..1418
<221> polyA_site
<222> 1437..1447
<400> 309
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gaagagctgt ggaggccacc ctctacaaag ctttatagaa cttctggatc taactcaca 180

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acaagcttcc agaagagact agagacctta ggccaggaga tgaaggagtt cagtagcaaaa 240
gtcacacctg tccaattccc tgagctttgc tcaactcagct a atg gga tgg caa agg 296
Met Gly Trp Gln Arg
-15

tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa 344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
-10 -5 1

ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt 389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys
5 10 15

taacaaadga aaacgtcttg gtggcggcag casctttgct ctgagtgccct acaaaagctaa 449
tgcttggtgc tagaaacatc atcattatta aacttcagaa aagcagcagc catgttcagt 509
caggctcatg ctgcctcact gcttaagtgc ctgcaggagc cgcttgccaa rctccccttc 569
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<210> 310
<211> 1641
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 208..339

<221> sig_peptide
<222> 208..294
<223> Von Heijne matrix
score 5.59999990463257
seq LFLQLLVSHIEIVC/AT

<221> polyA_site
<222> 1631..1641

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atgatcatgc agaggcagaa gccaggcacc tggctctatga atcagaccaa aacaaggatg 120
gcaagcttac caaggaggag atcgttgaca agtatgactt atttggttggc agccaggcca 180
cagatgtttg ggaggcccta gtacggc atg atg agt tot gag cta cgg agg aac 234
Met Met Ser Ser Glu Leu Arg Arg Asn
-25

cct cat ttc ctg aaa agt aat tta ttt tta cag ctt ctg gtt tca cat 282
Pro His Phe Leu Lys Ser Asn Leu Phe Leu Gln Leu Leu Val Ser His
-20 -15 -10 -5

gaa att gtt tgc gct act gag act gtt act aca aac ttt tta aga cat 330
Glu Ile Val Cys Ala Thr Glu Thr Val Thr Thr Asn Phe Arg His
1 5 10

gaa aag gcg taatgaaaac catccgctcc ccattcctcc tctctctgta 379

Glu Lys Ala

15

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gggactggag ggaagccgtg cttctgagga acaactctaa ttagtacact tgtgtttgta 439
ratttacacw wtgtattatg tattaacatg gcgtgtttat ttttgtattt ttctctgggt 499
gggagtatka tatgaaggat caaratccctc aactcacaca tgтарасааа cattasctct 559
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<210> 311
 <211> 884
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 <213> Homo sapiens

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 <222> 69..557

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 <222> 69..224
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 score 4.69999980926514
 seq LGLALGRLEGGSA/RH

<221> polyA_signal
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<221> polyA_site
 <222> 870..883

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      Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
            -50      -45      -40
cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc 158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Gly Met Arg Val
            -35      -30      -25
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg 206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
            -20      -15      -10
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg 254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
            -5      1      5      10
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc 302

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09975350.107501

Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
15 20 25
ccg ggc ctg cac cag ctc acc aag cta ckt ttc ett caa act gag gac 350
Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp
30 35 40
agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg 398
Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val
45 50 55
cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg 446
Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu
60 65 70
gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg 494
Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu
75 80 85 90
ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct 542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala
95 100 105
cra rac acc cga tgg tgaaccctg ctgascacg ctgttctccg ggcctraatg 597
Xaa Xaa Thr Arg Ser
110
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<212> DNA
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<221> sig_peptide
<222> 134..274
<223> Von Heijne matrix
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seq TWLGLLSFQNLHC/FP

<221> polyA_site
<222> 718..729

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tgtaatgcaa gtcccttaac tccttggttg ctaacattaa ctcccttaag taataatcaa 120
tgaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa 169
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
-45 -40
tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt 217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35 -30 -25 -20
ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac 265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Ser Ser Phe Gln Asn
-15 -10 -5
ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa 313
Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys
1 5 10
gga ktc aac act tgagcctagg gtgggtacac acaaaaratt ctaatttacc 365
Gly Xaa Asn Thr

09070350.101501

15

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attttattgta	ttgtataasc	taaaaacatt	tatttttgg	gaatcraaac	aattccatgt	485
ascaactcttt	tttctgttca	cgggtgttgg	gataaaacct	taaattccgc	aagcatcagt	545
tttttgaaaa	aatgggaatt	gaccggatag	wwacaggcaa	agwtataaat	agctacaaaca	605
tcatttaact	tttataaaca	tgcttctctc	ctattgaara	catctgatat	tttgctgtga	665
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<220>
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 <222> 78..731

<221> sig_peptide
 <222> 78..227
 <223> Von Heijne matrix
 score 5.09999990463257
 seq RTALILAVCCGSA/SI

<221> polyA_site
 <222> 1002..1013

<400> 313

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aattttattt	actttctc	atg cat cat	ggc ctc aca	cca ctg tta	ctt ggt	110
		Met His His	Gly Leu Thr	Pro Leu Leu Leu	Gly	
		-50	-45	-40		
gta cat gag	caa aaa	cag caa	gtg gtg	aaa ttt	tta atc aag	aaa aaa
Val His Glu	Gln Lys	Gln Gln	Val Val	Lys Phe	Leu Ile Lys	Lys Lys
	-35		-30		-25	
gca aat tta	aat gca	ctg gat	aga tat	gga aga	act gct ctc	ata ctt
Ala Asn Leu	Asn Ala	Leu Asp	Arg Tyr	Gly Arg	Thr Ala Leu	Ile Leu
	-20		-15		-10	
gct gta tgt	tgt gga	tcg gca	agt ata	gtc agc	ctt cta	ctt gag
Ala Val Cys	Cys Gly	Ser Ala	Ser Ile	Val Ser	Leu Leu Leu	Glu Gln
	-5		1		5	
aac att gat	gta tct	tct caa	gat cta	tct gga	cag acg	gcc aaa
Asn Ile Asp	Val Ser	Ser Gln	Asp Leu	Ser Gly	Gln Thr	Ala Lys
	10		15		20	
tat gct gtt	tct agt	cgt cat	aat gta	att tgc	cag tta	ctt tct
Tyr Ala Val	Ser Ser	Ser Arg	His Asn	Val Ile	Cys Gln	Leu Ser
	30		35		40	
tac aaa raa	aaa cag	atr cta	aaa gtc	tct tct	gaa aac	agc aat
Tyr Lys Xaa	Lys Gln	Xaa Leu	Lys Val	Ser Ser	Glu Asn	Ser Asn
	45		50		55	
raa caa gac	tta aag	ctg aca	tca gag	gaa gag	tca caa	agg ctt
Xaa Gln Asp	Leu Lys	Leu Thr	Ser Ser	Glu Glu	Glu Ser	Gln Arg
	60		65		70	
gga agt gaa	aat agc	cag cca	gag gaa	atg tct	caa gaa	cca gaa
Gly Ser Glu	Asn Ser	Gln Pro	Glu Glu	Met Ser	Gln Glu	Pro Glu
	75		80		85	
aat arg ggt	ggt gat	aga aag	gtt gaa	raa raa	aat aar	aag cac
Asn Xaa Gly	Gly Asp	Arg Lys	Val Glu	Xaa Xaa	Met Lys	Lys His
	90		95		100	
agt wct cat	atg gga	ttc cca	raa aac	ctg mct	aac ggt	gcc act
Ser Xaa His	Met Gly	Phe Pro	Xaa Asn	Leu Xaa	Asn Gly	Ala Thr
						Ala

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110      115      120
gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct 638
Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro
125      130      135
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac 686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp
140      145      150
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag 731
Phe Ser Gly His Pro Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
155      160      165
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaattattaca 791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc 851
tttctcttag ttataaaaa gaaaaagacc tcttgcataa aaatagtagc ttgcaggaag 911
aaattgtcat gctaaractg gaactagack taatgaaaca tcagagccag ctaaraaaa 971
araaatattt ggaggaaatt gaaagtgtgg aaaaaaaaaa aa 1013

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<221> sig_peptide
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<223> Von Heijne matrix
score 7.59999990463257
seq CVLVLAAGAGAVA/VP

<221> polyA_signal
<222> 937..942

<221> polyA_site
<222> 962..973

<400> 314
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Met Val Cys Val
-15
ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg 105
Leu Val Leu Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10 -5 1 5
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct 153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
10 15 20
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc 201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
25 30 35
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat 249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
40 45 50
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt 297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe
55 60 65
gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac 345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr
70 75 80 85
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc 393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro

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          90          95          100
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta 441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu
          105          110          115
att cac agg gtg aag cca rat ttg gtg ttg tgt aac gga cca gga aca 489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr
          120          125          130
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata 537
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile
          135          140          145
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs 585
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr
          150          155          160
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att 633
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile
          170          175          180
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tgc gtg tac ctt 681
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu
          185          190          195
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa 733
Gly Arg Ile Val
          200
cagtartatg tactcaaatt ggggggaaaa aaacctaca tgtttcttgt aaaggcgtct 793
gacagtcctg araattattg atggtaaggga ataaaaaatg twcagatrac tcagtgaara 853
aactgaggct tctcttatga aacaacatt gataaacgta actacyaaat gtttatgcct 913
ctgtaaacca aattctcttt ctarataaaa atatgtatta ctacctgcaa aaaaaaaaaa 973

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<222> 126..527

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<222> 126..182
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      seq ILPHGVFYAGGFA/IV

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<222> 834..839

<221> polyA_site
<222> 856..867

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gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc 120
ggtcac atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc 170
      Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
          -15          -10          -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg 218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
          1          5          10
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag 266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu
          15          20          25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc 314

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Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
30 35 40
atc gac agg gaa aac ttc gtg gac att gtt rat gcc aag ttg aaa att 362
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile
45 50 55 60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc 410
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Tyr Val His Ser Ser
65 70 75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag 458
Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
80 85 90
ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 506
Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
95 100 105
ggg gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 557
Gly Asp Glu Val Lys Lys Glu
110 115
ctagtccatc cttccctcat ctctaccata tggccactgg ggtgggtggcc catctcagtg 617
acagacactc ctgcaaccga gktttccagc caccagtggg atgatgggtat gtgccagcac 677
atggtaattt tgggtgaatt ctaacttggg cacaacgaat gctatttgtc atttttaaac 737
tgaatccgaa agaaactcct attataaatt taagataatg taatgtattt gaaagtgtct 797
tgtataaaaa agcacatgat aaaaggaatc agaattaata aaatgtttgt tgatctttaa 857
aaaaaaaaa h 868

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<211> 519
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<222> 66..320

<221> sig_peptide
<222> 66..113
<223> Von Heijne matrix
score 3.5
seq TALAAXTWLGWVG/VR

<221> polyA_signal
<222> 490..495

<221> polyA_site
<222> 508..519

<400> 316
aattagcgcg taacgcasag actgcttgct gcggcagaga cgccagakgt gcagctccag 60
cagca atg gca gtg acg gcg ttg gcg gcg mrg acg tgg ctt gcc gtg tgg 110
Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
-15 -10 -5
ggc gtg agg acc atg caa gcc cga ggc ttc ggc tcg gat cag tcc gag 158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
1 5 10 15
aat gtc gac cgg ggc gcg ggc tcc atc cgg gaa gcc ggt ggg gcc ttc 206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
20 25 30
gga aag aga gag cag gct gaa gag gaa cga tat ttc cga gca cag agt 254
Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser
35 40 45
aca gaa caa ctg gca rct ttg aaa aaa crc cat gaa gaa gar atc gtt 302
Thr Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val

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50 55 60
 cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca 350
 His His Arg Glu Gly Asp
 65
 taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat 410
 ggccacatgtc attgccact tctgtgtaaa catgtttctg gttaaactaa tatttgtctg 470
 tgtgtacta acagattata ataaattgtc atcagtga aa aaaaaaaa 519

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 <222> 73..948

 <221> sig_peptide
 <222> 73..159
 <223> Von Heijne matrix
 score 4.40000009536743
 seq IVLHLVLQGMVYT/EY

 <221> polyA_site
 <222> 1016..1028

 <400> 317
 agcttttaaag gccctggccag gggaggagca cagatatattt cctgtataat tccagaatgt 60
 cttcagagag cc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac 111
 Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
 -25 -20
 cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act 159
 His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
 -15 -10 -5
 gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc 207
 Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
 1 5 10 15
 ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt 255
 Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Gly Val Asn Leu Phe
 20 25 30
 ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca 303
 Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala
 35 40 45
 aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt 351
 Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe
 50 55 60
 cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga 399
 Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg
 65 70 75 80
 tcc aas cac tgc akt gtg tgt aac tgg tgt gtg cac cgt ttc rac cat 447
 Ser Xaa His Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His
 85 90 95
 cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc 495
 His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa
 100 105 110
 ttc ctc atc tac gtc ttg acc ttg acg gcc tgc gct gcc acc gtc gcc 543
 Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala
 115 120 125
 att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta 591
 Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu
 130 135 140

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tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac	639
Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp	
145 150 155 160	
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc	687
Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val	
165 170 175	
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac	735
Phe Met Leu Gly Phe Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr	
180 185 190	
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag	783
Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu	
195 200 205	
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc	831
Trp Tyr Arg Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala	
210 215 220	
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat	879
Trp Tyr Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His	
225 230 235 240	
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt	927
Gly Leu Arg Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys	
245 250 255	
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta	978
His Glu Arg Lys Lys Gln Glu	
260	
gttcccgttt atttacacat gtggatcctc gttttccaaa aaaaaaaaaa	1028
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score 4.90000009536743	
seq FACVPGASPTTLA/FP	
<221> polyA_signal	
<222> 419..424	
<221> polyA_site	
<222> 441..452	
<400> 318	
acagcgtgas tcgcccgcga gaagaatatg aaaaagcaga gcganctcgg ttaaggga	60
gcgcgcgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cgg	110
Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg	
-55 -50 -45	
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac	158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn	
-40 -35 -30	
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt	206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys	
-25 -20 -15	
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc	254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu	
-10 -5 1 5	

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aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
      10      15      20
ggg ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
      25      30      35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
      40      45      50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
      55      60      65
aaaaaaaaa      452

<210> 319
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<220>
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<222> 628..804

<221> sig_peptide
<222> 628..711
<223> Von Heijne matrix
score 4.19999980926514
seq LMPVIPALQEXA/GG

<221> polyA_site
<222> 864..875

<400> 319
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gaaaccgctt tatcatcctt gtgtatgtac tggcagttatt aagttngtcc atcaagaatg      120
cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaattttatt ctccagatat gccttcacgg ctccaattc aagacatatt      240
tgctggactg gttacaagta ttggcactgc aatacgatat tggtttcatt atacacttgt      300
ggcctttgca tggttgggag ttgttcctct tacagcatgt gattattcat gcctctgatt      360
ggagttattt aaacattgca taactactta atattataaa gcaattatgc atcatattat      420
tatttgactg atgttttagt atttgatgtc agagtgtcat gtattaggaa agccttactt      480
araaratggt catcggaact aaraatgakt ttaacaggtc agttttttga gtgaatgtgg      540
gaaaraacac agcatacaga atggctaacc atgaaagttc atgaaagcgt kgaaaaaatc      600
aaatcaaatc ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa      654
Met Leu Xaa Leu Ser Arg Ala Thr Lys
      -25      -20

rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag      702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu
      -15      -10      -5
gcc gan gca gcc gga tca cga ggt cag gag ttt gaa act agc ctg gcc      750
Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala
      1      5      10
aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg      798
Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg
      15      20      25
ttg car tgaactgaga tcgcaccact gcactccagc ttgggcaaca gagcaagact      854
Leu Gln
      30
ttgtctcgca aaaaaaaaaa a      875

<210> 320

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<211> 531
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLISNWNANPASS/RR

<221> polyA_signal
 <222> 496..501

<221> polyA_site
 <222> 521..531

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          Met His Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
          -10          -5          1
cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc      159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
          5          10          15
gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc      207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
          20          25          30
tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
          35          40          45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
          50          55          60          65
cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
          70          75          80
ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaaatta      406
Leu Gly Arg Gln Leu
          85
ttttaratgt ctaactttat gttattgctc acgggtattt gactgaattg ttgatttagg      466
ataagtcaat tctctggagg aaattaccaa ataaatgat atgtattttc taccacaaaa      526
aaaaa                                         531
  
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 <213> Homo sapiens

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 <222> 70..366

<221> sig_peptide
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 score 3.5
 seq MHLISNWNANPASS/RR

<221> polyA_site

<222> 1233..1244

<400> 321

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cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga      111
      Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
      -10                               -5                               1
cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tgc acc ctc      159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
      5                               10                               15
gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc      207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
      20                               25                               30
tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
      35                               40                               45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
      50                               55                               60
cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
      70                               75                               80
ttg gga cgc caa ttg tagtcggtct tctcttgccc aaccagacac tggcatccac      406
Leu Gly Arg Gln Leu
      85
tgtcttctgg cagtggctga accagagcca caatgcctgt gtcaactatg caaaccgcga      466
tgcaccaagg ccttcacctg catccaagtt catccaggga tacctgggag ctgtcatcag      526
cgccgctctc attgctgtgg gccttatktc ctggttcaga aagcccaacaa gtccacccca      586
gccaccgcgc ttctcatcca gagggtttgt cegttccctg ctgtagccag tgccaatatc      646
tgcaatgtgg tctctgatcg gtacggggag ctggagggaag ggattgatgt cctggacagc      706
gatggcaaac tcgtgggtgc ctccaagatc gcagcccgac acgcccctgt ggagacggcg      766
ctgacgcgag tggctctgcc catgcccatc ctggtgctac ccccgatcgt catgtccatg      826
ctggagaaga cggctctcct gcaggcacgc ccccggtcgc tcctccctgt gcaaacgctc      886
gtgtgcctgg cagccttcgg cctggccctg ccgctggcca tcagcctctt cccgcaaatg      946
tcagagattg aaacatccca attagagccg gagatagccc agggcacgag cagccggaca      1006
gtgtgttaca acaaggggtt gtgagtgtgg tcagcgccct ggggacggag cactgtgcag      1066
ccggggagct gaggggcarg gccgtagact caccgctgca cctgcaggga gcagcacgcc      1126
aaccaccagca gtctctgggc ccctgggaga gtgctcaacc tacagtggag ggagactgac      1186
ccattcacat ttttaacatag gcaagaggag ttctaacaca ttctgtacaa aaaaaaaa      1244
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<210> 322

<211> 631

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 111..434

<221> sig_peptide

<222> 111..185

<223> Von Heijne matrix

score 3.90000009536743

seq WIAAVTIAAGTAA/IG

<221> polyA_site

<222> 618..631

<400> 322

Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
 30 35 40
 aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc 243
 Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
 45 50 55 60
 ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa 291
 Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu
 65 70 75
 ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg 339
 Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met
 80 85 90
 att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac 387
 Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp
 95 100 105
 aca rag cac gtg gcc ara gtc ctc cag cac ata gaa gtg aat ggc 435
 Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly
 110 115 120
 atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc 483
 Ile Asn Leu Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser
 125 130 135 140
 aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att 531
 Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile
 145 150 155
 tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgt 577
 Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu
 160 165
 caatcagtggt gccccaact tcaccatctt ctccccccta ctctcacttc cgctcatgtgt 637
 tttatacaac tctcaaatct ttcttgagaga aggaggatat acatacataa tatgaaatgt 697
 gtttgttctt cacagtcacc cgattttact gatatttatt tgcattttac caataaaaag 757
 aaaatgcaag ctcaaaaaaa aaaa 781

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 <211> 931
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 19..312

 <221> sig_peptide
 <222> 19..63
 <223> Von Heijne matrix
 score 8.39999961853027
 seq AMWLLCVALAVLA/WG

 <221> polyA_signal
 <222> 896..901

 <221> polyA_site
 <222> 921..931

 <400> 324
 aagtgtgtgt taccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg 51
 Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
 -15 -10 -5
 gcg gtc ttg gca tgg gcc ttc ctc tgg gtt tgg gac tcc tca gaa cga 99
 Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
 1 5 10
 atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc 147
 Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr

	15	20	25	
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc				195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro				
30	35	40		
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc				243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys				
45	50	55	60	
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa rgt ctt				291
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu				
65	70	75		
acc tct gaa ccc ctc ama gcc tagggacagg arcggccggc ttacctgggtg				342
Thr Ser Glu Pro Leu Xaa Ala				
80				
ggttggggga cgtcggcagc tcrctacta cgccagcagg attganganc acagaaacag				402
ttgchsttgg ttgtattcag tacctkcaatt tccgttggga actccaccwg tacttgttat				462
kctgtggaac ttttttttat ttgtagaagg agcaagaata ttgaccttac tataatgacac				522
acgaaacaat ctatgctgta tcgtgctgc tcaatcctta aagttaactt ctaatgatag				582
taaaaracct tctcgtcgcc tttaaaatgc agcttggtgct aktaacatgc atgtgtcaaa				642
ttgaaraatt agacatagat gactaratar aaagtaattt tgtaggtaatt ttaragttc				702
aactccaccc agctttcakt gaaggaacct ttcaataat aratttttgc ttaccatara				762
raaaaratca aatgacaaag caaatattga ccattaagct ggaatatggt gataattgaa				822
cagttgtata aatgaaktaa ttgaattgta cacatacaat ggggtgaattt tatggcatgt				882
caaagtatac ctcaataaag ctattttttt aaattgcmma aaaaaaaaaa				931
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<222> 64..612				
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<222> 64..234				
<223> Von Heijne matrix				
score 3.79999995231628				
seq QLWLVMFCGAGS/VT				
<221> polyA_site				
<222> 839..849				
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acatacgggc aagttttataa gggctgctat gtcaaaacgg gccagcttgc agccatcaag				60
gtt atg gat gtc aca ggg gat gaa gag gaa gaa atc aaa caa gaa att				108
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile				
-55 -50 -45				
aac atg ttg aag aaa tat tct cat cac cgg aat att gct aca tac tat				156
Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr				
-40 -35 -30				
ggt gct ttt atc aaa aag aac cca cca ggc atg gat gac caa ctt tgg				204
Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp				
-25 -20 -15				
ttg gtg atg gag ttt tgt ggt gct ggc tct gtc acc gac ctg atc aag				252
Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys				
-10 -5 1 5				
aac aca aaa ggt aac acg ttg aaa gag gag tgg att gca tac atc tgc				300
Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys				
10 15 20				
msg gaa atc tta cgg ggg ctg art cac ctg cac cag cat aaa gtg att				348
Xaa Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile				

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      25              30              35
cat cga rat att aaa ggg caa aat gtc ttg ctg act gaa aat gca gaa      396
His Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu
      40              45              50
gtt aaa cta gtg gac ttt gga rtc akt gct cag ctt gat cga aca gtg      444
Val Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val
      55              60              65              70
ggc agg arg aat act ttc att gga act ccc tac tgg atg gca cca raa      492
Gly Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa
      75              80              85
gtt att gcc tgt gat gaa aac cca sat gcc aca tat gat ttc aar art      540
Val Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa
      90              95              100
gac ttg tgg tct ttg ggt atc acc gcc att gaa atg gca gaa ggg ctc      588
Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu
      105              110              115
ccc ctc tct gtg aca tgc acc cca tgagagctct cttcctcatc ccccggaatc      642
Pro Leu Ser Val Thr Cys Thr Pro
      120              125
cagcgctctcg gctgaagtct aagaagtggg caaaaaaatt ccagtcattt attgagagct      702
gcttggtataa aaatcacagc cagcgaccag caacagaaca attgatgaag catccattta      762
tacgagacca acctaattgag cgacagggtcc gcattcaact caaggaccat attgatagaa      822
caaagaagaa gcgaggaataa aaaaaaa      849

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<211> 644
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 39..458

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<222> 39..80
<223> Von Heijne matrix
      score 4.40000009536743
      seq FLTALLWRGRIP/RQ

<221> polyA_signal
<222> 613..618

<221> polyA_site
<222> 633..644

<400> 326
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Met Phe Leu Thr Ala Leu
      -10
ctc tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg      104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
      -5              1              5
cgg cgg cgg ttc gtg tgg ttg cgc gcc aag cag aac atg atc cgc cgc      152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
      10              15              20
ctg gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg      200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
      25              30              35              40
acc cgg gag cag gag cgc gcc cac gcc gcg ttg cgc agg agg gag gcc      248
Thr Arg Glu Gln Glu Arg Gly His Ala Ala Leu Arg Arg Arg Glu Ala
      45              50              55

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ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga	296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg	
60 65 70	
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc	344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val	
75 80 85	
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc	392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr	
90 95 100	
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag	440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu	
105 110 115 120	
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata	488
Leu Trp Thr Ser Leu Tyr	
125	
tcgaatatct agagctctaa acccccacat acttaaaagt ctaattgctg tcctgtggtt	548
tcattagtct gataggaaga tagggatttc ctcagtcaca gatgatattt tgaaggaag	608
ctgcaataaaa gccacaatga ttgaaaaaa aaaaaa	644

<210> 327
 <211> 918
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 9..185

<221> sig_peptide
 <222> 9..50
 <223> Von Heijne matrix
 score 3.70000004768372
 seq AALVTVLFTGVRR/LH

<221> polyA_site
 <222> 906..918

<400> 327	
agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg	50
Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg	
-10 -5	
ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc	98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser	
1 5 10 15	
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc	146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser	
20 25 30	
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaggcca	195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln	
35 40 45	
gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra ktgtactgc tgtcacagga	255
aaaggagcgt ggattacaas catggcasct caggcagcar aaktgtcagg aaraacaaag	315
gaagcaggaa aatgctctta aacccaaagg ggcttcactg aaaaacccacg tccaaktca	375
ataaaaagca actcctgcct cccttcctca cctgtctctt ggatttcttt tctatcacct	435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaa	495
agctgggaacm ccaaraacaa gctgttarat cactgcctgg gaggcttgcc ttartactct	555
catctctgggt tccattccag ttcagctaag tcttgcttta aaatttttac ctccctagctg	615
ggtgcggtgg ctcacgcctg taatcccagg actttgggag gctgaggcgg gcagatcaca	675
agatcaggag tctgagacca gcctggccaa cccagcctgg tcaacatggt gaacacctgt	735
ccctactaaa gatacaaaac attagccggg cgtggtgggg tgcgcttgta atcccagcta	795
ctcaggaggc tgaggcagga gaatcgctta aactcgggag gtagagggtg cagtgaacca	855

aggtcacacc attgcactcc aacctgggag acaggggag actctgtctc aaaaaaaaaa 915
aaa 918

<210> 328
<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..316

<221> sig_peptide
<222> 14..121
<223> Von Heijne matrix
score 5.19999980926514
seq PLRLNLLILIEG/SV

<221> polyA_signal
<222> 442..447

<221> polyA_site
<222> 458..471

<400> 328
attatataga gcc atg ggg cct tac aac gtg gca gtg cct tca gat gta 49
Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
-35 -30 -25
tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta 97
Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
-20 -15 -10
aat ctg ctg atc ctt att gag ggc agt gtc gtc ttc tat cag ctg tat 145
Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
-5 1 5
tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt tcc atg gct ctg 193
Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
10 15 20
atc ctg ttc tgc aac tac tat gtt tta ttt aaa ctt ctg cgg gac aga 241
Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
25 30 35 40
wta kta tta ggc agg gca tac tcc tac cca ctg aac agt tat gaa ctg 289
Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
45 50 55
aag gca aac twa gct gcc tct caw caa tgagggagaa ctcagataaa 336
Lys Ala Asn Xaa Ala Ala Ser Xaa Gln
60 65
aatattttca tacgtttctat ttttttcttg tgatttttat aaatatttaa gatattttat 396
attttgtata ctattatggt ttgaaagtcg ggaagagtaa gggatattaa atgtatccgt 456
aaacaaaaaa aaaaam 472

<210> 329
<211> 1504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..1092

<221> sig_peptide
<222> 70..234

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<223> Von Heijne matrix
score 4.09999990463257
seq AVCAALLASHPTA/EV

<221> polyA_signal

<222> 1475..1480

<221> polyA_site

<222> 1493..1504

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tgcgcggaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att      111
      Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
      -55                -50                -45
ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat      159
Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
      -40                -35                -30
ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct      207
Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
      -25                -20                -15                -10
gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg      255
Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
      -5                1                5
gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag      303
Asp Val Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys
      10                15                20
caa agg ttt cag aga tta gac tgt ata tat cta aat gct ggg atc atg      351
Gln Arg Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met
      25                30                35
cct aat cca caa cta aat atc aaa gca ctt ttc ttt ggc ctc ttt tca      399
Pro Asn Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser
      40                45                50                55
aga aaa gtg att cat atg ttc tcc aca gct gaa ggc ctg ctg acc cag      447
Arg Lys Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln
      60                65                70
ggg gat aag atc act gct gat gga ctt cag gag gtg ttt gag acc aat      495
Gly Asp Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn
      75                80                85
gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctc ctc tgt      543
Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys
      90                95                100
cac agt gac aat cca tct cag ctc atc tgg aca tca tct cgc agt gca      591
His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala
      105                110                115
agg aaa tct aat ttc agc ctc gag gac ttc cag cac agc aaa ggc aag      639
Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys
      120                125                130                135
gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct      687
Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala
      140                145                150
ttg aac agg aac ttc aac cag cag ggt ctc tat tcc aat gtg gcc tgt      735
Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys
      155                160                165
cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct cgg ttt      783
Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe
      170                175                180
ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca      831
Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Arg Phe Phe Ala
      185                190                195
aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg      879

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Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Xaa Gln Lys Thr Val
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 Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
 15 20 25
 gag caa gak tat cta aar ata raa aaa gga gac ggt gcc tca ggg agt 534
 Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys Gly Asp Gly Gly Ser Gly Ser
 30 35 40 45
 aaa gga agg cca ktt gan caa aca gaa ktg ttc ctc tgc att tca aaa 582
 Lys Gly Arg Pro Xaa Xaa Gln Thr Glu Xaa Phe Leu Cys Ile Ser Lys
 50 55 60
 cct tct tcc ttt cta tagccctgtg gtggaagatt ttattaaaa cctacgtgaa 637
 Pro Ser Ser Phe Leu
 65
 gttgataagg cgcttgctga tgacttgaaa aaaaacttcc caagtttgaa gggtcagact 697
 taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa 757
 aaaaaaaa 765

 <210> 331
 <211> 1041
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 230..469

 <221> sig_peptide
 <222> 230..307
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VLCTNQVLITARA/VP

 <221> polyA_signal
 <222> 1004..1009

 <221> polyA_site
 <222> 1027..1040

 <400> 331
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 tcaactccaga tacatggaaa gatggtgcta ggaataccac agaaagtgtt ggaagaaagc 180
 tgaatgaaaa taaagctttg acttcaaaaa aagccagaat tgatccata atg gaa gaa 238
 Met Glu Glu
 -25
 ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag 286
 Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
 -20 -15 -10
 gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga 334
 Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
 -5 1 5
 tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg 382
 Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
 10 15 20 25
 tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc 430
 Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
 30 35 40
 tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgktk 479
 Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
 45 50

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acc tgagatcact tcttaagtca ctttttctt ttgttatatt ctgtttgtag 595
Thr
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tgttttctta catttttatg ttctgagttt tgaaatagtt ttatgaaatt tcttttattt 715
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tcagtttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat 835
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taatcccgag actttgggag gccgagggcg gccgattgct tgaggtaag ttgttgagac 955
cagcctggcc aacatggcga aacccccatct actaaaaata caaaaattag ccaggcatgg 1015
tggtgggtgc ctgtaatccc aactacctag gaggctgagg caggagaatc gcttgaaccc 1075
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<210> 333
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..425

<221> sig_peptide
<222> 36..119
<223> Von Heijne matrix
score 11.6000003814697
seq LLLLVQLRLFLRA/DG

<221> polyA_signal
<222> 1215..1220

<221> polyA_site
<222> 1240..1250

<400> 333
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Met Asn Trp Glu Leu Leu
-25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg ttg cag ctg 101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Val Gln Leu
-20 -15 -10
ctg cgc ttc ctg agg gct gac gcc gac ctg acg cta cta tgg gcc gag 149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5 1 5 10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg 197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
15 20 25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg 245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
30 35 40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag 293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
45 50 55
ctg gaa agg gtg aaa aga aga tgc cta gag aat gcc aat tta aaa gaa 341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
60 65 70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac act ggt tcc cat 389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
75 80 85 90
gaa agc gcc tac caa agc tgt tct cca gga att tgg tagaatcgac 435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp

	95	100	
attctgtgtca	acaatgtgga	aatgtcccag	cgttctctgt
gtctacagaa	agctaagag	agcttaacta	cttagggacg
kctgcctcac	atgatcgaga	ngaarcaagg	aaagattgtt
tatcatactt	gtacctcttt	ccattggata	ctgtgctagc
ktttaatggc	cttcracag	aacttgccac	ataccceargt
cccaggacct	gtgcaatcaa	atatttgga	aaattcccta
tataggcaat	aatggagacc	agtcaccacaa	gatgacaacc
gttaatcagc	atggccaatg	atttgaaga	agtttggatc
agtaacatat	ttgtggcaat	acatgccaac	ctgggcctgg
gaagaaaagg	attgagaact	ttaagagtgg	tgtggatgca
ctttaagaca	aaacatgact	gaaaagagca	ctgtactttt
atggaaaaca	tgaaaacagc	gaactctctt	tcaagccact
attttacttt	ttaatatgata	tgctctctta	taatacaaga
ataaaaagatt	gccatgaatc	ttgcaaaaaa	aaaaa

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 <212> DNA
 <213> Homo sapiens

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 <222> 155..751

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 <222> 155..340
 <223> Von Heijne matrix
 score 3.70000004768372
 seq SILGIISVPLSIG/YC

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 <222> 912..917
 <221> polyA_site
 <222> 937..947

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 ccttgacctg accgacactg gttcccatga agcgggtacc aaagctgttc tccaggagtt 120
 tggtagaatac gacattcttg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc 175
 Met Ser Gln Arg Ser Leu Cys
 -60

atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac 223
 Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
 -55 -50 -45 -40

tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag 271
 Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
 -35 -30 -25

agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata 319
 Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
 -20 -15 -10

tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg 367
 Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg
 -5 1 5

ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata 415
 Gly Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile
 10 15 20 25

ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa 463
 Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu
 30 35 40

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aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac      511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn
      45      50      55
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc      559
Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile
      60      65      70
agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct ttc      607
Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro Phe
      75      80      85
ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg tgg      655
Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp Trp
      90      95      100      105
ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt ggt      703
Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser Gly
      110      115      120
gtg gat gcm rac tct tct tat ttt aaa atc ttt aag aca aaa cat gac      751
Val Asp Ala Xaa Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His Asp
      125      130      135
tgaaaaganc acctgtactt ttcaagccac tggagggaga aatggaaaac atgaaaacag      811
caatctctct atgtctctga ataatacaag actaatttgt gatcttactt ttaatatagat      871
atgactttgc ttccaacatg grtgaaata aaaaaataat aataaaaagat tgccatgrrrt      931
cttgcaaaaa aaaaaa                                     947

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<212> DNA
<213> Homo sapiens

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<222> 46..120
<223> Von Heijne matrix
      score 6.30000019073486
      seq AFSLSVMAALTFG/CF

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<222> 584..589

<221> polyA_site
<222> 606..619

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Met Asn Thr Val
      -25
ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg gcs      105
Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met Ala
      -20      -15      -10
gcg ctc acc ttc ggc tgc ttc atc ayy acc gcc ttc aaa gac agg agc      153
Ala Leu Thr Arg Ser Phe Gly Cys Phe Ile Xaa Thr Ala Phe Lys Asp Arg Ser
      -5      1      5      10
gtc ccg gtg cgg ctg cac gtc tcg cga atc atg cta aaa aat gta gaa      201
Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val Glu
      15      20      25
gat ttc act gga cct aga gaa aga agt gat ctg gga ttt atc aca ttt      249
Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly Phe Ile Thr Phe
      30      35      40
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag      297

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09973360.101501

Asp	Ile	Thr	Ala	Asp	Leu	Glu	Asn	Ile	Phe	Asp	Trp	Asn	Val	Lys	Gln		
45						50				55							
ttg	ttt	ctt	tat	tta	tca	gca	gaa	tat	tca	aca	aaa	aat	aat	gct	ctg	345	
Leu	Phe	Leu	Tyr	Leu	Ser	Ala	Glu	Tyr	Ser	Thr	Lys	Asn	Asn	Ala	Leu		
60					65				70				75				
aac	caa	ktt	gtc	cta	tg	gac	aag	att	gtt	ttg	aga	ggg	gat	aat	ccg	393	
Asn	Gln	Xaa	Val	Leu	Trp	Asp	Lys	Ile	Val	Leu	Arg	Gly	Asp	Asn	Pro		
			80						85				90				
aag	ctg	ctg	ctg	aaa	gat	atg	aaa	aca	aaa	tat	ttt	ttc	ttt	gac	gat	441	
Lys	Leu	Leu	Leu	Lys	Asp	Met	Lys	Thr	Lys	Tyr	Phe	Phe	Phe	Asp	Asp		
			95					100					105				
gga	aat	ggg	ctc	wag	gga	aac	agg	aat	gtc	act	ttg	acc	ctg	tct	tgg	489	
Gly	Asn	Gly	Leu	Xaa	Gly	Asn	Arg	Asn	Val	Thr	Leu	Thr	Leu	Ser	Trp		
			110				115					120					
aac	gtc	gta	cca	aat	gct	gga	att	cta	cct	ctt	gtg	aca	gga	tca	gga	537	
Asn	Val	Val	Pro	Asn	Ala	Gly	Ile	Leu	Pro	Leu	Val	Thr	Gly	Ser	Gly		
			125				130				135						
cac	gta	tct	gtc	cca	ttt	cca	gat	aca	tat	gaa	ata	acg	aag	agt	tat	585	
His	Val	Ser	Val	Pro	Phe	Pro	Asp	Thr	Tyr	Glu	Ile	Thr	Lys	Ser	Tyr		
140					145					150				155			
taaattattc	tgaatttgaa	acaaaaaaaa	aaaahm													621	

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<211> 699

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 35..568

<220>

<221> sig_peptide

<222> 35..100

<223> Von Heijne matrix

score 10.7

seq LLTLALLGGPTWA/GK

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<222> 667..672

<220>

<221> polyA_site

<222> 685..699

<400> 336

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			Met	His	Arg	Pro	Glu	Ala	Met								
			-20														
ctg	ctg	ctg	ctc	acg	ctt	gcc	ctc	ctg	ggg	ggc	ccc	acc	tgg	gca	ggg	103	
Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly		
-15					-10				-5				1				
aag	atg	tat	ggc	cct	gga	gga	ggc	aag	tat	ttc	agc	acc	act	gaa	gac	151	
Lys	Met	Tyr	Gly	Pro	Gly	Gly	Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp		
			5					10				15					
tac	gac	cat	gaa	atc	aca	ggg	ctg	cgg	gtg	tct	gta	ggg	ctt	ctc	ctg	199	
Tyr	Asp	His	Glu	Ile	Thr	Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu		
			20				25					30					
gtg	aaa	agt	gtc	cag	gtg	aaa	ctt	gga	gac	tcc	tgg	gac	gtg	aaa	ctg	247	
Val	Lys	Ser	Val	Gln	Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu		

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      35              40              45
gga gcc tta ggt ggg aat acc cag gaa gtc acc ctg cag cca ggc gaa      295
Gly Ala Leu Gly Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu
50              55              60              65
tac atc aca aaa gtc ttt gtc gcc ttc caa act ttc ctc cgg ggt atg      343
Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Thr Phe Leu Arg Gly Met
70              75              80
gtc atg tac acc agc aag gac cgc tat ttc tat ttt ggg aag ctt gat      391
Val Met Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp
85              90              95
ggc cag atc tcc tct gcc tac ccc agc caa gag ggg cag gtg ctg gtg      439
Gly Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
100             105             110
ggc atc tat ggc cag tat caa ctc ctt ggc atc aag agc att ggc ttt      487
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe
115             120             125
gaa tgg aat tat cca cta gag gag ccg acc act gag cca cca gtt aat      535
Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn
130             135             140             145
ctc aca tac tca gca aac tca ccc gtg ggt cgc taggggtggg tatggggcca      588
Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
150             155
tccgagctga ggccatctgg gtgggtggtg ctgatggtac tggagtaact gagtcgggac      648
gtggaatctg aatccaccaa taaataaagg ttctgcaaaa aaaaaaaaaa a      699

<210> 337
<211> 497
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 68..337

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<222> 68..124
<223> Von Heijne matrix
score 10
seq LVLLGVSIPLVSA/QN

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<222> 462..467

<220>
<221> polyA_site
<222> 482..497

<400> 337
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caccacc atg aag ttc tta gca gtc ctg gta ctc ttg gga gtt tcc atc      109
Met Lys Phe Leu Ala Val Leu Val Leu Gly Val Ser Ile
-15              -10
ttt ctg gtc tct gcc cag aat ccg aca aca gct gct cca gct gac acg      157
Phe Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
-5              1              5              10
tat cca gct act ggt cct gct gat gat gaa gcc cct gat gct gaa acc      205
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr
15              20              25
act gct gct gca acc act gcg acc act gct gct cct acc act gca acc      253

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Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr
    30          35          40
acc gct gct tct acc act gct cgt aaa gac att cca gtt tta ccc aaa    301
Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys
    45          50          55
tgg gtt ggg gat ctc ccg aat ggt aga gtg tgt ccc tgagatggaa    347
Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
    60          65          70
tcagcttgag tcttctgcaa ttggtcacaa ctattcatgc ttctgtgat ttcatccaac    407
tacttacott gctacgata tcccttttat ctctaatacag tttattttct tccaataaa    467
aaataactat gagcaaaaaa aaaaaaaaaa    497

<210> 338
<211> 598
<212> DNA
<213> Homo sapiens

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<222> 39..413

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<222> 39..83
<223> Von Heijne matrix
      score 4.6
      seq LLTHNLLSSHVRG/VG

<220>
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<222> 566..571

<220>
<221> polyA_site
<222> 583..598

<400> 338
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                        Met Lys Leu Leu Thr His
                        -15                      -10
aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg tcc cgt ggc ttc ccc    104
Asn Leu Leu Ser Ser His Val Arg Gly Val Gly Ser Arg Gly Phe Pro
                        -5                      1                      5
ctg cgc ctc cag gcc acc gag gtc cgt atc tgc cct gtg gaa ttc aac    152
Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys Pro Val Glu Phe Asn
    10          15          20
ccc aac ttc gtg gcg cgt atg ata cct aaa gtg gag tgg tcg gcg ttc    200
Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val Glu Trp Ser Ala Phe
    25          30          35
ctg gag gcg gcc gat aac ttg cgt ctg atc cag gtg ccg aaa ggg ccg    248
Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile Gln Val Pro Lys Gly Pro
    40          45          50          55
gtt gag gga tat gag gag aat gag gag ttt ctg agg acc atg cac cac    296
Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe Leu Arg Thr Met His His
    60          65          70          75
ctg ctg ctg gag gtg gaa gtg ata gag ggc acc ctg cag tgc ccg gaa    344
Leu Leu Leu Glu Val Glu Val Ile Glu Gly Thr Leu Gln Cys Pro Glu
    75          80          85          90
tct gga cgt atg ttc ccc atc agc cgc ggg atc ccc aac atg ctg ctg    392
Ser Gly Arg Met Phe Pro Ile Ser Arg Gly Ile Pro Asn Met Leu Leu
    90          95          100

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agt gaa gag gaa act gag agt tgattgtgcc aggcgccagt tttttctgtt 443
 Ser Glu Glu Glu Thr Glu Ser
 105 110
 atgactgtgt atttttgttg atctataccc tgtttccgaa ttctgccgtg tgtatcccca 503
 acccttgacc caatgacacc aaacacagtg tttttgagct cggtattata tatttttttc 563
 tcattaaagg tttaaaacca aaaaaaaaaa aaaaa 598

<210> 339
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 <212> DNA
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<220>
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 <222> 235..642

<220>
 <221> sig_peptide
 <222> 235..336
 <223> Von Heijne matrix
 score 8.7
 seq HLLALLVFSVLLA/LR

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 <222> 1540..1545

<220>
 <221> polyA_site
 <222> 1564..1579

<400> 339
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 tcggggcccg gggattgccg gcgcacacagg gccgagggct ggggctggcg gggccgctcg 120
 ctgcctctcg ctgcgcacag cggcggcagg cgccggcgag ggccacgggg agaggagacg 180
 cagccccgcg ggtggcacgc tcggccgggc cccggcccg cgtcacagg cgcg atg 237
 Met
 ctc ttc tcg ctc cgg gag ctg gtg cag tgg cta ggc ttc gcc acc ttc 285
 Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr Phe
 -30 -25 -20
 gag atc ttc gtg cac ctg ctg gcc ctg ttg gtg ttc tct gtg ctg ctg 333
 Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu
 -15 -10 -5
 gca ctg cgt gtg gat ggc ctg gtc ccg ggc ctc tcc tgg tgg aac gtg 381
 Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn Val
 1 5 10 15
 ttc gtg cct ttc ttc gcc gct gac ggg ctc agc acc tac ttc acc acc 429
 Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr
 20 25 30
 atc gtg tcc gtg cgc ctc ttc cag gat gga gag aag cgg ctg gcg gtg 477
 Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val
 35 40 45
 ctc cgc ctt ttc tgg gta ctt acg gtc ctg agt ctc aag ttc gtc ttc 525
 Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val Phe
 50 55 60
 gag atg ctg ttg tgc cag aag ctg gcg gag cag act cgg gag ctc tgg 573
 Glu Met Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu Trp
 65 70 75
 ttc ggc ctc att acg tcc ccg ctc ttc att ctc ctg cag ctg ctc atg 621
 Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu Met
 80 85 90 95

09978360.101501

atc cgc gcc tgt cgg gtc aac tagcctcacc gaggtgccgg agagggagcg 672
 Ile Arg Ala Cys Arg Val Asn
 100
 ctggacaact agaattgtga cctcgagcgg agggccctact tgcagcgcac cggaggagag 732
 gctctctagt ctgaaggcac cgccggcgtg cgccgagctg agtgccgggt ttccctattc 792
 caatcctggt tgaatgggt tcttcagcag ggcttaaaag agcagccctc atccctgaaaa 852
 tgtatttcct ttgttttaat gctttgagta gataatcctg aattgaggtc atgaggaggc 912
 cccccaggcg agacagtcct gaaccctctc gacacttgga aactgaatat aagtaaaatg 972
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 caaagctgga ctcaggaatg ttctcccaacc agcagcgcta acctaagagc tccctgtgtg 1092
 gtctatccag accagacttc ggtagatgcc ttgttagat ctatcacatg taaacgagct 1152
 tgtatctcct tccctgtgtg acgagagaga ttggcttttt attccagttc aggcagagac 1212
 agaagaatgt tgaataagag cagcattaga gtctgtctg gttatctgtt gcccaagaaa 1272
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 gacttttgac cactttgggc tggcactctt agcacacctg agacagattt aagcctccct 1392
 aagagactga agagaggaac aggtgtcaga tactcatagg cactgagatc tacaaatggg 1452
 aagcttgtag gtggcccatc ttgtttggcc tacgaacttt ggtttgatgc cagtcagggtg 1512
 cccatgaga acccttgctg agatgcaaat aaagtaagag aatgttttcc caaaaaaaaa 1572
 aaaaaaa 1579

<210> 340
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 <221> CDS
 <222> 42..755
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 <222> 42..200
 <223> Von Heijne matrix
 score 5.8
 seq ILSLQVLLTITVTS/TV

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 <221> polyA_signal
 <222> 860..865

<220>
 <221> polyA_site
 <222> 878..893

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 Met Ala Asp Pro Asp
 -50
 ccc cgg tac cct cgc tcc tcg atc gag gac gac ttc aac tat ggc agc 104
 Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp Phe Asn Tyr Gly Ser
 -45 -40 -35
 agc gtc gcc tcc gcc acc gtc cac atc cga atg gcc ttt ctg aga aaa 152
 Ser Val Ala Ser Ala Thr Val His Ile Arg Met Ala Phe Leu Arg Lys
 -30 -25 -20
 gtc tac agc att ctt tct ctg cag gtt ctc tta act aca gtc act tca 200
 Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser
 -15 -10 -5
 aca gtt ttt tta tac ttt gag tct gta cgg aca ttt gta cat gag agt 248
 Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe Val His Glu Ser
 1 5 10 15
 cct gcc tta att ttg ctg ttt gcc ctc gga tct ctg ggt ttg att ttt 296

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Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe
      20      25      30
gcg ttg att tta aac aga cat aag tat ccc ctt aac ctg tac cta ctt      344
Ala Leu Ile Leu Asn Arg His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu
      35      40      45
ttt gga ttt acg ctg ttg gaa gct ctg act gtg gca gtt gtt act      392
Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val Ala Val Val Val Thr
      50      55      60
ttc tat gat gta tat att att ctg caa gct ttc ata ctg act act aca      440
Phe Tyr Asp Val Tyr Ile Ile Leu Gln Ala Phe Ile Leu Thr Thr Thr
      65      70      75      80
gta ttt ttt ggt ttg act gtg tat act cta caa tct aag aag gat ttc      488
Val Phe Phe Gly Leu Thr Val Tyr Thr Leu Gln Ser Lys Lys Asp Phe
      85      90      95
agc aaa ttt gga gca ggg ctg ttt gct ctt ttg tgg ata ttg tgc ctg      536
Ser Lys Phe Gly Ala Gly Leu Phe Ala Leu Leu Trp Ile Leu Cys Leu
      100      105      110
tca gga ttc ttg aag ttt ttt tta tat agt gag ata atg gag ttg gtc      584
Ser Gly Phe Leu Lys Phe Phe Leu Tyr Ser Glu Ile Met Glu Leu Val
      115      120      125
tta gcc gct gca gga gcc ctt ctt ttc tgt gga ttc atc atc tat gac      632
Leu Ala Ala Ala Gly Ala Leu Leu Phe Cys Gly Phe Ile Ile Tyr Asp
      130      135      140
aca cac tca ctg atg cat aaa ctg tca cct gaa gag tac gta tta gct      680
Thr His Ser Leu Met His Lys Leu Ser Pro Glu Glu Tyr Val Leu Ala
      145      150      155      160
gcc atc agc ctc tac ttg gat atc atc aat cta ttc ctg cac ctg tta      728
Ala Ile Ser Leu Tyr Leu Asp Ile Ile Asn Leu Phe Leu His Leu Leu
      165      170      175
cgg ttt ctg gaa gca gtt aat aaa aag taataaaag tatctcagct      775
Arg Phe Leu Glu Ala Val Asn Lys Lys
      180      185
caactgaaga acaacaaaaa aaatttaacg agaaaaaagg attaaagtaa ttggaagcag      835
tatatagaaa ctgtttcatt aagtaataaa gtttgaaacca ataaaaaaa aaaaaaaa      893

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      score 3.9
      seq VAVYCSFISFANS/RS

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Met Ser Thr Asn Asn Met Ser Asp Pro Arg
-70                                     -65
agg ccg aac aaa gtg ctg agg tac aag ccc ccg ccg agc gaa tgt aac      100
Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Glu Cys Asn
-60                                     -55                                     -50
ccg gcc ttg gac gac ccg acg ccg gac tac atg aac'ctg ctg ggc atg      148
Pro Ala Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met
-45                                     -40                                     -35                                     -30
atc ttc agc atg tgc ggc ctc atg ctt aag ctg aag tgg tgt gct tgg      196
Ile Phe Ser Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp
-25                                     -20                                     -15
gtc gct gtc tac tgc tcc ttc atc agc ttt gcc aac tct cgg agc tgc      244
Val Ala Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser
-10                                     -5                                     1
gag gac acg aag caa atg atg agt agc ttc atg ctg tcc atc tct gcc      292
Glu Asp Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala
5                                     10                                     15
gtg gtg atg tcc tat ctg cag aat cct cag ccc atg acg ccc cca tgg      340
Val Val Met Ser Tyr Leu Gln Asn Pro Met Met Thr Pro Pro Trp
20                                     25                                     30                                     35
tgataaccagc ctagaagggt cacattttgg accctgtgcta tccactaggc ctgggctttg      400
gctgctaaac ctgctgccct cagctgccat cctggaacttc cctgaatgag gccgtctcgg      460
tgccccccagc tggatagagg gaacctggccc ctttctctagg gaacacccta ggcttaccct      520
tcctgcctcc cttccctgcg ctgctgctgg gggagatgct gtccatgttt ctagggtat      580
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aaaa

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score 6.2
seq GLFRAAWLPGSRP/SP

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Met Ser Gly Gly Pro Glu Ala Arg Pro Pro Met Leu Val
-80                                     -75
gaa ggc gga gga ccg gag tcc ctg cag aag gcc ccg tgc act cgg ggg      98
Glu Gly Gly Gly Pro Glu Ser Leu Gln Lys Ala Pro Cys Thr Arg Gly
-70                                     -65                                     -60
cct ccg tca cat ccc gtg ccc cct gcg ctg gcc ttc aca gta ggt aat      146
Pro Pro Ser His Pro Val Pro Pro Ala Leu Ala Phe Thr Val Gly Asn
-55                                     -50                                     -45                                     -40
ggc tcc ggc ccg ggt gtt cgc tgt cca cgg aac atg gca gag ggg cac      194
Gly Ser Gly Pro Gly Val Arg Cys Pro Arg Asn Met Ala Glu Gly His
-35                                     -30                                     -25
ccc ggc ccg gaa aga cgc cag agc cag cag ggg ctg ttt cgg gcc gcg      242

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Pro Gly Pro Glu Arg Arg Gln Ser Gln Gln Gly Leu Phe Arg Ala Ala
-20 -15 -10
tgg ctc ccc ggg tct cgg cgg tct ccc ctc ttc tgc gtc tgt tcc gtg 290
Trp Leu Pro Gly Ser Arg Pro Ser Pro Leu Phe Cys Val Cys Ser Val
-5 1 5
act tgc cct ggg tgg gat gta ccg cag gtg cat cgc gtc gag gtg ggg 338
Thr Ser Pro Gly Trp Asp Val Pro Gln Val His Arg Val Glu Val Gly
10 15 20 25
cac ggc cgc cgg caa gaa acc cac cct gtc cgg agg cgg gcg 380
His Gly Arg Arg Gln Glu Thr His Pro Val Arg Arg Arg Ala
30 35
tgagacaagc ccagcccgca cgcgctcctc ttctcttggt ttttgatcag tttattcaga 440
attgctctat aatttaccaa ttgtatgtat ttaacctatt ctgtgggaaa aaaaaggctc 500
ttcattatat ctttatttct gcaaaaaaaaa aaaaaaaaa 538

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<223> Von Heijne matrix
score 4.7
seq DTFLLSFLSTTWL/KT

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Met Pro Arg Gly Arg Arg Leu Gly Met Val Phe Ala Pro Pro
-45 -40
aga ccc gga cag agg caa gca ggg gcg ccg tgg gtg cca gag agg cgg 97
Arg Pro Gly Gln Arg Gln Ala Gly Ala Pro Trp Val Pro Glu Arg Arg
-35 -30 -25 -20
aag agg agg cct gat ggg gat acc ttc ctg ctg tcc ttc ctg agc aca 145
Lys Arg Arg Pro Asp Gly Asp Thr Phe Leu Leu Ser Phe Leu Ser Thr
-15 -10 -5
acc tgg ctg aaa acc tgg agg tca caa cag tac aaa gaa tca aag tca 193
Thr Trp Leu Lys Thr Trp Arg Ser Gln Gln Tyr Lys Glu Ser Lys Ser
1 5 10
aga tct tgt gcc aga gag caa atg aac tct tcc tct tgc tgagaaaaacc 242
Arg Ser Cys Ala Arg Glu Gln Met Asn Ser Ser Ser Cys
15 20 25
caccctgctc acctaaacc ttgccttgcc tggtaattcc atccatgcgc ctggaaggcc 302
ccagacatca aggcctctgag gggccaggca cggggagaaac ccagcagtgc cctgccctgc 362
agctctgagct accagattcc ttgtgaagat aatttgaggga ccatgactca cccaaccaca 422
tttcttgagg cctcaaatg aaaaattcagg atgggctttt ctatatgact ggctgatact 482
caactatgct atggtcttta catgccatga acattctttc ctgccagagt tctaagaatc 542
tgtgtttctc gccttagacc ttctgcagat gagccacacag gaagctccac gtgtagctga 602
gctacatgca ccaggcctca gtttgcctca agtccctctg gtactctctc atggcctgtg 662
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attgcttgaa cttgaaaaaa aaaaaaaaaa 752

096038

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      seq VLFALFVAFLLRG/KL
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<222> 523..537
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<223> Von Heijne matrix
score 5.6
seq ACLSLGPFSLWL/QL

<220>

<221> polyA_site

<222> 1586..1602

<400> 345

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			Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln		
							-45					-40		
ctg	ccc	tgg	gag	gac	ggc	agg	tcc	ggg	ttg	ctc	ggc	ggc	ctc	cct
Leu	Pro	Trp	Glu	Asp	Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu
				-35				-30					-25	101
cgg	aag	tgt	tcc	gtc	ttc	cac	ctg	ttc	gtg	gcc	tgc	ctc	tcg	ctg
Arg	Lys	Cys	Ser	Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu
			-20					-15					-10	149
ttc	ttc	tcc	cta	ctc	tgg	ctg	cag	ctc	agc	tgc	tct	ggg	gac	gtg
Phe	Phe	Ser	Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val
		-5					1			5				197
cgg	gca	gtc	agg	gga	caa	ggg	cag	gag	acc	tcg	ggc	cct	ccc	cgt
Arg	Ala	Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg
	10				15					20				25
tgc	ccc	cca	gag	ccg	ccc	cct	gag	cac	tgg	gaa	gaa	gac	gca	tcc
Cys	Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser
					30				35					40
ggc	ccc	cac	cgc	ctg	gca	gtg	ctg	gtg	ccc	ttc	cgc	gaa	cgc	ttc
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
			45				50					55		341
gag	ctc	ctg	gtc	ttc	gtg	ccc	cac	atg	cgc	cgc	ttc	ctg	agc	agg
Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	Arg
			60				65				70			389
aag	atc	cgg	cac	cac	atc	tac	gtg	ctc	aac	cag	gtg	gac	cac	ttc
Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	His	Phe
	75					80				85				437
ttc	aac	cgg	gca	gcg	ctc	atc	aac	gtg	ggc	ttc	ctg	gag	agc	agc
Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu	Glu	Ser	Ser
	90				95					100				105
agc	acg	gac	tac	att	gcc	atg	cac	gac	gtt	gac	ctg	ctc	cct	ctc
Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	Leu	Leu	Pro	Leu
			110					115					120	533
gag	gag	ctg	gac	tat	ggc	ttt	cct	gag	gct	ggg	ccc	ttc	cac	gtg
Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	Gly	Pro	Phe	His	Val
			125					130				135		581
tcc	cgg	gag	ctc	cac	cct	ctc	tac	cac	tac	aag	acc	tat	gtc	ggc
Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	Tyr	Lys	Thr	Tyr	Val	Gly
			140				145					150		629
atc	ctg	ctg	ctc	tcc	aag	cag	cac	tac	cgg	ctg	tgc	aat	ggg	atg
Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	Tyr	Arg	Leu	Cys	Asn	Gly	Met
	155				160					165				677
aac	cgc	ttc	tgg	ggc	tgg	ggc	cgc	gag	gac	gac	gag	ttc	tac	cgg
Asn	Arg	Phe	Trp	Gly	Trp	Gly	Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg
	170				175				180				185	725
att	aag	gga	gct	ggg	ctc	cag	ctt	ttc	cgc	ccc	tcg	gga	atc	aca
Ile	Lys	Gly	Ala	Gly	Leu	Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr
			190					195				200		773
ggg	tac	aag	aca	ttt	cgc	cac	ctg	cat	gac	cca	gcc	tgg	cgg	aag
Gly	Tyr	Lys	Thr	Phe	Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys
			205				210					215		821
gac	cag	aag	cgc	atc	gca	gct	caa	aaa	cag	gag	cag	ttc	aag	gtg
														869

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Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp
 220 225 230
 agg gag gga ggc ctg aac act gtg aag tac cat gtg gct tcc cgc act 917
 Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr
 235 240 245
 gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc ctc aac atc atg ttg 965
 Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu
 250 255 260 265
 gac tgt gac aag acc gcc aca ccc tgg tgc aca ttc agc tgagctggat 1014
 Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
 270 275
 ggacagtggag gaagcctgta cctacaggcc atattgtctca ggctcaggac aaggcctcag 1074
 gtcgtgggcc cagctctgac aggatgtgga gtggccaggga ccaagacagc aagctacgca 1134
 attgcagcca cccggccgcc aaggcaggct tgggctgggc caggacacgt ggggtgcctg 1194
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 tggggagggc tgaacaggac aacctctcat caccctcact ttgttctctt cctgtggggc 1374
 tgcctcgtgc agagacacag tgtaggggcc atgcagctgg cgtagggtggc agttgggcct 1434
 ggtgagggtt aggaattcag aaaccagagc acaagcccca cagaggggga acagccagca 1494
 ccgctctagc tggttgttgc catgccggaa tgtgggccta gtgttgccag atcttctgat 1554
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 seq LLKVVVFVFASLC/AW

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 <222> 933..948

 <400> 346
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 ggggagcggc acctggaag atg cgc cca ttg gct ggt ggc ctg ctc aag gtg 112
 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val
 -20 -15 -10
 gtg ttc gtg gtc ttc gcc tcc ttg tgt gcc tgg tat tgg ggg tac ctg 160
 Val Phe Val Val Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu
 -5 1 5
 ctc gca gag ctc att cca gat gca ccc ctg tcc agt gct gcc tat agc 208
 Leu Ala Glu Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser
 10 15 20
 atc cgc agc atc ggg gag agg cct gtc ctc aaa gct cca gtc ccc aaa 256
 Ile Arg Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys
 25 30 35
 agg caa aaa tgt gac cac tgg act ccc tgc cca tct gac acc tat gcc 304

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Arg Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
40          45          50          55
tac agg tta ctc agc gga ggt ggc aga agc aag tac gcc aaa atc tgc    352
Tyr Arg Leu Leu Ser Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys
        60          65          70
ttt gag gat aac cta ctt atg gga gaa cag ctg gga aat gtt gcc aga    400
Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg
        75          80          85
gga ata aac att gcc att gtc aac tat gta act ggg aat gtg aca gca    448
Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala
        90          95          100
aca cga tgt ttt gat atg tat gaa ggc gat aac tct gga ccg atg aca    496
Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr
       105       110       115
aag ttt att cag agt gct gct cca aaa tcc ctg ctg ttc atg gtg acc    544
Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr
       120       125       130       135
tat gac gac gga agc aca aga ctg aat aac gat gcc aag aat gcc ata    592
Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile
       140       145       150
gaa gca ctt gga agt aaa gaa atc agg aac atg aaa ttc agg tct agc    640
Glu Ala Leu Gly Ser Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser
       155       160       165
tgg gta ttt att gca gca aaa ggc ttg gaa ctc cct tcc gaa att cag    688
Trp Val Phe Ile Ala Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln
       170       175       180
aga gaa aag atc aac cac tct gat gct aag aac aac aga tat tct ggc    736
Arg Glu Lys Ile Asn His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly
       185       190       195
tgg cct gca gag atc cag ata gaa ggc tgc ata ccc aaa gaa cga agc    784
Trp Pro Ala Glu Ile Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
       200       205       210       215
tgacactgca gggctctgag taaatgtggt ctgtataaac aaatgcagct ggaatcgctc    844
aagaatctta tttttctaaa tccaacagcc catatttgat gagtatatttg ggtttggtgt    904
aaaccaatga acatttgcta gttgtaccaa aaaaaaaaaa aaaa    948

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      seq VLFSSASSFPSISG/NI

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<222> 673..687

<400> 347
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acaaga atg cgg gtt tat aaa agg aca cag ttg agg caa gag acc gga    108
      Met Arg Val Tyr Lys Arg Thr Gln Leu Arg Gln Glu Thr Gly
      -30          -25          -20

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ccc aaa agt tat gtg ctc ttt agt gcc tca agt ttt cca agc atc tct      156
Pro Lys Ser Tyr Val Leu Phe Ser Ala Ser Ser Phe Pro Ser Ile Ser
      -15                      -10                      -5
ggt aac ata agg agt aga aat tat ttt caa aaa caa aat aat cac tgg      204
Gly Asn Ile Arg Ser Arg Asn Tyr Phe Gln Lys Gln Asn Asn His Trp
      1           5           10           15
ttc cag acc agt gat tat taaccctttt tgaattatga accccttttaa      252
Phe Gln Thr Ser Asp Tyr
      20
aacctaataa aatttaagga cctctctccc caaaatatac atataaaaaa acaaggcagt      312
ctatggacct actgagtaac tctcaagata gtaagtaagg agagaaaagt ctatgtttcc      372
ctctttgata agtatgaaat atttggagga gatgctaatt ttgacaggtt tatgatattt      432
gcaatctttc attttttagt cagattatac tcaaaaattt gatccagAAC ttggccccccta      492
ttcttttatt agcactttaa cttgtaaaat gaaaagttta ccatcatctg tatgacatcc      552
taatgagggt aaaaagataa aatgcagtta tgattatgat aggtataact gtatccaggt      612
ttccacagca aaaaacaaac aaaacataca ccatgttctg gggttattga cagcctcctc      672
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                        -45
gat gga tac atc acc tta aat att aaa act cgg aaa cca gct ctc gtc      105
Asp Gly Tyr Ile Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val
      -40                      -35                      -30
tcc gtt ggc cct gca tcc tcc ttc tgg tgg cgt gtg atg gct ttg att      153
Ser Val Gly Pro Ala Ser Ser Phe Trp Trp Arg Val Met Ala Leu Ile
      -25                      -20                      -15
ctg ctg atc ctg tgc gtg ggg atg gtt gtc ggg ctg gtg gct ctg ggg      201
Leu Leu Ile Leu Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly
      -10                      -5           1           5
att tgg tct gtc atg cag cgc aat tac cta caa gat gag aat gaa aat      249
Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp Glu Asn Glu Asn
      10           15           20
cgc aca gga act ctg caa caa tta gca aag cgc ttc tgt caa tat gtg      297
Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val
      25           30           35

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<222> 81..152
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      score 6.2
      seq AILGSTWVALTTG/AL
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ttccttctct cgcatgtgacc atg acg aaa tta gcg cag tgg ctt tgg gga cta      113
                               Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu
                               -20                               -15

gcg atc ctg ggc tcc acc tgg gtg gcc ctg acc acg gga gcc ttg ggc      161
Ala Ile Leu Gly Ser Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly
-10                               -5                               1

ctg gag ctg ccc ttg tcc tgc cag gaa gtc ctg tgg cca ctg ccc gcc      209
Leu Glu Leu Pro Leu Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala
5                               10                               15

tac ttg ctg gtg tcc gcc ggc tgc tat gcc ctg ggc act gtg ggc tat      257
Tyr Leu Leu Val Ser Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr
20                               25                               30                               35

cgt gtg gcc act ttt cat gac tgc gag gac gcc gca cgc gag ctg cag      305
Arg Val Ala Thr Phe His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln
40                               45                               50

agc cag ata cag gag gcc cga gcc gac tta gcc cgc agg ggg ctg cgc      353
Ser Gln Ile Gln Glu Ala Arg Ala Asp Leu Ala Arg Arg Gly Leu Arg
55                               60                               65

ttc tgacagccta accccattcc tgtgcggaca gcccttcttc ccatttccca      406
Phe

ttaaagagcc agtttttttt ctaaaaaaaaa aaaaaaaaaa      445

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<212> DNA
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<221> sig_peptide
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<223> Von Heijne matrix
score 5.9
seq SCDCFVSVPPASA/IP

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                               Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Cys Asp
                               -20                               -15

tgc ttt gtc tcc gtg ccc ccg gcc tca gcc atc ccg gct gtg atc ttt      158
Cys Phe Val Ser Val Pro Pro Ala Ser Ala Ile Pro Ala Val Ile Phe
-10                               -5                               1                               5

gcc aag aac tgc gac cga ccc cgg gac gag gtg cag gag gtg gtg ttt      206
Ala Lys Asn Ser Asp Arg Pro Arg Asp Glu Val Gln Glu Val Val Phe
10                               15                               20

gtc ccc gca gcc act cac act cct ggg agc cgg ctc cag tgc acc tac      254
Val Pro Ala Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr
25                               30                               35

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0007360.101501

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Ile	Glu	Val	Glu	Gln	Val	Ser	Lys	Thr	His	Ala	Val	Ile	Leu	Ser	Arg	
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cct	tct	tgg	cta	tgg	ggg	gct	gag	atg	ggc	gcc	aac	gag	cat	ggg	gtc	350
Pro	Ser	Trp	Leu	Trp	Gly	Ala	Glu	Met	Gly	Ala	Asn	Glu	His	Gly	Val	
55					60					65				70		
tgc	att	ggc	aac	gag	gct	gtg	tgg	acg	aag	gag	cca	gtt	ggg	gag	ggg	398
Cys	Ile	Gly	Asn	Glu	Ala	Val	Trp	Thr	Lys	Glu	Pro	Val	Gly	Glu	Gly	
75									80					85		
gaa	gcc	ctg	ctg	ggc	atg	gac	cta	ctc	agg	ctg	gct	ttg	gaa	cgg	agc	446
Glu	Ala	Leu	Leu	Gly	Met	Asp	Leu	Leu	Arg	Leu	Ala	Leu	Glu	Arg	Ser	
90							95						100			
agc	tct	gcc	cag	gag	gcc	ttg	cat	gtg	atc	aca	ggg	tta	ctg	gag	cac	494
Ser	Ser	Ala	Gln	Glu	Ala	Leu	His	Val	Ile	Thr	Gly	Leu	Leu	Glu	His	
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tat	ggg	cag	ggg	ggc	aac	tgc	ctg	gag	gat	gct	gcg	cca	ttc	tcc	tac	542
Tyr	Gly	Gln	Gly	Gly	Asn	Cys	Leu	Glu	Asp	Ala	Ala	Pro	Phe	Ser	Tyr	
120							125				130					
cat	agc	acc	ttc	ctg	ctg	gct	gac	cgc	act	gag	gcg	tgg	gtg	ctg	gag	590
His	Ser	Thr	Phe	Leu	Leu	Ala	Asp	Arg	Thr	Glu	Ala	Trp	Val	Leu	Glu	
135						140				145					150	
aca	gct	ggg	agg	ctc	tgg	gct	gca	cag	agg	atc	cag	gag	ggg	gcc	cgc	638
Thr	Ala	Gly	Arg	Leu	Trp	Ala	Ala	Gln	Arg	Ile	Gln	Glu	Gly	Ala	Arg	
155							160							165		
aac	atc	tcc	aac	cag	ctg	agc	att	ggc	acg	gac	atc	tcg	gcc	caa	cac	686
Asn	Ile	Ser	Asn	Gln	Leu	Ser	Ile	Gly	Thr	Asp	Ile	Ser	Ala	Gln	His	
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ccg	gag	ctg	cgg	act	cat	gcc	cag	gcc	aag	ggc	tgg	tgg	gat	ggg	cag	734
Pro	Glu	Leu	Arg	Thr	His	Ala	Gln	Ala	Lys	Gly	Trp	Trp	Asp	Gly	Gln	
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Gly	Ala	Phe	Asp	Phe	Ala	Gln	Ile	Phe	Ser	Leu	Thr	Gln	Gln	Pro	Val	
200						205					210					
cgc	atg	gag	gct	gcc	aag	gcc	cgc	ttc	cag	gca	ggg	cgg	gag	ctg	ctg	830
Arg	Met	Glu	Ala	Ala	Lys	Ala	Arg	Phe	Gln	Ala	Gly	Arg	Glu	Leu	Leu	
215					220					225					230	
cgg	caa	cgg	caa	ggg	ggc	atc	acg	gca	gag	gtg	atg	atg	ggc	atc	ctc	878
Arg	Gln	Arg	Gln	Gly	Gly	Ile	Thr	Ala	Glu	Val	Met	Met	Gly	Ile	Leu	
235							240							245		
aga	gac	aag	gag	agt	ggg	atc	tgt	atg	gac	tcg	gga	ggc	ttt	cgc	acc	926
Arg	Asp	Lys	Glu	Ser	Gly	Ile	Cys	Met	Asp	Ser	Gly	Gly	Phe	Arg	Thr	
250							255						260			
acg	gcc	agc	atg	gtg	tct	gtc	ctg	ccc	cag	gat	ccc	acg	cag	ccc	tgc	974
Thr	Ala	Ser	Met	Val	Ser	Val	Leu	Pro	Gln	Asp	Pro	Thr	Gln	Pro	Cys	
265							270						275			
gtg	cac	ttt	ctt	acc	gcc	acg	cca	gac	cca	tcc	agg	tct	gtg	ttc	aaa	1022
Val	His	Phe	Leu	Thr	Ala	Thr	Pro	Asp	Pro	Ser	Arg	Ser	Val	Phe	Lys	
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Pro	Phe	Ile	Phe	Gly	Val	Gly	Val	Ala	Gln	Ala	Pro	Gln	Val	Leu	Ser	
295						300				305					310	
ccc	act	ttt	gga	gca	caa	gac	cct	ggt	cgg	acc	ctg	ccc	cga	ttc	cag	1118
Pro	Thr	Phe	Gly	Ala	Gln	Asp	Pro	Val	Arg	Thr	Leu	Pro	Arg	Phe	Gln	
315							320							325		
act	cag	gta	gat	cggt	cggt	cat	acc	ctc	tac	cggt	gga	cac	cag	gca	gcc	1166
Thr	Gln	Val	Asp	Arg	Arg	His	Thr	Leu	Tyr	Arg	Gly	His	Gln	Ala	Ala	
330							335							340		
ctg	ggg	ctg	atg	gag	aga	gat	cag	gat	cggt	ggg	cag	cag	ctc	cag	cag	1214
Leu	Gly	Leu	Met	Glu	Arg	Asp	Gln	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Gln	
345							350						355			
aaa	cag	cag	gat	ctg	gag	cag	gaa	ggc	ctc	gag	gcc	aca	cag	ggg	ctg	1262

Lys Gln Gln Asp Leu Glu Gln Glu Gly Leu Glu Ala Thr Gln Gly Leu
 360 365 370
 ctg gcc ggc gag tgg gcc cca ccc ctc tgg gag ctg gcc agc ctc ttc 1310
 Leu Ala Gly Glu Trp Ala Pro Pro Leu Trp Glu Leu Gly Ser Leu Phe
 375 380 385 390
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 Gln Ala Phe Val Lys Arg Glu Ser Gln Ala Tyr Ala
 395 400
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 gtagggcagg tttagcattgc tacaggcctc ttaccgggcc tacagctctt aggcacatct 180
 gtccatttga cta atg gcc att ttc tgg ata gtc cat gct cac ttc tgg 229
 Met Ala Ile Phe Trp Ile Val His Ala His Phe Trp
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 Ser Pro Leu Pro Pro Arg Leu Pro His Gly Arg Cys Cys Cys Leu Lys
 -50 -45 -40 -35
 gcc cct ctt cct cct gac gtg gga ccc ctt cag gta gcc cgg cat ctt 325
 Ala Pro Leu Pro Pro Asp Val Gly Pro Leu Gln Val Ala Pro His Leu
 -30 -25 -20
 ttc agc gtg ccc ctt cac att ctg act gtt cct ctt ctg gaa cct gca 373
 Phe Ser Val Pro Leu His Ile Leu Thr Val Pro Leu Leu Glu Pro Ala
 -15 -10 -5
 aga tgc tct ggg atc ctt gta ttt ttc ctg cac cag ccc gtt tca tcc 421
 Arg Cys Ser Gly Ile Leu Val Phe Phe Leu His Gln Pro Val Ser Ser
 1 5 10
 ctg agc ttc tgt tat ttt att gga gga tgg tgc tagaaacaca ggtctggatg 474
 Leu Ser Phe Cys Tyr Phe Ile Gly Gly Trp Cys
 15 20 25
 caggcaggag acacacgcgt ccacactagc atgcgtgtgt acacacatct acatgtgctt 534
 atcccccgcg ttcatgttaa aaaccatggg atcataccgg tgtttcagat tccatccac 594
 cccagcaggg tttctcgccc ccattgctta taaccttagc aggtgtttgag aacctggcgg 654
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aaaaaa						1560

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<223> Von Heijne matrix

score 3.7

seq LASSFLFTMGGLG/PI

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<220>

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<222> 1051..1066

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ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg aag ctg						104
Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu Lys Leu						
	-95		-90		-85	
aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg tat gct						152
Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val Tyr Ala						
	-80		-75		-70	
ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att tat gat						200
Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile Tyr Asp						
	-65		-60		-55	-50
gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa cat ggg						248
Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu His Gly						
	-45		-40		-35	
cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga caa tat						296
His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly Gln Tyr						
	-30		-25		-20	
att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga ggt tta						344
Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly Gly Leu						
	-15		-10		-5	
ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca aaa ctc						392
Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro Lys Leu						

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aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta ttg agt				440
Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu Leu Ser				
20	25	30		
ttt ttc atg gct aga gta ttc atg aga atg aaa ctg cgg ggc tat ctg				488
Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly Tyr Leu				
35	40	45		
atg ggt tagagtgcct ttgagaagaa atcagtggtat actggatttg ctcctgtcaa				544
Met Gly				
tgaagtttta aaggctgtac caatcctcta atatgaaatg tggaaaagaa tgaagagcag				604
cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga ctgaatttc				664
ttcttgggat taaagagaca agtttatcac agaatttttt ttctgtctgg cctattgcta				724
taccaatgat gttgagtgcc attttctttt tagtttttca ttaaaatata ttccatatct				784
acaactataa tatcaataaa agtgattatt ttttacaacc ctcttaacat tttttggaga				844
tgacatttct gattttcaga aattaacata aaatccagaa gcaagattcc gtaagctgag				904
aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag agtgtgtgat				964
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 score 4.5
 seq SFTVSMaIGLVLG/GF

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Met Ala	
-35	
aat aac aca aca agt tta ggg agt cca tgg cca gaa aac ttt tgg gag	164
Asn Asn Thr Thr Ser Leu Gly Ser Pro Trp Pro Glu Asn Phe Trp Glu	
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gac ctt atc atg tcc ttc act gta tcc atg gca atc ggg ctg gta ctt	212
Asp Leu Ile Met Ser Phe Thr Val Ser Met Ala Ile Gly Leu Val Leu	
-15	
gga gga ttt att tgg gct gtg ttc att tgt ctg tct cga aga aga aga	260
Gly Gly Phe Ile Trp Ala Val Phe Ile Cys Leu Ser Arg Arg Arg Arg	
1	
5	
10	
15	
gcc agt gct ccc atc tca cag tgg agt tca agc agg aga tct agg tct	308
Ala Ser Ala Pro Ile Ser Gln Trp Ser Ser Arg Arg Ser Arg Ser	
20	
25	
30	
tct tac acc cac ggc ctc aac aga act gga ttt tac cgc cac agt ggc	356

Ser Tyr Thr His Gly Leu Asn Arg Thr Gly Phe Tyr Arg His Ser Gly	
35 40 45	
tgt gaa cgt cga agc aac ctc agc ctg gcc agt ctc acc ttc cag cga	404
Cys Glu Arg Arg Ser Asn Leu Ser Leu Ala Ser Leu Thr Phe Gln Arg	
50 55 60	
caa gct tcc ctg gaa caa gca aat tcc ttt cca aga aaa tca agt ttc	452
Gln Ala Ser Leu Glu Gln Ala Asn Ser Phe Pro Arg Lys Ser Ser Phe	
65 70 75	
aga gct tct act ttc cat ccc ttt ctg caa tgt cca cca ctt cct gtg	500
Arg Ala Ser Thr Phe His Pro Phe Leu Gln Cys Pro Pro Leu Pro Val	
80 85 90 95	
gaa act gag agt cag ctg gtg act ctc cct tct tcc aat atc tct ccc	548
Glu Thr Glu Ser Gln Leu Val Thr Leu Pro Ser Ser Asn Ile Ser Pro	
100 105 110	
acc atc agc act tcc cac agt ctg agc cgt cct gac tac tgg tcc agt	596
Thr Ile Ser Thr Ser His Ser Leu Ser Arg Pro Asp Tyr Trp Ser Ser	
115 120 125	
aac agt ctt cga gtg ggc ctt tca aca ccg ccc cca cct gcc tat gag	644
Asn Ser Leu Arg Val Gly Leu Ser Thr Pro Pro Pro Pro Ala Tyr Glu	
130 135 140	
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Ser Ile Ile Lys Ala Phe Pro Asp Ser	
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ttc tgg ttc aca gtc atc acc ctc agc ttt ggc tac tac aca tgg gtt	97
Phe Trp Phe Thr Val Ile Thr Leu Ser Phe Gly Tyr Tyr Thr Trp Val	

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gtc ttc tgg cct cag agt atc cct tat cag aac ctt ggg ccc ctg ggc				145
Val Phe Trp Pro Gln Ser Ile Pro Tyr Gln Asn Leu Gly Pro Leu Gly				
10	15	20		
ccc ttc act cag tac ttg gtg gac cac cat cac acc ctg ctg tgc aat				193
Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys Asn				
25	30	35		
ggg tat tgg ctt gcc tgg ctg att cat gtg gga gag tcc ttg tat gcc				241
Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr Ala				
40	45	50		
ata gta ttg tgc aag cat aaa ggc atc aca agt ggt cgg gct cag cta				289
Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln Leu				
55	60	65		
ctc tgg ttc cta cag act ttc ttc ttt ggg ata gcg tct ctc acc atc				337
Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Thr Ile				
70	75	80	85	
ttg att gct tac aaa cgg aag cgc caa aaa caa act tgaagttgtc				383
Leu Ile Ala Tyr Lys Arg Lys Arg Gln Lys Gln Thr				
90	95			
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gtgcagtaat ttactcagtg atctttctac ttcttagaaa ctgtccctca aagctcttta				503
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 <222> 14..319
 <223> Von Heijne matrix

score 4.9
seq VPFFGVSIILVLG/ST

<220>

<221> polyA_signal

<222> 555..560

<220>

<221> polyA_site

<222> 576..591

<400> 355

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agcaccatct gtc atg gcg gct ggg ctg ttt ggt ttg agc gct cgc cgt      49
      Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg
      -100                                -95
ctt ttg gcg gca gcg gcg acg cga ggg ctg ccg gcc gcc cgc gtc cgc      97
Leu Leu Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg
-90                                -85                                -80                                -75
tgg gaa tct agc ttc tcc agg act gtg gtc gcc ccg tcc gct gtg gcg      145
Trp Glu Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala
      -70                                -65                                -60
gga aag cgg ccc cca gaa ccg acc aca ccg tgg caa gag gac cca gaa      193
Gly Lys Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu
      -55                                -50                                -45
ccc gag gac gaa aac ttg tat gag aag aac cca gac tcc cat ggt tat      241
Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr
      -40                                -35                                -30
gac aag gac ccc gtt ttg gac gtc tgg aac atg cga ctt gtc ttc ttc      289
Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe
      -25                                -20                                -15
ttt ggc gtc tcc atc atc ctg gtc ctt ggc agc acc ttt gtg gcc tat      337
Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr
      -10                                -5                                1                                5
ctg cct gac tac agg atg aaa gag tgg tcc cgc cgc gaa gct gag agg      385
Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg
      10                                15                                20
ctt gtg aaa tac cga gag gcc aat ggc ctt ccc atc atg gaa tcc aac      433
Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn
      25                                30                                35
tgc ttc gac ccc agc aag atc cag ctg cca gag gat gag tgaccagtgg      482
Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
      40                                45                                50
ctaagtgggg ctcaagaagc accgccttcc ccaccacctg cctgccattc tgacctcttc      542
tcagagcacc taattaaagg ggctgaaagt ctgaaaaaaa aaaaaaaaaa      591

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<210> 356

<211> 544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..217

<220>

<221> polyA_signal

<222> 489..494

<220>

<221> polyA_site

<222> 529..544

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<400> 356
t cta cct gtg agt act agg atc atc aat cat atc tac agc ttc ccc tca      49
  Leu Pro Val Ser Thr Arg Ile Ile Asn His Ile Tyr Ser Phe Pro Ser
    1           5           10           15
gtt gat tta tgg ata gtt tgt att ttc act gta tct gtc tca cac ctt      97
Val Asp Leu Trp Ile Val Cys Ile Phe Thr Val Ser Val Ser His Leu
    20           25           30
ttt gaa aag gga aca ttg tat ggc tac ttt tat gtg att aac tcc tcc      145
Phe Glu Lys Gly Thr Leu Tyr Gly Tyr Phe Tyr Val Ile Asn Ser Ser
    35           40           45
atc aat tta tgt gtc aat gat tgc ctt cct gta atg gat tca att tct      193
Ile Asn Leu Cys Val Asn Asp Cys Leu Pro Val Met Asp Ser Ile Ser
    50           55           60
ctg tct cca ttg ttt ctt tct cac tagagaagtt ctttaaaatt ctatgaaaa      247
Leu Ser Pro Leu Phe Leu Ser His
    65           70
gaaactgtgc taaattaaaa atctactcat gataacagga gacactcaaa attatgggtt      307
tcagtttcag gcttctcacc atgtcctcag attgtactcc ctttctagcc cttctgcagc      367
aaataaaacct ttgccatcag ttaccacaaa gacactcatga gaggaataat ggcatatcac      427
taaataataga gttctttgtc acttcttgat ttcaaattta caactaatat tcaacatttt      487
aattaaatct ttcttttctc ttcttcctaa aacatacatg caaaaaaaaa aaaaaaa      544

<210> 357
<211> 1689
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..575

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<222> 51..110
<223> Von Heijne matrix
      score 11.2
      seq AFLLLVALSYTLA/RD

<220>
<221> polyA_signal
<222> 1653..1658

<220>
<221> polyA_site
<222> 1674..1689

<400> 357
agaagcttgg accgcacacct agccgccgac tcacacaagg cagagttgcc atg gag      56
                                Met Glu
                                -20
aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac act      104
Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr Thr
    -15           -10           -5
ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca aag      152
Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr Lys
    1           5           10
gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt gac      200
Asp Ser Arg Pro Lys Leu Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp
    15           20           25           30
caa ctc atc tgg act cag aca tat gaa gaa gct cta tat aaa tcc aag      248

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Gln	Leu	Ile	Trp	Thr	Gln	Thr	Tyr	Glu	Glu	Ala	Leu	Tyr	Lys	Ser	Lys	
				35				40						45		
aca	agc	aac	aaa	ccc	ttg	atg	att	att	cat	cac	ttg	gat	gag	tgc	cca	296
Thr	Ser	Asn	Lys	Pro	Leu	Met	Ile	Ile	His	His	Leu	Asp	Glu	Cys	Pro	
			50					55					60			
cac	agt	caa	gct	tta	aag	aaa	gtg	ttt	gct	gaa	aat	aaa	gaa	atc	cag	344
His	Ser	Gln	Ala	Leu	Lys	Lys	Val	Phe	Ala	Glu	Asn	Lys	Glu	Ile	Gln	
			65				70					75				
aaa	ttg	gca	gag	cag	ttt	gtc	ctc	ctc	aat	ctg	gtt	tat	gaa	aca	act	392
Lys	Leu	Ala	Glu	Gln	Phe	Val	Leu	Leu	Asn	Leu	Val	Tyr	Glu	Thr	Thr	
			80				85				90					
gac	aaa	cac	ctt	tct	cct	gat	ggc	cag	tat	gtc	ccc	agg	att	atg	ttt	440
Asp	Lys	His	Leu	Ser	Pro	Asp	Gly	Gln	Tyr	Val	Pro	Arg	Ile	Met	Phe	
			95		100					105				110		
gtt	gac	cca	tct	ctg	aca	gtt	aga	gcc	gat	atc	act	gga	aga	tat	tca	488
Val	Asp	Pro	Ser	Leu	Thr	Val	Arg	Ala	Asp	Ile	Thr	Gly	Arg	Tyr	Ser	
			115					120					125			
aat	cgt	ctc	tat	gct	tac	gaa	cct	gca	gat	aca	gct	ctg	ttg	ctt	gac	536
Asn	Arg	Leu	Tyr	Ala	Tyr	Glu	Pro	Ala	Asp	Thr	Ala	Leu	Leu	Leu	Asp	
			130				135					140				
aac	atg	aag	aaa	gct	ctc	aag	ttg	ctg	aag	act	gaa	ttg	taaa	gaaaaa		585
Asn	Met	Lys	Lys	Ala	Leu	Lys	Leu	Leu	Lys	Thr	Glu	Leu				
			145				150				155					
aaatctccaa	gccctctctgt	ctgtcaggcc	ttgagacttg	aaaccagaag	aagtgtgaga											645
agactggcta	gtgtggaagc	atagtgaaca	caactgattag	gttatgtgtt	aatgttacaa											705
caactatattt	ttaagaaaaa	caagtttttag	aaatttggtt	tcaagtgtac	atgtgtgaaa											765
acaatattgt	atactaccat	agttagccat	gattttctaa	aaaaaaaaa	aatgttttgg											825
gggtgttctg	ttttctccaa	cttggctctt	cacagtgggt	cgtttaccaa	ataggattaa											885
acacacacaa	aatgtccaag	gaagggacaa	gacaaaacca	aaactagttc	aaatgatgaa											945
gaccaaaagac	caagttatca	tctcaccaca	ccacagggtt	tcactagatg	actgtaagta											1005
gacacagagct	taactcaacag	aagtatcaag	ccatgtgctt	tagcataaaa	gaatatttag											1065
aaaaaacatcc	caagaaaaatc	acatcactac	ctagagtcac	ctctggccag	gaactctaag											1125
gtacacactc	tcatcttagta	attaaaatttt	agtcagattt	tgcccaacct	aatgctctca											1185
gggaaagcct	ctggcgaagta	gctttctcct	tcagagggtc	aatttagtag	aaaggctatc											1245
caaagaacat	ctgcaactct	gaacacaccc	tgaagaaatc	ctgggaattg	accttgaat											1305
cgatttgtct	gtcaagggtcc	taaagtactg	gagtgaataa	aattcagcca	acatgtgact											1365
aattggaaga	agagcaaagg	gtgggtgacgt	gttgatgagg	cagatggaga	tcagaggtta											1425
ctaggggttta	ggaaacgtga	aaggctgtgg	catcagggta	ggggagcatt	ctgcctaaca											1485
gaaattagaa	ttgtgtgtta	atgtcttcac	tctatactta	atctcacatt	cattaatata											1545
tggaaattcct	ctactgcccc	gcccctactg	atttctttgg	ccctcggaact	atggtgtgtg											1605
atataatgct	ttgcagtatc	gtttgcttgt	cttgattaac	ttttttggat	aaaacctttt											1665
ttgaacagaa	aaaaaaaaaa	aaaa														1689

<210> 358
 <211> 1111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..977

<220>
 <221> sig_peptide
 <222> 69..128
 <223> Von Heijne matrix
 score 5.3
 seq VLLGSGLTILSQP/LM

<220>
 <221> polyA_signal

<222> 1076..1081

<220>

<221> polyA_site

<222> 1096..1111

<400> 358

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gtgccatc atg gcg gac gcg gcc agt cag gtg ctc ctg gcc tcc ggt etc	110
Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu	
-20 -15 -10	
acc atc ctg tcc cag cgc etc atg tac gtg aaa gtg etc atc cag gtg	158
Thr Ile Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val	
-5 1 5 10	
gga tat gag cct ctt cct cca aca ata gga cga aat att ttt ggg cgg	206
Gly Tyr Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg	
15 20 25	
caa gtg tgt cag ctt cct ggt etc ttt agt tat gct cag cac att gcc	254
Gln Val Cys Gln Leu Pro Gly Leu Phe Ser Tyr Ala Gln His Ile Ala	
30 35 40	
agt atc gat ggg agg cgc ggg ttg ttc aca ggc tta act cca aga ctg	302
Ser Ile Asp Gly Arg Arg Gly Leu Phe Thr Gly Leu Thr Pro Arg Leu	
45 50 55	
tgt tcg gga gtc ctt gga act gtg gtc cat ggt aaa gtt tta cag cat	350
Cys Ser Gly Val Leu Gly Thr Val Val His Gly Lys Val Leu Gln His	
60 65 70	
tac cag gag agt gac aag ggt gag gag tta gga cct gga aat gta cag	398
Tyr Gln Gln Ser Asp Lys Gly Glu Glu Leu Gly Pro Gly Asn Val Gln	
75 80 85 90	
aaa gaa gtc tca tct tcc ttt gac cac gtt atc aag gag aca act cga	446
Lys Glu Val Ser Ser Ser Phe Asp His Val Ile Lys Glu Thr Thr Arg	
95 100 105	
gag atg atc gct cgt tct gct gct acc ctc atc aca cat ccc ttc cat	494
Glu Met Ile Ala Arg Ser Ala Ala Thr Leu Ile Thr His Pro Phe His	
110 115 120	
gtg atc act ctg aga tct atg gta cag ttc att ggc aga gaa tcc aag	542
Val Ile Thr Leu Arg Ser Met Val Gln Phe Ile Gly Arg Glu Ser Lys	
125 130 135	
tac tgt gga ctt tgt gat tcc ata ata acc atc tat cgg gaa gag ggc	590
Tyr Cys Gly Leu Cys Asp Ser Ile Ile Thr Ile Tyr Arg Glu Glu Gly	
140 145 150	
att cta gga ttt ttc gcg ggt ctt gtt cct cgc ctt cta ggt gac atc	638
Ile Leu Gly Phe Phe Ala Gly Leu Val Pro Arg Leu Leu Gly Asp Ile	
155 160 165 170	
ctt tct ttg tgg ctg tgt aac tca ctg gcc tac ctc gtc aat acc tat	686
Leu Ser Leu Trp Leu Cys Asn Ser Leu Ala Tyr Leu Val Asn Thr Tyr	
175 180 185	
gca ctg gac agt ggg gtt tct acc atg aat gaa atg aag agt tat tct	734
Ala Leu Asp Ser Gly Val Ser Thr Met Asn Glu Met Lys Ser Tyr Ser	
190 195 200	
caa gct gtc aca gga ttt ttt gcg agt atg ttg acc tat ccc ttt gtg	782
Gln Ala Val Thr Gly Phe Phe Ala Ser Met Leu Thr Tyr Pro Phe Val	
205 210 215	
ctt gtc tcc aat ctt atg gct gtc aac aac tgt ggt ctt gct ggt gga	830
Leu Val Ser Asn Leu Met Ala Val Asn Asn Cys Gly Leu Ala Gly Gln	
220 225 230	
tgc cct cct tac tcc cca ata tat acg tct tgg ata gac tgt tgg tgc	878
Cys Pro Pro Tyr Ser Pro Ile Tyr Thr Ser Trp Ile Asp Cys Trp Cys	
235 240 245 250	
atg cta caa aaa gag ggg aat atg agc cga gga aat agc tta ttt ttc	926
Met Leu Gln Lys Glu Gly Asn Met Ser Arg Gly Asn Ser Leu Phe Phe	

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                255                260                265
cgg aag gtc ccc ttt ggg aag act tat tgt tgt gac ctg aaa atg tta      974
Arg Lys Val Pro Phe Gly Lys Thr Tyr Cys Cys Asp Leu Lys Met Leu
                270                275                280
att tgaagatgtg gggcagggac agtgacatct ctgtagctcc agatgcacag      1027
Ile
aattatggga gagaatgttg atttctatac agtgtggcgc gcttttttaa taatcattta      1087
atcttggtcaa aaaaaaaaaa aaaa      1111

<210> 359
<211> 554
<212> DNA
<213> Homo sapiens

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<222> 44..238

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<222> 44..160
<223> Von Heijne matrix
      score 3.9
      seq FKTIAPLLLYVSA/GP

<220>
<221> polyA_signal
<222> 443..448

<220>
<221> polyA_site
<222> 540..554

<400> 359
atcctcaaca gaataattgc tgacaaaactc tcttgcccag aaa atg tct act gga      55
                                Met Ser Thr Gly
att atg gag tac aaa aaa act aca aaa gca atg aaa aaa aag aag gat      103
Ile Met Glu Tyr Lys Lys Thr Thr Lys Ala Met Lys Lys Lys Lys Asp
-35                -30                -25                -20
gtt tta ttt aca tcc tat ttc aaa acc att gct ttc ttg cta ttg tat      151
Val Leu Phe Thr Ser Tyr Phe Lys Thr Ile Ala Phe Leu Leu Leu Tyr
-15                -10                -5
gtc tct gca ggc cca ata tcg cga atc ttc ata aga agt tta gaa ttg      199
Val Ser Ala Gly Pro Ile Ser Arg Ile Phe Ile Arg Ser Leu Glu Leu
1                5                10
ttc ctt atg ttt cct tct aac aaa cac tgg tat att tca tgaaagtgtgta      248
Phe Leu Met Phe Pro Ser Asn Lys His Trp Tyr Ile Ser
15                20                25
tattttattc acttccaaaa cagtttagctc ataattcaga acattgagggt ttgcaaaaatg      308
actgaaggaa acttttaccta aacaatagtt gccagttctg ctgagaatta tcacgggccc      368
acaacggctg tgtgtttttc catcacagata ttctaatttt tttattatgc agctaatttt      428
tttttagact cgcgaaataa atagcaagtc agtctgtgca taagcatatg tttaaatcta      488
ccaggagaaa tgtctggaat ctttttggtt attaaaatta aaattcagga taaaaaaaaa      548
aaaaaa      554

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<211> 1773
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
<222> 114..524

<220>
<221> sig_peptide
<222> 114..164
<223> Von Heijne matrix
      score 5.2
      seq ATLAVGLTIFVLS/VV

<220>
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<222> 1739..1744

<220>
<221> polyA_site
<222> 1758..1773

<400> 360
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agaggggaaaa gccccagggtt acaggaggcc tctgggtgaa ggccagagcct aac atg    116
                               Met
ggg ttc gga gcg acc ttg gcc gtt ggc ctg acc atc ttt gtg ctg tct    164
Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu Ser
-15                               -10                               -5
gtc gtc act atc atc atc tgc ttc acc tgc tcc tgc tgc ctt tac    212
Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu Tyr
1                               5                               10                               15
aag acg tgc cgc cga cca cgt ccg gtt gtc acc acc acc aca tcc acc    260
Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Ser Thr
20                               25                               30
act gtc gtg cat gcc cct tat cct cag cct cca agt gtg ccg ccc agc    308
Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro Ser
35                               40                               45
tac cct gga cca agc tac cag gcc tac cac acc atg ccg cct cag cca    356
Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln Pro
50                               55                               60
ggg atg cca gca gca ccc tac cca atg cag tac cca cca cct tac cca    404
Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Tyr Pro
65                               70                               75                               80
gcc cag ccc atg gcc cca ccg gcc tac cac gag acc ctg gct gga gga    452
Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly Gly
85                               90                               95
gca gcc gcg ccc tac ccc gcc agc cag cct cct tac aac ccg gcc tac    500
Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala Tyr
100                               105                               110
atg gat gcc ccg aag gcg gcc ctc tgagcattcc ctggcctctc tggtgccac    554
Met Asp Ala Pro Lys Ala Ala Leu
115                               120
ttggttatgt tgtgtgtgtg cgtgagtggt gtgcaggcgc ggttccctac gccccatgtg    614
tgctgtgtgt gtccaggcac gggttccttac gccccatgtg tgctgtgtgt gtccctgcctg    674
tatatgtggc ttccctctgat gctgacaagg tggggaacaa tccttgccag agtgggcttg    734
gaccagactt tgttctcttc ctcacctgaa attatgcttc ctaaaatctc aagccaaact    794
caagaatagg ggtggtgggg ggcaccctgt gaggttgccc ctgagaggtg ggggcctctc    854
cagggcacat ctggagtctt tctccagctt accctagggt gaccaaagtag ggccgtgtac    914
accaggggtg cgcagctttc tgtgtgatgc agatgtgtcc tggtttcggc agcgtagcca    974
gctgtcgtct gaggccatgg ctcgctcccc gagttggggg tacccgttgc agagccaggg    1034
acatgatgca ggcgaagctt gggatctggc caagttggac tttgatcctt tgggcagatg    1094
tccattgct cctctggagcc tgtcatgcct gttgggggac aggcagcctc ctgatgccag    1154
aacacctcag gcagagccct actcagctgt acctgtctgc ctggactgtc cctgtcccc    1214
gcattctccc tgggaccacg tggagggccg catgcacaca cagcctagct gccccaggg    1274

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agctctgctg cccttgcctg ccctgcctct cccacaggtg agcagggtct ctgtccacca 1334
gcacactcag ttctcttccc tgcagtgttt tcattttatt tttagccaaac attttgcctg 1394
ttttctgttt caaacatgat agttgatatg agactgaaac ccttgggttg tggaggga 1454
ttggctcaga gatggacaac ctggcaactg tgagtccctg ctccccgaca ccagcctcat 1514
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ccaatggggc atctggacca aagggtgggtg gtggggccct ggatggcagc tctggcccag 1634
acatgaatac ctctgtgtcc tcctccctct attactgttt caccagagct gtcttagctc 1694
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tgcaaaaaaa aaaaaaaaaa 1773

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<210> 361
<211> 917
<212> DNA
<213> Homo sapiens

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<222> 26..487

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<222> 26..64
<223> Von Heijne matrix
      score 6.4
      seq MALLLSVLRVLG/GF

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<221> polyA_signal
<222> 883..888

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<220>
<221> polyA_site
<222> 901..917

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Met Ala Leu Leu Ser Val Leu Arg
-10 -5
gta ctg ctg ggc ggc ttc ttc gcg ctc gtg ggg ttg gcc aag ctc tgc 100
Val Leu Leu Gly Gly Phe Phe Ala Leu Val Gly Leu Ala Lys Leu Ser
1 5 10
gag gag atc tgc gct cca gtt tgc gag cgg atg aat gcc ctg ttc gtg 148
Glu Glu Ile Ser Ala Pro Val Ser Glu Arg Met Asn Ala Leu Phe Val
15 20 25
cag ttt gct gag gtg ttc ccg ctg aag gta ttt ggc tac cag cca gat 196
Gln Phe Ala Glu Val Phe Pro Leu Lys Val Phe Gly Tyr Gln Pro Asp
30 35 40
ccc ctg aac tac caa ata gct gtg ggc ttt ctg gaa ctg ctg gct ggg 244
Pro Leu Asn Tyr Gln Ile Ala Val Gly Phe Leu Glu Leu Leu Ala Gly
45 50 55 60
ttg ctg ctg gtc atg ggc cca ccg atg ctg caa gag atc agt aac ttg 292
Leu Leu Leu Val Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu
65 70 75
ttc ttg att ctg ctc atg atg ggg gct atc ttc acc ttg gca gct ctg 340
Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Leu
80 85 90
aaa gag tca cta agc acc tgt atc cca gcc att gtc tgc ctg ggg ttc 388
Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe
95 100 105
ctg ctg ctg ctg aat gtc ggc cag ctc tta gcc cag act aag aag gtg 436
Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val

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      110              115              120
gtc aga ccc act agg aag aag act cta agt aca ttc aag gaa tcc tgg      484
Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp
125              130              135              140
aag tagagcatct ctgtctcttt atgccatgca gctgtcacag caggaacatg      537
Lys
gtagaacaca gagtctatca tcttgttacc agtataatat ccagggtcag ccagtgttga      597
aagagacatt ttgtctacct ggcactgctt tctcttttta gctttactac tcttttga      657
ggagtacatg ttatgcataa taacattcct catatcatat gaaaatacaa aataagcaga      717
aaagaaattt aaatcaacca aaattctgat gccccaaata accactttta atgccttggt      777
gtaagtatac ctctgaacct ttttctgtgc ctttaaacag atatatattt tttttaaagt      837
aaaaaaaac catatatcct attttatttc ctctttttaa aacctataaa actataaac      897
tgcaaaaaaa aaaaaaaaaa

```

```

<210> 362
<211> 641
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 80..388

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```

<220>
<221> sig_peptide
<222> 80..187
<223> Von Heijne matrix
      score 3.6
      seq RALSTFLFGSIRG/AA

```

```

<220>
<221> polyA_signal
<222> 609..614

```

```

<220>
<221> polyA_site
<222> 627..641

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```

<400> 362
gccagtgccg agacgcaggg gtcggcgccg ggtgagagcg tgcggccggg taaggcggtg      60
tggccggatt caccacaac atg gca aat ctt ttt ata agg aaa atg gtg aac      112
              Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn
              -35              -30
cct ctg ctc tat ctc agt cgt cac acg gtg aag cct cga gcc ctc tcc      160
Pro Leu Leu Tyr Leu Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser
-25              -20              -15              -10
aca ttt cta ttt gga tcc att cga ggt gca gcc ccc gtg gct gtg gaa      208
Thr Phe Leu Phe Gly Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu
              -5              1              5
ccc ggg gca gca gtg cgc tca ctt ctc tca ccc gcc ctc ctg ccc cat      256
Pro Gly Ala Ala Val Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His
10              15              20
ctg ctg cct gcg ctg ggg ttc aaa aac aag act gtc ctt aat aag cgc      304
Leu Leu Pro Ala Leu Gly Phe Lys Asn Lys Thr Val Leu Asn Lys Arg
25              30              35
tgc aag gac tgt tac ctg gtg aag agg cgg ggt cgg tgg tac gtc tac      352
Cys Lys Asp Cys Tyr Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr
40              45              50              55
tgt aaa acc cat ccg agg cac aag cag aga cag atg tagacccttt      398
Cys Lys Thr His Pro Arg His Lys Gln Arg Gln Met
60              65

```

```

ccctccagac  tcacgcacat  actcgtcatc  gcatcacttg  ggagaatggg  tgtatcttat  458
ggaaggaatt  atcacatcaa  ggagtcaggg  gaaagtgact  ggaagcaaac  gccctaaaaa  518
ttacccatca  cgtttcagtg  taaatgagta  actatagaag  acattgcgtt  atcttatctc  578
caaaacggtc  caactaaaaa  acattttcct  attaaaaatg  accttccgaa  aaaaaaaaaa  638
aaa

```

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<210> 363
<211> 854
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS
<222> 186..443

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```

<220>
<221> sig_peptide
<222> 186..407
<223> Von Heijne matrix
      score 3.9
      seq ISCTCLLLYLTHC/IL

```

```

<220>
<221> polyA_signal
<222> 827..832

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<220>
<221> polyA_site
<222> 839..854

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<400> 363
aaatgttaat  attagaaga  gtctcatagt  gcttatgtga  catcattctt  tgcctaaagg  60
ctttgtacct  actgtaatga  agctaaactc  cttggccacg  gatataaggc  tcacgatctg  120
gacctggactc  attttcactc  ccattcttcag  tcattccccta  actccccac  agtcagtcctc  180
caaag  atg  cca  tat  gct  ttc  act  tct  cca  tgc  cct  tgc  tca  ttt  gtc  tca  230
      Met Pro Tyr Ala Phe Thr Ser Pro Cys Pro Cys Ser Phe Val Ser
                        -70                                -65                                -60
ttg  cct  gaa  ata  tcc  ttt  tat  ttc  acc  aaa  ctg  ctg  ctc  atc  ctc  aag  278
Leu Pro Glu Ile Ser Phe Thr Lys Leu Leu Leu Ile Leu Lys
                        -55                                -50                                -45
gcc  ctg  cct  gag  tca  cct  ttc  ctt  ctt  gct  tcc  tcc  ccc  ttg  cct  cct  326
Ala Leu Pro Glu Ser Pro Phe Leu Leu Ala Ser Ser Pro Leu Pro Pro
                        -40                                -35                                -30
ctc  ccc  act  acc  cta  aga  aaa  ttc  atc  cct  ccc  cct  tca  tta  ata  tca  374
Leu Pro Thr Thr Leu Arg Lys Phe Ile Pro Pro Pro Ser Leu Ile Ser
                        -25                                -20                                -15
tgc  aca  tgc  ttg  tta  tta  tat  tta  aca  cat  tgt  ata  tta  ggt  att  tgt  422
Cys Thr Cys Leu Leu Leu Tyr Leu Thr His Cys Ile Leu Gly Ile Cys
                        -10                                -5                                1                                5
ttt  gct  tat  cct  ttt  atc  cta  tgaaattgtg  aacaatttgt  tgaataattg  473
Phe Ala Tyr Pro Phe Ile Leu
      10
aataatcaca  tatcaaaaat  tagagagggt  atttgtctct  tccctgtagg  actccatttt  533
caggcagtg  ctgctaagaa  tccccttgac  ctgggattgg  aagttgtttc  tcccactgct  593
gagctccttt  atattagctc  ttcacctctc  actcctttgt  ttcttctctt  ggcactttac  653
ctctttctac  ccatttaatt  tgataaatgt  ctcattgcat  ctttaaaact  gaagtgaca  713
catgtctgg  ttactcttat  aactcaaaaa  tgtttagctt  aatgcagaat  ggagaatagc  773
tacttagtaa  atttttaaaa  tacatgctac  catttttaag  gggagaagaa  gacaaatatac  833
atgacaaaaa  aaaaaaaaaa  a

```

```

<210> 364

```

<211> 1568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..1259

<220>
 <221> sig_peptide
 <222> 75..1004
 <223> Von Heijne matrix
 score 4.4
 seq VLILLPSLALIL/PS

<220>
 <221> polyA_signal
 <222> 1536..1541

<220>
 <221> polyA_site
 <222> 1553..1568

<400> 364
 agaaaagggtg tagtgttttg ggcgggtcaac gggctatgct ggcttgacag ggctggggctc 60
 ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac cgg tgg 110
 Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp
 -310 -305 -300
 ctg gag ccc cca gag gat atc ttc tgg aca gga tcc gtc ctg gag ctg 158
 Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu
 -295 -290 -285
 gga ctc cac tgc ccc cct cca gag gtt cgg gta act agg cta cag gaa 206
 Gly Leu His Cys Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu
 -280 -275 -270
 cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt 254
 Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu
 -265 -260 -255
 caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat 302
 Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn
 -250 -245 -240 -235
 gag gtg tac tgc tca gaa gca tct cct gcc agt gac agt gcc atc tct 350
 Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser
 -230 -225 -220
 gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt 398
 Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser
 -215 -210 -205
 tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc ctg gag agg 446
 Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg
 -200 -195 -190
 atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc atc cag cta 494
 Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu
 -185 -180 -175
 gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc atg gtc agt 542
 Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser
 -170 -165 -160 -155
 gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga gca ggc acc 590
 Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr
 -150 -145 -140
 gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa acc ctg ttc 638
 Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe
 -135 -130 -125

ctg acc gat gag gag aag cgt ctg ctg ggg cag gaa ggg gtt tcc ctg	686
Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu	
-120 -115 -110	
ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc ctc aag aag	734
Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys	
-105 -100 -95	
gtc agg agg aaa atc cgt aac aag cag tca gct cag gac agt cgg cgg	782
Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg	
-90 -85 -80 -75	
cgg aag aag gag tac att gat ggg ctg gag agc agg gtg gca gcc tgt	830
Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys	
-70 -65 -60	
tct gca cag aac caa gaa tta cag aaa aaa gtc cag gag ctg gag agg	878
Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg	
-55 -50 -45	
cac aac atc tcc ttg gta gct cag ctc cgc cag ctg cag acg cta att	926
His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile	
-40 -35 -30	
gct caa act tcc aac aaa gct gcc cag acc agc act tgt gtt ttg att	974
Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile	
-25 -20 -15	
ctt ctt ttt tcc ctg gct ctc atc atc ctg ccc agc ttc agt cca ttc	1022
Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe	
-10 -5 1 5	
cag agt cga cca gaa gct ggg tct gag gat tac cag cct cac gga gtg	1070
Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val	
10 15 20	
act tcc aga aat atc ctg acc cac aag gac gta aca gaa aat ctg gag	1118
Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu	
25 30 35	
acc caa gtg gta gag tcc aga ctg agg gag cca cct gga gcc aag gat	1166
Thr Gln Val Val Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp	
40 45 50	
gca aat ggc tca aca agg aca ctg ctt gag aag atg gga ggg aag cca	1214
Ala Asn Gly Ser Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro	
55 60 65 70	
aga ccc agt ggg cgc atc cgg tcc gtg ctg cat gca gat gag atg	1259
Arg Pro Ser Gly Arg Ile Arg Ser Val Leu His Ala Asp Glu Met	
75 80 85	
tgagctggaa cagacccttc tggcccaact cctgatcaca aggaatcctg ggcttcctta	1319
tgagcttcctt cccactggga ttccctactta ggtgtctgcc ctacggggct caaatcactt	1379
caggacacccc caagagatgt cctttagtct ctgcctgagg cctagtctgc atttggttgc	1439
atatatgaga gggtagctca aatacttctg ttatgtatct gtgattttat ttcttctttg	1499
ggatagggt tgaggggaaa taagttttga gtgagaata aacgttttag ctgaaaaaaa	1559
aaaaaaaa	1568

<210> 365

<211> 506

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 98..376

<220>

<221> sig_peptide

<222> 98..151

<223> Von Heijne matrix

score 12.3

seq HILFLLLPVAAA/QT


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<220>
<221> polyA_signal
<222> 471..476

<220>
<221> polyA_site
<222> 491..506

<400> 365
gacatccgct attgctactt ctctgctccc ccacaggtcc tctggacttc tctggaccac 60
agtctctctgc cagacccctg ccagacccca gtccacc atg atc cat ctg ggt cac 115
Met Ile His Leu Gly His
-15
atc ctc ttc ctg ctt ttg ctc cca gtg gct gca gct cag acg act cca 163
Ile Leu Phe Leu Leu Leu Leu Pro Val Ala Ala Ala Gln Thr Thr Pro
-10 -5 1
gga gag aga tca tca ctc cct gcc ttt tac cct gcc act tca ggc tct 211
Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr Pro Gly Thr Ser Gly Ser
5 10 15 20
tgt tcc gga tgt ggg tcc ctc tct ctg ccg ctc ctg gca ggc ctc gtg 259
Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro Leu Leu Ala Gly Leu Val
25 30 35
gct gct gat gcg gtg gca tcg ctg ctc atc gtg ggg gcg gtg ttc ctg 307
Ala Ala Asp Ala Val Ala Ser Leu Leu Ile Val Gly Ala Val Phe Leu
40 45 50
tgc gca cgc cca cgc cgc agc ccc gcc caa gaa tat ggc aaa gtc tac 355
Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln Glu Tyr Gly Lys Val Tyr
55 60 65
atc aac atg cca ggc agg ggc tgacctcct gcagcttgga cctttgactt 406
Ile Asn Met Pro Gly Arg Gly
70 75
ctgacctctc cctcctggat ggtgtgtggt ggcacaggaa ccccgcccc aacttttgga 466
tgttaataaaa acaattgaaa caccaaaaaa aaaaaaaaaa 506

<210> 366
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..254

<220>
<221> sig_peptide
<222> 72..134
<223> Von Heijne matrix
score 4.2
seq LINLAASRTLSFC/IS

<220>
<221> polyA_signal
<222> 506..511

<220>
<221> polyA_site
<222> 528..542

<400> 366
gaccttaaga agagetaaac gggctgccac ctgtagctga agagtgcctt aacgccgagg 60

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cccacggctc c atg cga gag atg cct gtt cct tct ctg ata aat ttg gca      110
      Met Arg Glu Met Pro Val Pro Ser Leu Ile Asn Leu Ala
      -20                      -15                      -10
gct tca cgt acc cta agt ttt tgc att tct tct gac aac cac gtg tcc tca      158
Ala Ser Arg Thr Leu Ser Phe Cys Ile Ser Asp Asn His Val Ser Ser
      -5                      1                      5
cct gga ccc gcc aac cca tcc tgt ggc ctc cac cct cac tgg ctt cgt      206
Pro Gly Pro Ala Asn Pro Ser Cys Gly Leu His Pro His Trp Leu Arg
      10                      15                      20
cca ctt aaa ctt tta acg tac aca tgt aga gag ctg aaa ctc cag ggg      254
Pro Leu Lys Leu Leu Thr Tyr Thr Cys Arg Glu Leu Lys Leu Gln Gly
      25                      30                      35                      40
taacatggga caggtcctct tgatttaatg aaaacagaag atcaactgga cggggtagca      314
agaaataagg ctttaagaagc actggtttct ctgcagaaga cagcaagatg ccccgaggaa      374
tgttttgtgaa aaaggatgac tggatgggaa gcaagctgaa gaaaaagaag gaaagaaaga      434
gagaaatcag taaatcacca cacaagaggt ggagaagagg acttataaat attgtttcta      494
tgacatttga aaataaatgt tttactccat gctaaaaaaa aaaaaaaa      542

<210> 367
<211> 1629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..1140

<220>
<221> sig_peptide
<222> 148..240
<223> Von Heijne matrix
      score 10
      seq LVLLLVTRSPVNA/CL

<220>
<221> polyA_signal
<222> 1590..1595

<220>
<221> polyA_site
<222> 1614..1629

<400> 367
gtctgctgcc gccattgtgc ggcgctgggc cctcagagg gtctcctgctg ctgccgggtgc      60
cttggaccct cccctcgtct tctcgttcta ctgccccagg agccccgcgg gtccgggact      120
cccgctcgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
      Met Trp Leu Trp Glu Asp Gln Gly Gly
      -30                      -25
ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg      222
Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Val Thr
      -20                      -15                      -10
cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta      270
Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu
      -5                      1                      5                      10
ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag      318
Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln
      15                      20                      25
gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc      366
Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly
      30                      35                      40
agc cac gac gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct      414

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Ser His Asp Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala
45 50 55
aag aat gga gca aca ggc gtg gag ttg gac att gag ttt act tct gac 462
Lys Asn Gly Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp
60 65 70
ggg att cct gtc tta atg cac gat aac aca gta gat agg acg act gat 510
Gly Ile Pro Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp
75 80 85 90
ggg act ggg cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg 558
Gly Thr Gly Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu
95 100 105
aat cct gca gca aac cac aga ctc agg aat gat ttc cct gat gaa aag 606
Asn Pro Ala Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys
110 115 120
atc cct acc cta atg gaa gct gtt gca gag tgc cta aac cat aac ctc 654
Ile Pro Thr Leu Met Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu
125 130 135
aca atc ttc ttt gat gtc aaa ggc cat gca cac aag gct act gag gct 702
Thr Ile Phe Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala
140 145 150
cta aag aaa atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg 750
Leu Lys Lys Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val
155 160 165
gtc tgt tct ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat 798
Val Cys Ser Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp
175 180 185
cgg gat gta ata aca gca tta act cac aga cct tgg agc cta agc cat 846
Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His
190 195 200
aca gga gat ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata 894
Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile
205 210 215
ttt gtt atg atg gac att ttg ctc gat tgg agc atg cat aat atc ttg 942
Phe Val Met Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu
220 225 230
tgg tac ctg tgt gga att tca gct ttc ctc atg caa aag gat ttt gta 990
Trp Tyr Leu Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val
235 240 245 250
tcc ccg gcc tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt 1038
Ser Pro Ala Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val
255 260 265
ggg tgg act gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat 1086
Gly Trp Thr Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His
270 275 280
ctt ggt tcc agc tat atc act gac agc atg gta gaa gac tgc gaa cct 1134
Leu Gly Ser Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro
285 290 295
cac ttc tagactttca cgggtgggacg aaacgggttc agaaaactgcc aggggcctca 1190
His Phe
300
tacaggagata tcaaaatacc ctttgtgcta gccagggcc tggggaatca ggtgactcac 1250
acaaatgcaa tagttgggtca ctgcattttt acctgaacca aagctaaaac cgggtgtgcc 1310
accatgcacc atggcatgcc agagttcaac actgttgctc ttgaaaatct ggggtctgaaa 1370
aaacgcacaa gagccccctgc cctgccttag ctgaggcaca caggggagacc cagtgaggat 1430
aagcacagat tgaattgtac aatttgcaga tgcagatgta aatgcatggg acatgcatga 1490
taactcagag ttgacattttt aaaacttgcc acacttattt caaatatttg tactcagcta 1550
tgttaacatg tactgtagac atcaaaacttg tggccatact aataaaaatta ttaaaaaggag 1610
cacaaaaaaa aaaaaaaaaa 1629

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<210> 368

<211> 1665

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 109..738

<220>
<221> sig_peptide
<222> 109..405
<223> Von Heijne matrix
score 4.5
seq LAPGSFLAAVVDA/LE

<220>
<221> polyA_signal
<222> 1633..1638

<220>
<221> polyA_site
<222> 1650..1665

<400> 368
cccagcggttc etctcccgccg cccaggtcac cgcacagcag cgctctgttc cgtctcgcgc 60
gagtcacagc agctcccccag gcccttcacc agcacagcag cagcaggc atg gca gca 117
Met Ala Ala
agc gtg gag cag cgc gag ggc acc atc cag gtg cag ggc cag gcc ctc 165
Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu
-95 -90 -85
ttc ttc cga gag gcc ctg ccc ggc agt ggg cag gct cgc ttc tct gta 213
Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val
-80 -75 -70 -65
ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg 261
Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu
-60 -55 -50
ggt aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att 309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile
-45 -40 -35
gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct 357
Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro
-30 -25 -20
att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc 405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala
-15 -10 -5
ttg gag ctg ggc ccc ccg gtt gtg atc agt cca tca ctg agt ggc atg 453
Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met
1 5 10 15
tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg gcc ttt 501
Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe
20 25 30
gtg cca gtg gcc ccc atc tgc act gac aaa atc aat gct gcc aac tat 549
Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala Ala Asn Tyr
35 40 45
gcc agt gtg aag act cca gct ctg att gta tat gga gac cag gac ccc 597
Ala Ser Val Lys Thr Pro Pro Ala Leu Ile Val Tyr Gly Asp Gln Asp Pro
50 55 60
atg ggt cag acc agc ttt gag cac ctg aag cag ctg ccc aac cac cgg 645
Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro Asn His Arg
65 70 75 80
gtg ctg atc atg aag ggg gcg ggg cac ccc tgt tac ctg gac aaa cca 693
Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu Asp Lys Pro

099738ED-101501

	85	90	95	
gag gag tgg cat aca ggg ctg ctg gac ttc ctg cag ggg ctc cag				738
Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly Leu Gln				
	100	105	110	
tgaagccag cactgctgca ggggggtggc tgectgctg ctctgagctc tetettgcac				798
gctctctctt ctctcccagg ctctggctca tgcacatgca acaggtgcgt ctgtctatat				858
gtctgggttc ttgtcttttg ttgtctgttt gtcttttcta cctctttctc ttgcagtgat				918
agactgaggg ggtaaaatca agagaaaaaa ctctcaggaa tcaaggaaaca taatcctgtg				978
gagggtaatc cattacatga gcttctcctg ttcttccact ttctgcctg gctttcactc				1038
ctctcccctg tctgcccagg ctttccctcc caccactcc tacttctgca aatgcccttg				1098
aggccagccc ttaccccaac acccacttcc ccactctctt agggcccaga tacatacatg				1158
cccacatgca cgcttacctg tttagagcca tccttgcttc caaatatgca ccttcgcttg				1218
agggcaactg cataggtaca tctaactctg gactggcatg cacattgtca tgtgcagctt				1278
tgcataatac cacatgcata catgagcctc cacacaagca cttgcacaca tgtggactcc				1338
taaccatgct aacctcactg gctgggaagg tggggacccc atggggcagc ccttgaggga				1398
ggcccttttg caaggcttag ggtgtggcca gccctgaaag ctacttggac acagggttca				1458
gctggcccca gccagaagt gaccccaga aaggaggggc caccgctttg cccctgctt				1518
ttacccttcc ttctgggtgc tctacacctc aggttaccag gcctgaggca tctcagccaa				1578
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gtgatgcaat taaaaaaaa aaaaaaa				1665
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	score 4.4			
	seq LISLVASLFMGFG/VL			
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ctgcgcagct gttcttccgg tggcggagcg gcggattagc cttcgcgggg caaa atg				57
			Met	
gag ctc gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc				105
Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val				
-65 -60 -55				
ttc ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc				153
Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr				
-50 -45 -40 -35				
gcc tgg ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat				201
Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp				
-30 -25 -20				
atc tat aaa gag ctc ctc atc tcc tta gtg gcc tca ctc ttc atg gcc				249
Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Ser Leu Phe Met Gly				
-15 -10 -5				
ttt gga gtc ctc ttc ctg ctg ctc tgg gtt ggc atc tac gtg				291

Phe Gly Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val	
1 5 10	
tgagcacccca aggggtaacaa ccagatggcgt tcaactgaaac ctgcttttgt aaattacttt	351
tttttactgt tgctggaaat gtcccacctg ctgctcataa taaatgcaga tgtataacaa	411
aaaaaaaaaaaa aaaa	425
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<222> 508..513	
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<221> polyA_site	
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<400> 370	
gttgaccagg gcgatgcaag acac atg gca gtc tgg cct gaa gtt tcc caa	51
Met Ala Val Trp Pro Glu Val Ser Gln	
1 5	
aac agg ctg act agg gcc cta ctg ctt ccc aac tac cag ctg agg ggg	99
Asn Arg Leu Thr Arg Gly Leu Leu Leu Pro Asn Tyr Gln Leu Arg Gly	
10 15 20 25	
tcc gtc ccg aaa agg gag aag agg cct aag agg aaa cat caa cat ctt	147
Ser Val Pro Lys Arg Glu Lys Arg Pro Lys Arg Lys His Gln His Leu	
30 35 40	
ttt act cct agc gag cgg cat tct gtc tgc ctt gat tgt ctt ctg gaa	195
Phe Thr Pro Ser Glu Arg His Ser Val Cys Leu Asp Cys Leu Leu Glu	
45 50 55	
ata tcg ctt tca ggg aaa caa tgg cga aat gtc atc agt ttc aac tgc	243
Ile Ser Leu Ser Gly Lys Gln Trp Arg Asn Val Ile Ser Phe Asn Cys	
60 65 70	
ttt tgc act act aag acg ctt ttc tgg gtt aat tagcagcaat acagacaacg	296
Phe Cys Thr Thr Lys Thr Leu Phe Trp Val Asn	
75 80	
atctttttatt caacaacctc tctcgagata ttttaaataa ttctctcacac tcgaaaaaca	356
tcgagaagcg actatttgca aaacctgaaga gggtggaata ccaaatggct gaactggaat	416
attttctagt tagcgagggt ttgagagggt cgtaggtct ccagaaattc acctcaaaa	476
cgtacaggat gtaattgccag tggtaggaat cattaaagac accttgagta gattcaaaaa	536
aaaaaaaaaaaa	546
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<221> CDS	
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<222> 32..91	
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score 7.4
seq LVFCVGLLTKA/ES

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<222> 452..457

<220>

<221> polyA_site

<222> 472..485

<400> 371

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ctttcagcag gggacagccc gattggggac a atg gcg tct ctt ggc cac atc      52
                                Met Ala Ser Leu Gly His Ile
                                -20                                -15
ttg gtt ttc tgt gtg ggt ctc ctc acc atg gcc aag gca gaa agt cca      100
Leu Val Phe Cys Val Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro
                                -10                                -5                                1
aag gaa cac gac ccg ttc act tac gac tac cag tcc ctg cag atc gga      148
Lys Glu His Asp Pro Phe Thr Tyr Asp Tyr Gln Ser Leu Gln Ile Gly
                                5                                10                                15
ggc ctc gtc atc gcc ggg atc ctc ttc atc ctg ggc atc ctc atc gtg      196
Gly Leu Val Ile Ala Gly Ile Leu Phe Ile Leu Gly Ile Leu Ile Val
                                20                                25                                30                                35
ctg agc aga aga tgc cgg tgc aag ttc aac cag cag cag agg act ggg      244
Leu Ser Arg Arg Cys Arg Cys Lys Phe Asn Gln Gln Gln Arg Thr Gly
                                40                                45                                50
gaa ccc gat gaa gag gag gga act ttc cgc agc tcc atc cgc cgt ctg      292
Glu Pro Asp Glu Glu Glu Gly Thr Phe Arg Ser Ser Ile Arg Arg Leu
                                55                                60                                65
tcc acc cgc agg cgg tagaaacacc tggagcgatg gaatccggcc aggactcccc      347
Ser Thr Arg Arg Arg
                                70
tggcacctga catctcccac gctccacctg cgcgcccacc gcccccctcg ccgccccttc      407
cccagcccctg cccccgcaga ctccccctgc cgccaagact tccaataaaa cgtgcgttcc      467
tctcaaaaaa aaaagaaa
                                485
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<210> 372

<211> 1394

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 46..675

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<221> sig_peptide

<222> 46..87

<223> Von Heijne matrix

score 5.9

seq LTLGLSLILAGL/IV

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<222> 1363..1368

<220>

<221> polyA_site

<222> 1382..1394

00070350.101501

<400> 372
ctccgagttg ccacccagga aaaagagggc tcctctggga gatgt atg ctt act ctc 57
Met Leu Thr Leu
tta ggc ctt tca ctc atc ttg gca gga ctt att gtt ggt gga gcc tgc 105
Leu Gly Leu Ser Leu Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
-10 -5 1 5
att tac aag cac ttc atg ccc aag agc acc att tac cgt gga gag atg 153
Ile Tyr Lys His Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
10 15 20
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag 201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
25 30 35
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac 249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
40 45 50
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac 297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
55 60 65 70
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg 345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
75 80 85
gac ttg ttg ctg ggg aac tgc tat ctg atg ccc ctc aat act tct att 393
Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
90 95 100
gtt atg cct cca gaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt 441
Val Met Pro Leu Glu Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
105 110 115
ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct 489
Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
120 125 130
gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa 537
Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
135 140 145 150
ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg 585
Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Asp Leu Leu
155 160 165
ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac 633
Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His
170 175 180
ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag 675
Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu
185 190 195
taagaggcaa cagatagagt gtccttggtg acaagaagtc agagatttac aatatgacct 735
taacattaag gtttatggga tactcaagat atttactcat gcatttactc tattgcttat 795
gccttataaaa aaggaaaaaa aaaaactact aaccactgca agctctgtgc aaattttgat 855
ttaattggca ttgcttggtt tttgaaactg aaattacctg agtttcaatt tttcttggaa 915
tttatagggt tttagattctt gaaagcagca tgaatataac acctaaccatc ctgacaataa 975
attccatccg ttgttttttt tggttggttt tttttctctt tcctttaagt aagctcttta 1035
ttcatcttat ggtgcagcaa ttttaaaatt tgaatatatt taaattgttt ttgaactttt 1095
tgtgtaaaat atatcagatc tcaacattgt tggtttcttt tgtttttcat ttgtacaac 1155
tttcttgaat ttagaataat catctttgca gctctgttag gtgctctgta attaacctga 1215
cttatatgtg aacaattttc atgagacagt catttttaaa taatgcaggt attctttctc 1275
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taggttctat gaattctaca accctataat aaatttttact ctatacaaaa aaaaaaaaa 1394

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<213> Homo sapiens

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<222> 329..943

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<222> 329..745
<223> Von Heijne matrix
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      seq SLSLALKTGPTSG/LC

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<221> polyA_site
<222> 1322..1333

<400> 373
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cgctgggtgag gaaccctgga ctctcagcat cacaagaggg aacaccagga gccaacatga      120
gctcgggacct gaactgctgt ggcgccggagc agcgtgctgt gtgctgtgtg gggtggcgagc      180
cagtcgtgtgt gtgcgctgct cagccccagg tgcaagaggg tcagagagaa tctaccagca      240
gagaagtctgt cgtgaggacc aacagagctt tacgggggtcc cggacctact ccttggctgg      300
gcaggcatgg ccaggacccc tggcggagc atg gca ccc aca agg aag gac aag      352
                                Met Ala Pro Thr Arg Lys Asp Lys
                                -135
ctg ttg caa ttc tac ccc agc ctg gag gat cca gca tct tcc agg tac      400
Leu Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr
-130 -125 -120
cag aac ttc agc aaa gga agc aga cac ggg tgg gag gaa gcc tac ata      448
Gln Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile
-115 -110 -105 -100
gac ccc att gcc atg gag gat tat tac aac tgg ggg cgg ttc tgg aag ccc      496
Asp Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro
-95 -90 -85
cca gaa ggt gag gcg aag gac aaa gcc gga ggt gga gga agt ggt gtg      544
Pro Glu Gly Glu Ala Lys Asp Lys Ala Gly Gly Gly Ser Gly Val
-80 -75 -70
gga gct cag gcc aga agc cat acc tcc agg cag gag agg agg ctg gcc      592
Gly Ala Gln Gly Arg Ser His Thr Ser Arg Gln Glu Arg Arg Leu Gly
-65 -60 -55
ctg ggt tgg gat gat gat gcc aat tcc tac gag aat gtg ctg att tgc      640
Leu Gly Ser Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys
-50 -45 -40
aag cag aaa acc aca gag aca ggt gcc cag cag gag gac gta ggt gcc      688
Lys Gln Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Asp Val Gly Gly
-35 -30 -25 -20
ctc tgc aga ggg gac ctc agc ctg tca ctg gcc ctg aag act ggc ccc      736
Leu Cys Arg Cys Gly Asp Leu Ser Leu Ala Leu Lys Thr Gly Pro
-15 -10 -5
act tct ggt ctc tgt ccc tct gcc tcc ccg gaa gaa gat ggg gaa tct      784
Thr Ser Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Gly Glu Ser
1 5 10
gag gat tat cag aac tca gca tcc atc cat caa tgg cgc gag tcc agg      832
Glu Asp Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg
15 20 25
aag gtc att ggg caa ctc cag aga gaa gca tcc cct ggc ccg gtg gga      880
Lys Val Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly
30 35 40 45
agc cca gac gag gag gac ggg gaa ccg gat tac gtg aat ggg gag gtg      928
Ser Pro Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val
50 55 60
gca gcc aca gaa gcc tagggcagac caagaagaaa ggagccaagg caaagagggg      983
Ala Ala Thr Glu Ala

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65
 ccactgtgct catggaccaca tcgctgcect ccaaggacca ttccagag ctactcaact 1043
 ttttaagcccc tgccatgggt gctcctggaa ggagaaccag ccaccctgag gaccacctgg 1103
 ccactgcgtgc acagcctggg aaaagacagt tactcacggg agctgcaggc ccgtcaccac 1163
 gccctctccc gaccacggct ttgtggggca ggcacctggt accatgggta acccggtccc 1223
 tggatatggac ggatgcgcag gatttaggat aagctgtcac ccagtcacca taacaaaacc 1283
 actgtccaac actggtatct gtgttctttt gtgctatgaa aaaaaaaaaa 1333

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 <211> 326
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 27..281

<220>
 <221> sig_peptide
 <222> 27..77
 <223> Von Heijne matrix
 score 8.2
 seq LLLITAILAVAG/FP

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 Met Lys Lys Val Leu Leu Ile Thr
 -15 -10
 gcc atc ttg gca gtg gct gtt ggt ttc cca gtc tct caa gac cag gaa 101
 Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln Glu
 -5 1 5
 cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggg ttt 149
 Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe
 10 15 20
 ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att cca 197
 Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro
 25 30 35 40
 ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata cct 245
 Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro
 45 50 55
 gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaagaa 291
 Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
 60 65
 ggaaaagtca cgataaacct ggtcacctga aattg 326

<210> 375
 <211> 703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..405
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 <221> sig_peptide
 <222> 61..213
 <223> Von Heijne matrix
 score 8.1
 seq VCLCGTFCFPCLG/CQ

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<221> polyA_signal
<222> 675..680

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<222> 692..703

<400> 375
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atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc ggt 108
Met Gln Ala Gln Ala Pro Val Val Val Thr Gln Pro Gly Val Gly
-50 -45 -40
ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt gac 156
Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
-35 -30 -25 -20
tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc ccg 204
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
-15 -10 -5
tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg tgt 252
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
1 5 10
gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc atc 300
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
15 20 25
cct gga cct att tgt gat gac tat atg gca act ctt tgc tgt cct cat 348
Pro Gly Pro Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
30 35 40 45
tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc atg 396
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
50 55 60
cgt act ttc taaaaactga tggtagaaaag ctcttaccga agcaacaaaa 445
Arg Thr Phe
ttcagcagac acctctccag cttgagttct tcaccatctt ttgcaactga aatatgatgg 505
atatgcttaa gtacaactga tggcatgaaa aaaatcaaat ttttgattta ttataaatga 565
atgttgtccc tgaacttagc taaatggtgc aacttagttt ctccctgtct tcataattac 625
gaattttcctg gcttataaac tttttaaat acatttgaaa tataaaccaa atgaaatatt 685
ttactcaaaa aaaaaaaaa 703

<210> 376
<211> 768
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..379

<220>
<221> sig_peptide
<222> 137..229
<223> Von Heijne matrix
score 4.4
seq TCCHLGLPHPVRA/PR

<220>
<221> polyA_signal
<222> 728..733

<220>
<221> polyA_site

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<222> 755..768

<400> 376

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aatgagattg aacttcagct ggattgaaa agaggctaga agttccgctt gccagcagcc      120
cccttagtag agcgga atg agt aat acc cac acg gtg ctt gtc tca ctt ccc      172
                Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro
                -30                -25                -20

cat ccg cac ccg gcc ctc acc tgc tgt cac ctc gcc ctc cca cac ccg      220
His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro
                -15                -10                -5

gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct agg      268
Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg
                1                5                10

tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc cta      316
Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu
                15                20                25

aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg gct      364
Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala
                30                35                40                45

gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta ttttatcctt      419
Asp Arg Cys Asp Leu
                50

gacttggtac aagttttggg atttctgaaa agaccatgca gataaccaca aatatcaaga      479
aagtcgtctt cagtatttaag tagaatttag atttaggttt ccttctgtct tcccacctcc      539
ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg agctgtattt      599
caagtaatat agttataaat taacaatgta gcagttattg atagagaaat tgagaaaact      659
gaaacgtgac cggagtattg gaaataacgt agtacctcac ctagcacaat gacacatagt      719
aggtgctcaa taaatttatg cttataattt ttgtcaaaaa aaaaaataa      768
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<210> 377

<211> 1007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..741

<220>

<221> sig_peptide

<222> 37..153

<223> Von Heijne matrix

score 7.2

seq SALAKLLLTCCSA/LR

<220>

<221> polyA_signal

<222> 969..974

<220>

<221> polyA_site

<222> 994..1007

<400> 377

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cgcaggctccc gaggagcgca gactgtgtcc ctgaca atg gga aca gcc gac agt      54
                Met Gly Thr Ala Asp Ser
                -35

gat gag atg gcc ccg gag gcc cca cag cac acc cac atc gat gtg cac      102
Asp Glu Met Ala Pro Glu Ala Pro Gln His Thr His Ile Asp Val His
                -30                -25                -20
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09978360.101501

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atc cac cag gag tct gcc ctg gcc aag ctc ctg ctc acc tgc tgc tct      150
Ile His Gln Glu Ser Ala Leu Ala Lys Leu Leu Leu Thr Cys Cys Ser
-15                               -10                               -5
gcg ctg cgg ccc cgg gcc acc cag gcc agg ggc agc agc cgg ctg ctg      198
Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg Gly Ser Ser Arg Leu Leu
1                               5                               10                               15
gtg gcc tgc tgg gtg atg cag atc gtg ctg ggg atc ttg agt gca gtc      246
Val Ala Ser Trp Val Met Gln Ile Val Leu Gly Ile Leu Ser Ala Val
20                               25                               30
cta gga gga ttt ttc tac atc cgc gac tac acc ctc ctc gtc acc tgc      294
Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr Thr Leu Leu Val Thr Ser
35                               40                               45
ggg gct gcc atc tgg aca ggg gct gtg gct gtg ctg gct gga gct gct      342
Gly Ala Ala Ile Trp Thr Gly Ala Val Ala Val Leu Ala Gly Ala Ala
50                               55                               60
gcc ttc att tac gag aaa cgg ggt ggt aca tac tgg gcc ctg ctg agg      390
Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr Trp Trp Ala Leu Leu Arg
65                               70                               75
act ctg cta gcg ctg gca gct ttc tcc aca gcc atc gct gcc ctc aaa      438
Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr Ala Ile Ala Ala Leu Lys
80                               85                               90                               95
ctt tgg aat gaa gat ttc cga tat ggc tac tct tat tac aac agt gcc      486
Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr Ser Tyr Tyr Asn Ser Ala
100                              105                              110
tgc cgc atc tcc agc tcg agt gac tgg aac act cca gcc ccc act cag      534
Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn Thr Pro Ala Pro Thr Gln
115                              120                              125
agt cca gaa gaa gtc aga agg cta cac cta tgt acc tcc ttc atg gac      582
Ser Pro Glu Glu Val Arg Arg Leu His Leu Cys Thr Ser Phe Met Asp
130                              135                              140
atg ctg aag gcc ttg ttc aga acc ctt cag gcc atg ctc ttg ggt gtc      630
Met Leu Lys Ala Leu Phe Arg Thr Leu Gln Ala Met Leu Leu Gly Val
145                              150                              155
tgg att ctg ctg ctt ctg gca tct ctg gcc cct ctg tgg ctg tac tgc      678
Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala Pro Leu Trp Leu Tyr Cys
160                              165                              170                              175
tgg aga atg ttc cca acc aaa ggg aaa aga gac cag aag gaa atg ttg      726
Trp Arg Met Phe Pro Thr Lys Gly Lys Arg Asp Gln Lys Glu Met Leu
180                              185                              190
gaa gtg agt gga atc tagccatgcc tctcctgatt attagtgcct ggtgcttctg      781
Glu Val Ser Gly Ile
195
caccgggcgt cccctgcattct gactgctgga agaagaacca gactgaggaa aagaggctct      841
tcaacagccc cagttatcctt ggccccatga ccgtggccac agccctgctc cagcagcact      901
tgccatttcc ttacaccctc tccccatcct gctccgcttc atgtcccttc ctgagtagtc      961
atgtgataat aaactctcat gttattgttc ccaaaaaaaa aaaaaa      1007

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<210> 378

<211> 527

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 80..265

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<221> sig_peptide

<222> 80..142

<223> Von Heijne matrix
score 5.4

seq TFCLIFGLGAVWG/LG

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<222> 517..527

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gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt      112
                               Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
                               -20                               -15

ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc      160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser
-10                               -5                               1                               5

cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc      208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr
                               10                               15                               20

gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc      256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu
                               25                               30                               35

ttt caa gcg tgactgaagc agcagcctgc acatgtggat ggtcatcagt      305
Phe Gln Ala
40

gcctcgccca gagatacctg gccttcaccc aaagggaacc tgctgccaca agtccctcag      365
gcagcaccgc cactgtggct ccttcgcact gactatgttg gactctgccca tagactgacc      425
ctcttgctcg gctgctgcag ttgtctgta atgcctgac atgttgcatc ctccccattt      485
ggataaataa aaacaaacaa atgcttctgt caaaaaaaaa aa                        527

<210> 379
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<212> DNA
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<220>
<221> CDS
<222> 612..644

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<222> 829..834

<220>
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<222> 850..861

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tgctggcccta tcatggggca tgccatgggg ctggctcctt cctaccggt tcactgcttg      180
accttcgcct cctcagcacc tccaagcccc cagcctacga ggaatgtggt caccgcccag      240
gcacaccacc ccccccttat actgtggccc caggccgccc ctgtactgt tccagtgaac      300
aaacctgctg ttctctctca tccagctgcc ctgcccaact tgaagggaaca aatgtggaag      360
gtgtttcttc ccaccagagt gccccccttc atcaggaggg tgagcccggg gcaggggtga      420
ccccctgctc cacaccccc tctgcgcgt atgcgcgttt aactggcgac tccggtattg      480
agctctgccc ttgtcctgcc tccggtgagg gtgagccagt caaggagggt aggggttagtg      540
ccaccctgcc agatctggag gactactccc cgtgtgcact acccccagag tctgtaccgc      600
agatcttttc c atg ggg ctg tct tcc agt gaa ggg gac atc cca      644

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	Met	Gly	Leu	Ser	Ser	Ser	Glu	Gly	Asp	Ile	Pro	
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taagtagttt	tgagagggtg	gatgggttac	ttgcccacca	gaaacagccc	tagtccaac							704
tccctgcggt	cctttggccc	ctccctgcct	acctagaatc	tgccctgaagg	ggctggagag							764
ggacagtatt	gggggactgt	gctagcttta	ccccgcgagg	acatacacag	gagcctttga							824
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atg gag aga	ggc ctg aaa	tca gca gac	cct cgg gat	ggc acc ggt tac									108
Met Glu Arg	Gly Leu Lys	Ser Ala Asp	Pro Arg Asp	Gly Thr Gly Tyr									
act ggc tgg	gca ggt att	gct gtg ctt	tac tta cat	ctt tat gat	gta								156
Thr Gly Trp	Ala Gly Ile	Ala Val Leu	Tyr Leu His	Leu Tyr Asp	Val								
ttt ggg gac	cct gcc tct	atg ttc tgt	aaa gta ttt	gac tta cta	gtt								204
Phe Gly Asp	Pro Ala Ser	Met Phe Cys	Lys Val Phe	Asp Leu Leu	Val								
ctc aat aaa	att tta tta	gga cta taaaaaaa	a										239
Leu Asn Lys	Ile Leu Leu	Gly Leu											
15		20											

<210> 381
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 <212> DNA
 <213> Homo sapiens

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 <222> 15..311

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 <222> 15..110
 <223> Von Heijne matrix
 score 3.5
 seq RIHLQQRXSGSQG/VR

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 <222> 507..512

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<220>
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<222> 531..542

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aag ctg ggc ctg cgt gag att cgc atc cac tta tgt cag cgc tcg scc      98
Lys Leu Gly Leu Arg Glu Ile Arg Ile His Leu Cys Gln Arg Ser Xaa
-20                               -10                               -5
ggc agc cag ggc gtc agg gac ttc att gag aaa cgc tac gtg gag ctg      146
Gly Ser Gln Gly Val Arg Asp Phe Ile Glu Lys Arg Tyr Val Glu Leu
          1                               5                               10
aag aag gcg aat ccc gac cta ccc atc cta atc cgc gaa tgc tcc gat      194
Lys Lys Ala Asn Pro Asp Leu Pro Ile Leu Ile Arg Glu Cys Ser Asp
          15                               20                               25
gtg cag ccc aag ctc tgg gcc cgc tac gca ttt ggc caa rag acg aat      242
Val Gln Pro Lys Leu Trp Ala Arg Tyr Ala Phe Gly Gln Xaa Thr Asn
          30                               35                               40
gtc cct ttg aac aac ttc agt gct gat cag gta acc aga rcc ctg gag      290
Val Pro Leu Asn Asn Phe Ser Ala Asp Gln Val Thr Arg Xaa Leu Glu
          45                               50                               55                               60
aac gtt cta agt ggt aaa gcc tgaagcctcc actgaggatt aagagcaaca      341
Asn Val Leu Ser Gly Lys Ala
          65

gccccagagc ctgggctctg ctggacttar tataatgtga aaaaaatgtg ttctcctatt      401
cotcataaag cttgtgctgt aaaatacttt ctcaggggtgt tcttgtcctc atctaccctc      461
taccoccttac tgtgcaacca ctgaggcaaa gttagcttaat ataaaaataa aactttatct      521
tgtctcatca aaaaaaaaaa a                                         542

<210> 382
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<213> Homo sapiens

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<222> 50..529

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<222> 50..130
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      seq VLWLSGLSEPGAA/RQ

<220>
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<222> 877..882

<220>
<221> polyA_site
<222> 899..909

<400> 382
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          -25
gtg tcc ggg ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc      106

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Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser	
gag -20 gga gct gcc cgg cag ccc cgg atc atg gaa gag	154
Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu	
aaa gcg cta gag gtt tat gat ttg att aga act atc cgg gac cca gaa	202
Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu	
aag ccc aat act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg	250
Lys Pro Asn Thr Leu Glu Leu Glu Val Val Ser Glu Ser Cys Val	
gaa gtt cag gag ata aat gaa gaa raa tat ctg gtt att atc agg ttc	298
Glu Val Gln Glu Ile Asn Glu Glu Xaa Tyr Leu Val Ile Ile Arg Phe	
acg cca aca gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc	346
Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys	
yta arw kta aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gma	394
Leu Xaa Xaa Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Xaa	
atc tac att tct gaa gga acc cac tca raa gar gaa gac atc aat wwk	442
Ile Tyr Ile Ser Glu Gly Thr His Ser Xaa Glu Glu Asp Ile Asn Xaa	
cag ata aat gac aaa gag cgw ktg gca kct gca atg gaa aac ccc awc	490
Gln Ile Asn Asp Lys Glu Arg Xaa Ala Xaa Ala Met Glu Asn Pro Xaa	
tta cgg gaa att gtg gaa cag tgt gtc ctt gaa cct gac tgawakctgt	539
Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp	
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gatttgtaac acttaaatga tcagacagaa taatatatttc tagttattat gtgtaagatg	779
agttgtctatt tttctgatgc tcattctgat acaactattt ttctgtgtcaa atatctactg	839
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<210> 383

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<221> CDS

<222> 240..416

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<221> sig_peptide

<222> 240..305

<223> Von Heijne matrix

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<222> 1117..1122

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<221> polyA_site

<222> 1139..1149

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tgaaccagcc acccgaggat ggcatctcct ccgtgaagtt cagccccaac acctccagc 180
tcctgtctgt ctctctctgg gacacgtccg tgcgtctcta cgatgtgcgc gccaaactcc 239
atg cgg ctg aag tac cag cac acc ggc gcc gtc ctg gac tgc gcc ttc 287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
-20 -15 -10
tac gat cca acg cat gcc tgg agt gga gga cta gat cat caa ttg aaa 335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
-5 1 5 10
atg cat gat ttg aac act gat caa gaa aat ctt gtt ggg acc atg atg 383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
15 20 25
ccc cta tca gat gtg ttg aat act gtc cac aaa tgaatgtgat ggctmctgga 436
Pro Leu Ser Asp Val Leu Asn Thr Val His Lys
30 35
akttgggatc aaacagttaa actgtgggat ccamaactc cttgtaatgc tgggaccttc 496
tctcmkctcg aaaaggtata taccctctca gtgtctggag accggctgat tgtgggaaca 556
gcaggcgcca gagtgttgtt gtgggactta cggaacatgg gttactgtca gcagcgacgg 616
gagtcacgcc tgaaatacca gactcgtcgc atacgagcgt ttccaaacaa gcagggttat 676
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caagtgcacg atgcagaaac aaaccccaag tcaccatgta cttgacaaga ttctatttc 1096
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<212> DNA
<213> Homo sapiens

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<222> 111..446

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<223> Von Heijne matrix
score 4.90000009536743
seq PSLAAGLLFGSLA/GL

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agaccgtgag aggcctgggg tagtctccag tctggacaga gaagagaaaa atg cag 116
Met Gln
gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt gcc tac gca 164
Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly Tyr Ala
-45 -40 -35

gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa gca ggb agc 212
 Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala Gly Ser
 -30 -25 -20 -15
 gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta gcc ggc ctg 260
 Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala Gly Leu
 -10 -5 1
 ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg gtt ttc cta 308
 Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val Phe Leu
 5 10 15
 gct aca tct ggt acc ttg gct ggc att atg gga atg agg ttc tac cac 356
 Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe Tyr His
 20 25 30
 tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc akt ttg ctg 404
 Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Xaa Leu Leu
 35 40 45 50
 atg gtc gcc aaa att gga gtt agt atg ttc aac aga ccc cat 446
 Met Val Ala Lys Ile Gly Val Ser Met Phe Asn Arg Pro His
 55 60
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 gc atg gga ggc aat ggc tcc aca tgt aaa ccc gac act gaa aga caa 167
 Met Gly Gly Asn Gly Ser Thr Cys Lys Pro Asp Thr Glu Arg Gln
 -55 -50 -45
 ggc act ctc tcc aca gca gcc cca aca act agc cct gca ccc tgt ctc 215
 Gly Thr Leu Ser Thr Ala Ala Pro Thr Ser Pro Ala Pro Cys Leu
 -40 -35 -30
 tct aac cac cac aac aaa aaa cat tta atc ctt gcc ttt tgt gct ggg 263

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Ser Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys Ala Gly
 -25 -20 -15 -10
 gtt cta ctg aca ctg ctg ctg ata gcc ttt atc ttc ctc atc ata aag 311
 Val Leu Leu Thr Leu Leu Leu Ile Ala Phe Ile Phe Leu Ile Ile Lys
 -5 1 5
 agc tac aga aaa tat cac tcc aag ccc cag gcc cca gat cct cac tca 359
 Ser Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Asp Pro His Ser
 10 15 20
 gat cct cca kcc rrg ctt tca tcc atc cca ggg gaa tca ctt acc tat 407
 Asp Pro Pro Xaa Xaa Leu Ser Ser Ile Pro Gly Glu Ser Leu Thr Tyr
 25 30 35
 gcc agc aca ags ktt caa act ctc aga aka ama gag cam yca ctt ggc 455
 Ala Ser Thr Xaa Xaa Gln Thr Leu Arg Xaa Xaa Glu Xaa Xaa Leu Gly
 40 45 50 55
 tgagaacccat tctgcagact ttgacccccc kgtctatgct caaattaaag taacaaacta 515
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 aaaaatttca aataaagtca aacccccac aaaaaaaaa a 916

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 <222> 2..433

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 <222> 2..232
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 score 4.40000009536743
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 ggg ccc atc gac tac aaa cgg aac ttg ccg cgt cga gga ctg tct ggc 97
 Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
 -60 -55 -50
 tac agc atg ctg gcc ata ggg att gga acc ctg atc tac ggg cac tgg 145
 Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
 -45 -40 -35 -30
 agc ata atg aag tgg aac cgt gag cgc agg cgc cta caa atc gag gac 193
 Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Leu Gln Ile Glu Asp
 -25 -20 -15
 ttc gag gct cgc atc gcg ctg ttg cca ctg tta cag gca gaa acc gac 241

09973360.101501

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
 -10 -5 1
 cgg agg acc ttg cag atg ctt cgg gag aac ctg gag gag gag gcc atc 289
 Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
 5 10 15
 atc atg aag gac gtg ccc gac tgg aag gtg ggg gac tct gtg tyc cac 337
 Ile Met Lys Asp Val Pro Asp Trp Lys Val Gly Xaa Ser Val Xaa His
 20 25 30 35
 aca acc cgc tgg gtg ccc ccc ttg atc ggg gag ctg tac ggg ctg cgc 385
 Thr Thr Arg Trp Val Pro Pro Leu Ile Gly Leu Tyr Gly Leu Arg
 40 45 50
 acc aca aag gag gct ctc cat gcc agc cac ggc ttc atg tgg tac acg 433
 Thr Thr Lys Glu Ala Leu His Ala Ser His Gly Phe Met Trp Tyr Thr
 55 60 65
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 <222> 34..363

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 <223> Von Heijne matrix
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 seq LLSLSLPLVLLG/WE

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 <222> 536..541

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 agc ctc agc tct ctt cct ctt gtt ctc cta ggg tgg gag tac agc agc 102
 Ser Leu Ser Ser Leu Pro Leu Val Leu Leu Gly Trp Glu Tyr Ser Ser
 -10 -5 1 5
 caa acg ctg aac tta gtc cca tcc act tcc atc tta tcc ttt gtg ccc 150
 Gln Thr Leu Asn Leu Val Pro Ser Thr Ser Ile Leu Ser Phe Val Pro
 10 15 20
 ttc atc ccc ctg cat ctt gtc ctt ttt gcc ctc tgg tac ctc cca gtg 198
 Phe Ile Pro Leu His Leu Val Leu Phe Ala Leu Trp Tyr Leu Pro Val
 25 30 35
 ccc cat cat ctc tac ccc cag gga ctc gga rat cat gca gca raa gca 246
 Pro His His Leu Tyr Pro Gln Gly Leu Gly Xaa His Ala Ala Xaa Ala
 40 45 50
 gaa raa ggc aaa cga raa gaa gga gga acc caa kta gct ttg tgg ctt 294
 Glu Xaa Gly Lys Arg Xaa Glu Gly Gly Thr Gln Xaa Ala Leu Trp Leu
 55 60 65
 cgt gtc caa ccc tct tgc cct tcg cct gtg tgc ctg gag cca gtc cca 342

09973660.101501

Arg Val Gln Pro Ser Cys Pro Ser Pro Val Cys Leu Glu Pro Val Pro
 70 75 80 85
 cca cgc tgc cgt ttc ctc ctg tagtgctcac aggtcccagc accgatggca 393
 Pro Arg Ser Arg Phe Leu Leu

90
 ttccctttgc cctgagtcgt carcgggtcc cttttgtgct tccttcccct caggtagcct 453
 ctctccccct gggccactcc cgggggtgag ggggtttacc ccttcccagt gttttttatt 513
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<210> 388
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<220>
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 <222> 50..286

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 score 4.80000019073486
 seq VLLAIGMFFTAWF/FV

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 <222> 385..390

<220>
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 <222> 405..416

<400> 388
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 Met Glu Leu

-35
 gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc ttc ccc 106
 Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe Pro
 -30 -25 -20

cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc gcc tgg 154
 His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala Trp
 -15 -10 -5

ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat atc tat 202
 Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile Tyr
 1 5 10 15

aaa gag ctc ctc atc tcc tta gtg gcc tca ctc ttc atg ggc ttt gga 250
 Lys Glu Leu Leu Ile Ser Leu Val Ala Ser Leu Phe Met Gly Phe Gly
 20 25 30

gtc ctc ttc ctg ctg ctc tgg gtt ggc atc tac gtg tgagcaccga 296
 Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val
 35 40

agggtaacaa ccagatggct tcaactgaaac ctgcttttgt aaattacttt tttttactgt 356
 tgctggaagt gtccccactg ctgctcataa taaatgcaga agtatagcaa aaaaaaaaaa 416
 ccc 419

<210> 389
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 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> 50..637

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 seq LGAAALALLANT/DV

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 Met Ser Phe
 ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc att ggt gca 106
 Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser Ile Gly Ala
 -30 -25 -20
 gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc aac aca gac 154
 Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala Asn Thr Asp
 -15 -10 -5 1
 gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac ctg gag gat 202
 Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Gly Tyr Leu Gly Asp
 5 10 15
 ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc aaa gca aag 250
 Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys
 20 25 30
 gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg cgg agg cca 298
 Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val Arg Arg Pro
 35 40 45
 ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc tcc ctg aaa 346
 Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys
 50 55 60 65
 agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg gta aag gas 394
 Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val Val Lys Xaa
 70 75 80
 cac atc rgg act gaa ktg aag gat ttc cag cct tat ttc aaa gga gaa 442
 His Ile Xaa Thr Glu Xaa Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu
 85 90 95
 atc ttc ctg gat gaa aar aaa aag ttc tat ggt cca caa agg cgg aag 490
 Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys
 100 105 110
 atg atg ttt atg gga ttt atc cgt ctg gga atg tgg tac aac ttc ttc 538
 Met Met Phe Met Gly Phe Ile Arg Leu Gly Met Trp Tyr Asn Phe Phe
 115 120 125
 cga rcc tgg aac gga rgc ttc tct gga aac ctg gaa gga raa ggc ttc 586
 Arg Xaa Trp Asn Gly Xaa Phe Ser Gly Asn Leu Glu Gly Xaa Gly Phe
 130 135 140 145
 att ctt ggg gga att ttc gtg gtg gga tca asg aaa gca ggg cat tct 634
 Ile Leu Gly Gly Ile Phe Val Val Gly Ser Xaa Lys Ala Gly His Ser
 150 155 160
 tct tgarcmccga gaaaagaat ttggagacaa agtaaaccta ctttctgttc 687
 Ser
 tgggaagctgc taagatgac aaaccacaga ctttgcctc agagaaaaaa tgattgtgtg 747
 aaactgcccc gctcagggat aaccagggac attcactgt gtccatggga tgattgtgtt 807
 caactcgtgt cctaaggag tgagaaaccc atttatact tactctcagt atggattatt 867
 aatgtatttt aatattctgt ttaggccccc taaggcaaaa taccctccaaa acaagactga 927
 caaaaatctg aaaaactaat gaggattatt aagctaaaac ctgggaaata ggaggtctaa 987

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aaggtgagca agtcacttga ggtcgggagt tcgagaccag cctgagcaac atggcgaaac 1107
cccgtctcta ckaaaaaaac araaatcacc cgggtgtggt ggcaggcacc tgtagtccca 1167
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aa

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<210> 390
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<221> polyA_site
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Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Phe
-15
cca aca ggt ttt tct tcc ccc agt ccc tca gct gct gct gct cag 158
Pro Thr Gly Phe Ser Ser Pro Ser Pro Ser Ala Ala Ala Ala Gln
-5 1 5 10
gag gtc aga tct gcc act gat ggt aat acc agc acc act ccg ccc acc 206
Glu Val Arg Ser Ala Thr Asp Gly Asn Thr Ser Thr Thr Pro Pro Thr
15 20 25
tct gcc aar aar aka aag tta aac agc agc agc agt agc agt aac 254
Ser Ala Lys Lys Xaa Lys Leu Asn Ser Ser Ser Ser Ser Ser Asn
30 35 40
agt agt aac gag aga gaa gac ttt gat tcs acc tct tcc tcc tct tcc 302
Ser Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Ser
45 50 55
act cct cct tta caa ccc agg gat tgc gca tcc cct tca acc tgc tcc 350
Thr Pro Pro Leu Gln Pro Arg Asp Ser Pro Ser Pro Ser Thr Ser Ser
60 65 70 75
ttc tgc ctg ggg gtt tca gtg gct gct tcc agc cac gta ccg ata swg 398
Phe Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Xaa
80 85 90
aar aag ctg cgt ttt gaa rac acc ctg gag ttt gta ggg ttt gat gcg 446
Lys Lys Leu Arg Phe Glu Xaa Thr Leu Glu Phe Val Gly Phe Asp Ala
95 100 105
aar atg gct gar gaa tcc tcc tcc tcc tcc tcc tca tct tca cca ack 494
Lys Met Ala Glu Lys Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
110 115 120
gct gca aca tct cag cag cag caa ctt aaa aat aag agt ata ttg aat 542
Ala Ala Thr Ser Gln Gln Gln Gln Leu Lys Asn Lys Ser Ile Leu Asn
125 130 135
ctc ttc tgt ggc ttc ggt gca tca tgc aaa cgg cct agc caa atc ttc 590
Leu Phe Cys Gly Phe Gly Ala Ser Cys Lys Arg Pro Ser Gln Ile Phe

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140          145          150          155          642
tac cac cgt ctc tagctttgct aacagcaaac ctggctctgc taagaagtta
Tyr His Arg Leu
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caaaaaaaaaaaa aaa 715

<210> 391
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<212> DNA
<213> Homo sapiens

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<222> 120..434

<220>
<221> sig_peptide
<222> 120..185
<223> Von Heijne matrix
score 6.30000019073486
seq FALVNLWLRLSTGC/FW

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<222> 899..904

<220>
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<222> 918..931

<400> 391
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gccttcgtga gaccggtgca ggcctggggg agtcctctgt ctggacagag aagagaaaa 119
atg cag gga cac tgg ctc agt agt gcc ttt gca ttg gtt tgg ctt tgg 167
Met Gln Gly His Trp Leu Ser Ser Ala Phe Ala Leu Val Trp Leu Trp
-20 -15 -10
cta cgc agc act ggt tgc ttc tgg tgg gat cat tgg cta tgt aaa agc 215
Leu Arg Ser Thr Gly Cys Phe Trp Trp Asp His Trp Leu Cys Lys Ser
-5 1 5 10
agg cag cgt gcc gtc cct gcc tgc agg gct gct ctt tgg cag tct agc 263
Arg Gln Arg Ala Val Pro Gly Cys Arg Ala Ala Leu Trp Gln Ser Ser
15 20 25
cgg cct ggg tgc tta cca gct gtc tca gga tcc aag gaa cgt ttg ggt 311
Pro Gly Cys Leu Pro Ala Val Ser Gly Ser Lys Glu Arg Leu Gly
30 35 40
ttt cct agc tac atc tgg tac ctt ggc tgg cat tat ggg aat gag gtt 359
Phe Pro Ser Tyr Ile Trp Tyr Leu Gly Trp His Tyr Gly Asn Glu Val
45 50 55
cta cca ctc tgg aaa att cat gcc tgc agg ttt aat tgc agg tgc cag 407
Leu Pro Leu Trp Lys Ile His Ala Cys Arg Phe Asn Cys Arg Cys Gln
60 65 70
ttt gct gat ggt cgc caa agt tgg agt tagtatgtkc aacagacccc 454
Phe Ala Asp Gly Arg Gln Ser Trp Ser
75 80
atttagcagaa gtcatgttcc agcttagatg atgaaraatt aaaaatctgc atcttccact 514
attttcaata tattaagaga aataagtgca gcatttttgc atctgacatt ttacctaaaa 574
aaaaaaaaacmc caaacttgcc aaaaagggtgg aaatcagtc atgattacaa acctacagag 634
gtggcgagta tgtaacacaa gagcttaata agaccctcat agagcttgat tcttgatat 694
tgatgtgtgc ttttctttct gtatctgtag gtaaatctca agggtaaaat gttagggtgc 754
agctttcagg gctctgaaac cchattccct gctctgagga acagtgtgaa aaaaagtctt 814
ttaggaratt tacaatatct gttcttttgc tcatcttara ccacagactg actttgaaat 874

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takgttaagt gaaatatcaa tgaaaataaa gtttactata aataawaaaa aaaaaaa 931

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..447

<220>
 <221> sig_peptide
 <222> 4..147
 <223> Von Heijne matrix
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<220>
 <221> polyA_signal
 <222> 858..863

<220>
 <221> polyA_site
 <222> 880..891

<400> 392
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 -45 -40 -35
 gcg ttc atg cta ctc atg cga aac att gtc agg gtg gtc gtc ctg gac 96
 Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp
 -30 -25 -20
 aaa gtc aca gac ctg ctg ctg ttc ttt ggg aag ctg ctg gtg gtc gga 144
 Lys Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly
 -15 -10 -5
 ggc gtg ggg gtc ctg tcc ttc ttt ttt ttc tcc ggt cgc atc ccg ggg 192
 Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly
 1 5 10 15
 ctg ggt aaa gac ttt aag agc ccc cac ctg aac tat tac tgg ctg ccc 240
 Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro
 20 25 30
 ayc atg acc tcc atc ctg ggg gcc tat gtc atc gcc agy ggc ttc ttc 288
 Xaa Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe
 35 40 45
 agc gtt ttc ggc atg tgt gtg gac acg ctg ttc ctg tgc ttc ctg gaa 336
 Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu
 50 55 60
 gac ctg gag cgg aca acg gct ccc tgg acg gcc cta cta cat gtc caa 384
 Asp Leu Glu Arg Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln
 65 70 75
 gag ctt cta aag att ctg ggc aag aag aac gag gcg ccc ccg gac aac 432
 Glu Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp Asn
 80 85 90 95
 aag aaa agg aaa aak tgacagctcc ggccctgac caggactgca cccaccccc 487
 Lys Lys Arg Lys Xaa
 100
 accgtccagc catccaacct cacttcgcct tacaggtctc cattttgtgg taaaaaaagg 547
 ttttagccca ggcgcctgtg ctcacgcctg twatccaaca ctttgaragg ctgagcgagg 607
 cggatcaccct kaktcaggak tycgagacca kccctggccaa catggtgaaa cctccgtctc 667
 tattaaaaat acaaaaatta gccgagagtg gtggcatgca cctgtcatcc cagctactcg 727

ggaggctgag gcaggagaat cgcttgaacc cgggaggcag aggttgcaat gagccagat 787
 cgccgactg cactccaacc tgggtgacag actctgtctc caaaacaaaa caaacaaaa 847
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<210> 393
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 <212> DNA
 <213> Homo sapiens

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 <222> 28..96
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 <221> polyA_site
 <222> 806..817

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 ctt ccc etc ttg ggg ctg ctg etc tcc etc ccc gcc ggg gcg gat gtg 102
 Leu Pro Leu Leu Gly Leu Leu Leu Ser Leu Pro Ala Gly Ala Asp Val
 -10 -5 1
 aag gct cgg agc tgc gga gag gtc cgc cag gcg tac ggt gcc aag gga 150
 Lys Ala Arg Ser Cys Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly
 5 10 15
 ttc agc ctg gcg gac atc ccc tac cag gag atc gca kgg gaa cac tta 198
 Phe Ser Leu Ala Asp Ile Pro Tyr Gln Glu Ile Ala Xaa Glu His Leu
 20 25 30
 aga atc tgt cct cag gaa tat aca tgc tgc acc aca gaa atg gar gac 246
 Arg Ile Cys Pro Gln Glu Tyr Thr Cys Cys Thr Thr Ala Met Glu Asp
 35 40 45 50
 aag tta agc caa caa agc aaa ctc gaa ttt gaa aac ctt gtg gaa gag 294
 Lys Leu Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu
 55 60 65
 aca agc cat ttt gtg cgc acc act ttt gtg tcc agg cat aag aaa ttt 342
 Thr Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Phe
 70 75 80
 gac gaw ttt ttc cga rag ctc kcg gag aat gca raa aag tca cta aat 390
 Asp Xaa Phe Phe Arg Xaa Leu Xaa Glu Asn Ala Xaa Lys Ser Leu Asn
 85 90 95
 gat rtg ttt gtm cgg acc tat ggc atg ctg tac wtg car aat kca gaa 438
 Asp Xaa Phe Val Arg Thr Tyr Gly Met Leu Tyr Xaa Gln Asn Xaa Glu
 100 105 110
 gtc ttc crg gac etc ttc aca rag ctg aaa agg tac tac act ggg ggt 486
 Val Phe Xaa Asp Leu Phe Thr Xaa Leu Lys Arg Tyr Tyr Thr Gly Gly
 115 120 125 130
 aat gtg aat ctg gag gaa atg etc aat gac ttt tgg gct cgg etc ctg 534
 Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Thr Ala Arg Leu Leu
 135 140 145
 gaa cgg atg ttt cag cwr awa aac cct cag tat cac ttc agt gaa gac 582
 Glu Arg Met Phe Gln Xaa Xaa Asn Pro Gln Tyr His Phe Ser Glu Asp
 150 155 160

tac ctg gaa tgt gtg agc aaa tac act gac cak ctc aag cca ttt gga	630
Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp Xaa Leu Lys Pro Phe Gly	
165 170 175	
gac gtg ccc cgg aaa ctg aag att cag gtk acc cgc gcc ttc atk gsk	678
Asp Val Pro Arg Lys Leu Lys Ile Gln Val Thr Arg Ala Phe Xaa Xaa	
180 185 190	
gcc agg acc ttt gtc cag ggg ctg act gtg ggc aga gaa gtt gca aac	726
Ala Arg Thr Phe Val Gln Gly Leu Thr Val Gly Arg Glu Val Ala Asn	
195 200 205 210	
cga gtt tcc aag gta att gaa aac gtg ctt tct ttc tca ttg gtg ttc	774
Arg Val Ser Lys Val Ile Glu Asn Val Leu Ser Phe Ser Leu Val Phe	
215 220 225	
ctt gtt tat tct gtt ttt aaa acc aat gtt taaaaaaaaaaa aaa	817
Leu Val Tyr Ser Val Phe Lys Thr Asn Val	
230 235	

<210> 394
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 <213> Homo sapiens

<220>
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 <222> 27..212
 <223> Von Heijne matrix
 score 3.59999990463257
 seq SWLSLLAALAHLA/AA

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<220>
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 <222> 1009..1020

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-60 -55	
ccg gtc ccg gtg gaa cag gcg gtg ctg gag acg ttc ttc tct cac ctg	101
Pro Val Pro Val Glu Gln Ala Val Leu Glu Thr Phe Ser His Leu	
-50 -45 -40	
ggt atc ttc tct tac gac aag gct aag gac aat gtg gag aag gaa cga	149
Gly Ile Phe Ser Tyr Asp Lys Ala Lys Asp Asn Val Glu Lys Glu Arg	
-35 -30 -25	
gag gcc aac aag agc gcg ggg gcc agc tgg ctg tcg ctg ctg gcg gcc	197
Glu Ala Asn Lys Ser Ala Gly Gly Ser Trp Leu Ser Leu Leu Ala Ala	
-20 -15 -10	
ttg gcg cac ctg gcc gcg gcc gag aag gtc tat cac agc ctc acc tac	245
Leu Ala His Leu Ala Ala Ala Glu Lys Val Tyr His Ser Leu Thr Tyr	
-5 1 5 10	
ctg ggg cag aaa cta ggt acc tcc gcc ccg ccc ccc gag ccc ctt gag	293
Leu Gly Gln Lys Leu Gly Thr Ser Ala Pro Pro Pro Glu Pro Leu Glu	
15 20 25	
gag gaa gta aag ggg gta tat tcc cca dtc gcc agt gcc ttg ggt btc	341
Glu Glu Val Lys Gly Val Tyr Ser Pro Xaa Gly Ser Gly Leu Gly Xaa	

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30 35 40
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 Pro Ser Leu Cys His Phe
 45
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 ctgctgtagat attggcgaaac tgggtagatg ctcttttgcaa ggctgtgacc caaacccgaaw 509
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 aaaaaacmcwd tyccckttttm cccccccgg grmcagaaga gcaaaacttt gcaaaacaac 629
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 gaaaaatgga aacactctta gcacttcatg tacatcttgc ctctgaaata agattcaaga 869
 gctgattcaa ctgattttta ctagtagaag caataagtat aagtagatga gaaggaaata 929
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 <222> 25..957

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 <222> 25..93
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LEAFSQAISAIQA/LR

 <220>
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 <222> 1368..1373

 <220>
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 <222> 1388..1399

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 -20 -15
 aac ctg gag gcc ttt tcc cag gcc att agt gcc atc cag gcg ctg cga 99
 Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
 -10 -5 1
 tcc agc gtg agc agg gtg ttc gac tgc ctg aag gat ggg atg cgg aac 147
 Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
 5 10 15
 aag gag acg ctg gag ggc cgg gag aag gcc ttt att gcg cac ttc cag 195
 Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
 20 25 30
 gac aac tta cat tgc gtc aac cgg gac ctc aat gag ctg gaa cgt ctg 243
 Asp Asn Leu His Ser Val Asn Arg Asp Leu Asn Glu Leu Glu Arg Leu
 35 40 45 50
 agc aat ctg gta ggc arg cca tct gar aac cat cct ctt cat aac agt 291
 Ser Asn Leu Val Gly Xaa Pro Ser Glu Asn His Pro Leu His Asn Ser
 55 60 65
 ggg ctg tta asc ctg gat cct gtg car gac aaa act cct ctc tat agt 339
 Gly Leu Leu Xaa Leu Asp Pro Val Gln Asp Lys Thr Pro Leu Tyr Ser

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caa ctc ctt	70	caa gca tat aag tgg	75	tca aac aag ttg	80	cag tac cat gca	387		
Gln Leu Leu	85	Gln Ala Tyr Lys Trp	90	Ser Asn Lys Leu	95	Gln Tyr His Ala			
gga cta gca		tct ggc ctt tta aat		cas car tca ktg		aag cgt ycc gct	435		
Gly Leu Ala		Ser Gly Leu Leu Asn		Xaa Gln Ser Xaa		Lys Arg Xaa Ala			
aat cag atg	100	gga gta tct gcc aaa	105	cgt aga cca aag	110	gct cag ccc aca	483		
Asn Gln Met		Gly Val Ser Ala Lys		Arg Arg Pro Lys		Ala Gln Pro Thr			
act ctt gtc	115	cta cca cct caa tat	120	gtt gat gat gtg	125	atc agc cgc att	531		
Thr Leu Val		Leu Pro Pro Gln Tyr		Val Asp Asp Val		Ile Ser Arg Ile			
gac agg atg	135	ttt cct gaa atg tcc	140	atc cac tta tcc	145	aga ccc aat gga	579		
Asp Arg Met		Phe Pro Glu Met Ser		Ile His Leu Ser		Arg Pro Asn Gly			
aca tca gca	150	atg ctt ctg gtg acc	155	ttg gga aar gtg	160	ttg aaa gtg awc	627		
Thr Ser Ala		Met Leu Leu Val Thr		Leu Gly Lys Val		Leu Lys Val Xaa			
gtc gtc rtr	165	cgg arm ctg ttc att	170	gat cga aca ata	175	gtw aag gga tat	675		
Val Val Xaa	180	Arg Xaa Leu Phe Ile	185	Asp Arg Thr Ile	190	Val Lys Gly Tyr			
wac gag aat	195	gtc tac rca gaa kat	200	ggc mag ctt gat	205	ata tgg tcc aaa	723		
Xaa Glu Asn		Val Tyr Xaa Glu Xaa		Gly Xaa Leu Asp		Ile Trp Ser Lys			
tcc aac tat	210	caa gta ttc cag aag	215	gtg aca gac cat	220	gcc acc act gcc	771		
Ser Asn Tyr		Gln Val Phe Gln Lys		Val Thr Asp His		Ala Thr Thr Ala			
ctg ctc cac	225	taw mag ctg ccc cag	230	atg ccg gat gtc	235	gtg gtc cga tcc	819		
Leu Leu His		Xaa Xaa Leu Pro Gln		Met Pro Asp Val		Val Val Arg Ser			
ttc awg acc	240	tgg tta aga agt tac	245	ata aag ctg ttc	250	cag gcc ccg tgc	867		
Phe Xaa Thr		Trp Leu Arg Ser Tyr		Ile Lys Leu Phe		Gln Ala Pro Cys			
cag cgc tgc	255	ggg aag ttt ctg cag	260	gac ggc ctt ccc	265	ccg aca tgg agg	915		
Gln Arg Cys		Gly Lys Phe Leu Gln		Asp Gly Leu Pro		Pro Thr Trp Arg			
gat ttc cga	270	acc ctc gaa gcc ttc	275	cat gac acc tgc	280	cgg cag	957		
Asp Phe Arg		Thr Leu Glu Ala Phe		His Asp Thr Cys		Arg Gln			
tagccccac	285	gctggcccca	290	gcctcagacc	295	ccaccagca	ccttcccaga	cacgcaggaa	1017
gccccacagaa		ggctcagctg		gttcctcact		gcccagatgt	gtacagctgc	tcctcccttt	1077
cataaaagcag		cgccatgtgt		gcagaggcca		ctcttgaaga	gcagactccc	tcgtgtggct	1137
atgggactaa		ttattccac		tagccagcgg		actgaaggca	aagaagacct	ttctagaacc	1197
tggtagaagg		aagctgtgca		gcattgtctc		cgctccatgtg	tgtcggcagt	gctgggtgtc	1257
gtcgtctccg		cgagctgtta		ctggaatgac		cccttgtgtt	catgggtatc	gtcatgcggg	1317
gttctgtgt		tttgtggg		ctgggttttg		gttaacttat	ttttataagc	aataaacctt	1377
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<210> 396
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 47..319

<220>
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 <222> 47..226

<223> Von Heijne matrix
score 3.90000009536743
seq SSLVPFFLFTCFG/HF

<220>
<221> polyA_site
<222> 656..666

<400> 396
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Met Thr Ser
-60
ttg ttt gct gtt gtg tta cag aga gag aag gaa cct cac ctg tgg ctc 103
Leu Phe Ala Val Val Leu Gln Arg Glu Lys Glu Pro His Leu Trp Leu
-55 -50 -45
agc tca ccc cac atc cgt ttc tca tta cgt gta aat aaa ctg tca gag 151
Ser Ser Pro His Ile Arg Phe Ser Leu Arg Val Asn Lys Leu Ser Glu
-40 -35 -30
ctg atg tta cag ctt tta cag ttt aaa gca ttc ccc tcg tct cta gtt 199
Leu Met Leu Gln Leu Leu Gln Phe Lys Ala Phe Pro Ser Ser Leu Val
-25 -20 -15 -10
cct ttt ttc ttg ttt aca tgt ttt ggg cac ttt ccc tca ttc acc acc 247
Pro Phe Phe Leu Phe Thr Cys Phe Gly His Phe Pro Ser Phe Thr Thr
-5 1 5
ttc cag ggc ttc ata gaa aat aac ttg tta caa aat cag ttc aat tct 295
Phe Gln Gly Phe Ile Glu Asn Asn Leu Leu Gln Asn Gln Phe Asn Ser
10 15 20
aat gtg gac ata gtg gca tgt tca taattagacc catatagggg acactgagct 349
Asn Val Asp Ile Val Ala Cys Ser
25 30
ttaaatacgtt gattctaaac tctatacatt aaaaaaatc agcccaggcc cctcaaagcc 409
tgaraaaaat taatttgcgc ttaatttaat gtcccaaac tcactcttgg aaaaatgcct 469
gttggaaaac tacaggtggg tcacatgktg gggctgtctc cgtgacactc agggattccag 529
tcaraacctc atccctcatat ctattgccta caaaaataga ccaagaatgt tgctgtctct 589
ttataatcct ttaaatattt aacattcaag ttttctttgt cttaaatcca gcctcttctct 649
aaaagcaaaa aaaaaaa 666

<210> 397
<211> 1131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..940

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<222> 80..130
<223> Von Heijne matrix
score 3.70000004768372
seq RIVSAALLAFVQT/HL

<220>
<221> polyA_signal
<222> 1101..1106

<220>
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<222> 1119..1130

00975360.101501

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agtttggtggg gctgggggat gagagctgca ccgcgcggga yaagtcgccc gcggcgcccc 60
amggagcaga acagagagc atg gag ctg gag agg atc gtc agt gca gcc ctc 112
Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu
-15 -10
ctt gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg 160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
-5 1 5 10
gat gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc 208
Asp Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly
15 20 25
ccc tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag 256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
30 35 40
atg atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca 304
Met Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
45 50 55
ata ggg gac atg atg cag aar ctc tca ggg cag ctg agc gat gcc vgg 352
Ile Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Xaa
60 65 70
aac aaa gag aac ctg caa ccg cag aac tct ggt gtc caa ggt cag gtg 400
Asn Lys Glu Asn Leu Gln Pro Gln Asn Ser Gly Val Gln Gly Gln Val
75 80 85 90
ccc atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag 448
Pro Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu
95 100 105
act agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act 496
Thr Arg Ser Ser Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Xaa
110 115 120
ggc gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg 544
Gly Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val
125 130 135
ttc cct acc tgt tcg gtg gag cag gcc cag tgg gtg ctg gcc aaa gct 592
Phe Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala
140 145 150
cgg ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa 640
Arg Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu
155 160 165 170
gag ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc 688
Glu Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg
175 180 185
ctc aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag 736
Leu Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys
190 195 200
tac atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg 784
Tyr Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met
205 210 215
gct ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag 832
Ala Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln
220 225 230
gta gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag 880
Val Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu
235 240 245 250
gcc gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag 928
Ala Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys
255 260 265
tac cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca 980
Tyr Arg Phe His
270
gatccacagag ggaatgcagga gccctatacc cctacacagg ggccccctaa ctccgtgcc 1040
ccttctctac tctcttgctc catagtgtta acctactctc ggagctgcct ccattgggac 1100

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agtaaagggtg gcccaaggaa aaaaaaaaaaaw t

1131

<210> 398
<211> 475
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 146..457

<220>
<221> sig_peptide
<222> 146..292
<223> Von Heijne matrix
score 5.19999980926514
seq CFLCLYPIPLCTS/HP

<220>
<221> polyA_signal
<222> 442..447

<220>
<221> polyA_site
<222> 465..475

<400> 398
attgtaacaa acagtaccaa tttatttttg cctgtgggttt ttgctttttt tccagttgat 60
gactttgtga acattcccag gtattggagc ctctgtggcc ttaaatgtgg ctccagttggag 120
ggagaccagg catagccagg ccagt atg gag cac ctc acg cac agc tct cag 172
Met Glu His Leu Thr His Ser Ser Gln
-45
aag ctg cag gcg gac gaa cat ctg acc aaa gag gtg tgg tgg agg ctc 220
Lys Leu Gln Ala Asp Glu His Leu Thr Lys Glu Val Trp Ser Arg Leu
-40 -35 -30 -25
ctg aaa gag aaa ggg cct gct ggt ctc atc ctc tgc ttc ctt tgc ctt 268
Leu Lys Glu Lys Gly Pro Ala Gly Leu Ile Leu Cys Phe Leu Cys Leu
-20 -15 -10
tac cct ata cct ctc tgc acg tcc cac ccc gtt tkg ctg tgt gcy cac 316
Tyr Pro Ile Pro Leu Cys Thr Ser His Pro Val Xaa Leu Cys Ala His
-5 1 5
ccc cag gat gtg tac ccg gtt gta gta aga gct gaa atc cat gct gag 364
Pro Gln Asp Val Tyr Pro Val Val Val Arg Ala Glu Ile His Ala Glu
10 15 20
ctg tac cag gaa ctt gca tat cta aaa aca gaa act gag tca ctg gcc 412
Leu Tyr Gln Glu Leu Ala Tyr Leu Lys Thr Glu Thr Glu Ser Leu Ala
25 30 35 40
cat ctc ttt gct ctt gtg ccc cag gcc aaa ata aag aat aga gtg 457
His Leu Phe Ala Leu Val Pro Gln Ala Lys Ile Lys Asn Arg Val
45 50 55
taragtga aa aaaaaaa 475

<210> 399
<211> 949
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..351

09976300.101501

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<220>
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<222> 100..207
<223> Von Heijne matrix
      score 4.19999980926514
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<220>
<221> polyA_site
<222> 940..949

<220>
<221> misc_feature
<222> 745
<223> n=a, g, c or t

<400> 399
aaaggaatac tgacagataa ggccggaaac aaaactgatg gcttgaaaaa catttttatg      60
gaatgtattt actatcattt tgttttacta tagaggtag atg gga ctc tta act      114
                               Met Gly Leu Leu Thr
                               -35
ttt ggg tac att gaa amc akc ckg aaa act gaa cac aat cct gat cat      162
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His
      -30                -25                -20
cac tcc tgc ctg gct gtc tcc tgg gag gct gcc ggg tgc cac gga gct      210
His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala Gly Cys His Gly Ala
      -15                -10                -5                1
ggg aca cag cag agc ccg cta ggt gtt gca ggg ccc tgg agg cca agg      258
Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly Pro Trp Arg Pro Arg
      5                10                15
cca ccc tgt gtg ggg tcc ctg ttg gca gcc agg tcc cta cac aaa caa      306
Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg Ser Leu His Lys Gln
      20                25                30
gta atc ctg ttt gcc ctc cta ggt ttt gca tat gac cac gca gcc      351
Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr Asp His Ala Ala
      35                40                45
taatttgggg tgtaggggaa cctctgctgg cccttgctcc ttgtatgttt gggtagcttt      411
aatggctggc cacatacccc tttctcccag ctactcattc actgacttgg gtaagttcta      471
gcacaatggc cacttagaaa cagaatgtga cacatcaaca ttaacttttc ctgaaaagaa      531
cagtttgccct aacatggacc cmaaagaagc ttggaattta taagactttc ctttataaga      591
tatagttgggg gtttttttgg gtggaggggg gttgtttttt gttttttggt ttcaaagacag      651
agtctcgctc agttgtccag gctggartgt aktggcatga tctcggtcca ctgcarectc      711
tgccctccag gttcatgcca ttctcctgcc tcancctccc gactagctgg gactacaggt      771
gtctgcggcc acgcctggct aatttttttg tatttttagt agagacgggg ttccaccatg      831
ttggtcagga ttgtctcgat ttctgacct cgtgatccgc ctgtctcgcc ctcccaaaag      891
gctgggatta caggcgtgag ccaccacgcc tggcctataa gatacgggaa aaaaaaaaa      949

<210> 400
<211> 940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 177..569

<220>
<221> sig_peptide
<222> 177..236
<223> Von Heijne matrix
      score 11.1999998092651

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09978360.101501

seq AFLLLVALSYTLA/RD

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<220>
<221> polyA_site
<222> 931..939

<220>
<221> misc_feature
<222> 482
<223> n=a, g, c or t

<400> 400
agaagataat cacttgggga aaggaaggtt cgtttctgag ttagcaacaa gtaaatgcag      60
cactagtggg tgggattgag gtatgccctg gtgcataaat agagactcag ctgtgctggc      120
acactcagaa gcttggaacc cactcctagcc gccgactcac acaaggcaga gttgcc atg      179
Met
-20
gaa aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac      227
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr
-15 -10 -5
act ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca      275
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
1 5 10
aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt      323
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
15 20 25
gac caa ctc atc tgg aca car aca tat gaa raa rct cta twt aaa tcc      371
Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Xaa Xaa Leu Xaa Lys Ser
30 35 40 45
aar aca agc aac aaa ccc ttg atg att att cat cac ttg gat gad tgc      419
Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Xaa Cys
50 55 60
cca cac agt caa gct tta aaa aaa ktg ttt gct gaa aat aaa raa atc      467
Pro His Ser Gln Ala Leu Lys Lys Xaa Phe Ala Glu Asn Lys Xaa Ile
65 70 75
cag aaa ttg gca ran cag ttt gtc cyc ctc aat ctg gtt tat gaa aca      515
Gln Lys Leu Ala Xaa Gln Phe Val Xaa Leu Asn Leu Val Tyr Glu Thr
80 85 90
act gac aaa cac ctt tct cct gat ggc caa tat ktc ccc cmg gat tat      563
Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Xaa Pro Xaa Asp Tyr
95 100 105
gtt tgt tgacccatct ctgacagtta gagccgatat cactggaaga tattcaaaac      619
Val Cys
110
gtctctatgc ttacgaacct gcagatacag ctctgttgct tgacaacatg aagaaagctc      679
tcaagttgct gaagactgaa ttgtaaagaa aaaaaatctc caagcccttc tgtctgtcag      739
gccttgagac ttgaaccag aagaagtgtg agaagactgg ctagtgtgga agcatagtga      799
acacactgat taggttatgt tttaatgtta caacaactat tttttaagaa aaacaagtgt      859
tagaaatttg gtttcaagtg tacatgtgtg aaaacaatat tgtatactac catagtgcag      919
catgattttc taaaaaaaaa a      940

<210> 401
<211> 887
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..459

<220>

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<221> sig_peptide
 <222> 67..135
 <223> Von Heijne matrix
 score 5.19999980926514
 seq IGVGLYLLASAAA/FY

<220>
 <221> polyA_signal
 <222> 856..861

<220>
 <221> polyA_site
 <222> 875..887

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<400> 401
agcggcgccga tccgggacg cgggcgggct ggcaccacg ggacaggaag gcacagagca    60
tggaga atg atg aac ttc cgt cag cgg atg gga tgg att gga gtg gga    108
      Met Met Asn Phe Arg Gln Arg Met Gly Trp Ile Gly Val Gly
            -20                    -15                    -10
ttg tat ctg tta gcc agt gca gca gca ttt tac tat gtt ttt gaa atc    156
Leu Tyr Leu Leu Ala Ser Ala Ala Ala Phe Tyr Tyr Val Phe Glu Ile
            -5                    1                    5
agt gag act tac aac agg ctg gcc ttg gaa cac att caa cag cac cct    204
Ser Glu Thr Tyr Asn Arg Leu Ala Leu Glu His Ile Gln Gln His Pro
            10                    15                    20
ggg gag ccc ctt gaa gga acc aca tgg aca cac tcc ttg aaa gct caa    252
Gly Glu Pro Leu Glu Gly Thr Thr Trp Thr His Ser Leu Lys Ala Gln
            25                    30                    35
tta ctc tcc ttg cct ttt tgg gtg tgg aca gtt att ttt ctg gta cct    300
Leu Leu Ser Leu Pro Phe Trp Val Trp Thr Val Ile Phe Leu Val Pro
            40                    45                    50                    55
cac tta car atk ttt ttg ttc cta tac tct tgt aca aaa vct gat ccc    348
Tyr Leu Gln Xaa Phe Leu Phe Leu Tyr Ser Cys Thr Lys Xaa Asp Pro
            60                    65                    70
aaa aca gtg ggc tac tgt wtc atc cct ata tgc ttg gca rtt att tsc    396
Lys Thr Val Gly Tyr Cys Xaa Ile Pro Ile Cys Leu Ala Xaa Ile Xaa
            75                    80                    85
aat cgc cac cag gat ttt gtc aag gct tct aat caa atc agc aaa cta    444
Asn Arg His Gln Asp Phe Val Lys Ala Ser Asn Gln Ile Ser Lys Leu
            90                    95                    100
caa ctg att gac acg taaaatcagt caccgttttt tccctacgat tacaaaaactg    499
Gln Leu Ile Asp Thr
            105
ccagtcctat atggagtcgt atcacaaagc tgcagtttct tcacagatct caggaagttg    559
tcgtggggga gaggcttttt aaaaacatgt gattagggag ctatctttat ctgaataata    619
acgaattttt aggtaaaacc tgagatagag tactacaaaa tcatgttgat gacttcagat    679
tttgggaagt aaatcatgtc tgttatttgc attctttaga aacttgacta agtacctgaa    739
ttcatatttc tattctactg tgcaacatag tgatgattca gaaatttttc ctttggggaa    799
aaaaatgaat atgaacattt ccattgtgtt aagtgtaaaa aggtccagka catgatcata    859
aatattaaat tttatacaaa aaaaaaaaaa

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<210> 402
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 65..1069

<220>

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<221> sig_peptide
<222> 65..112
<223> Von Heijne matrix
      score 12.5
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<220>
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<222> 1978..1983

<220>
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<222> 1999..2010

<400> 402
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cacc atg gct gtg ttt gtc gtg ctc ctg gcg ttg gtg gcg ggt gtt ttg      109
      Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu
      -15 -10 -5
ggg aac gag ttt agt ata tta aaa tca cca ggg tct gtt gtt ttc cga      157
Gly Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg
      1 5 10 15
aat gga aat tgg cct ata cca gga gag cgg atc cca gac gtg gct gca      205
Asn Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala
      20 25 30
ttg tcc atg gcc ttc tct gtg aaa gaa gac ctt tct tgg cca gga ctc      253
Leu Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu
      35 40 45
gca gtg ggt aac ctg ttt cat cgt cct cgg gct agc gtc atg gtg atg      301
Ala Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met
      50 55 60
gtg aag gga gtt aac aac tmc cct cta ccc cca ggc tgt gtc att tog      349
Val Lys Gly Val Glu Asn Asn Xaa Pro Leu Pro Pro Gly Cys Val Ile Ser
      65 70 75
tac cct ttg gag aat gca gtt cct ttt agt ctt gac agt gtt gca aat      397
Tyr Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn
      80 85 90 95
tcc att cac tcc tta ttt tct gag gaa act cct gtt gtt ttg cag ttg      445
Ser Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu
      100 105 110
gct ccc agt gag gaa aga gtg tat atg gta ggg aag gcm aac tca gtg      493
Ala Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val
      115 120 125
tgg aar acc ttt cag tca ctt gcg cca gct ccg kta atc rcc tgt ttc      541
Trp Lys Thr Phe Gln Ser Leu Ala Pro Ala Pro Xaa Ile Xaa Cys Phe
      130 135 140
aag aaa act ctg ttc tca gtt cac tcc ccc ycc att cma ctg agt agg      589
Lys Lys Thr Leu Phe Ser Val His Ser Pro Xaa Ile Xaa Leu Ser Arg
      145 150 155
aac aat gaa gtt gac cyg ctc ttt ctt tct gaa ctg caa gtg cta cat      637
Asn Asn Glu Val Asp Xaa Leu Phe Leu Ser Glu Leu Gln Val Leu His
      160 165 170 175
gat att tca agc ttg ctg tct cgt cat aag cat cta gcc aag gat cat      685
Asp Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His
      180 185 190
tct cct gat tta tat tca ctg gag ctg gca ggt ttg gat gaa att ggg      733
Ser Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly
      195 200 205
aag cgt tat ggg gaa gac tct gaa caa ttc aga gat gct tct aag atc      781
Lys Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile
      210 215 220

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03973360.101501

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ctt gtt gac gct ctg caa aag ttt gca gat gac atg tac agt ctt tat      829
Leu Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr
225                               230       235
ggg ggg aat gca gtg gta gag tta gtc act gtc aag tca ttt gac acc      877
Gly Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr
240                               245       250       255
tcc ctg att agg aag aca agg act atc ctt gag gca aaa caa gcg aag      925
Ser Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys
260                               265       270
aac cca gca agt ccc tat aac ctt gca tat aag tat aat ttt gaa tat      973
Asn Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr
275                               280       285
tcc gtg gtt ttc aac atg gta ctt tgg ata atg atc gcc ttg gcc ttg      1021
Ser Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu
290                               295       300
gct gtg att atc acc tct tac aat att tgg aac atg gaa tcc tgg ata      1069
Ala Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Glu Ser Trp Ile
305                               310       315
tgatagcgc atttatagga tgacaaacca gaagattcgg aatggattga atgttacctg      1129
tgccagaaat akaaaagggg gttggaaatt ggctgttttg ttaaaatata tcttttagtg      1189
tgcttttaag tagatagtat actttacatt tataaaaaaa aatcaaatTT tggtctttat      1249
tttgtgtgtg cctgtgatgt ttttctagag tgaattatag tattgacgtg aatccccactg      1309
tggtatagat tccataatat gcttgaatat tatgatatag ccatttaata acattgattt      1369
cattctgttt aatgaatttg gaaatatgca ctgaaagaaa tgtaaaacat ttagaatagc      1429
tcgtgttatg gaaaaaagtg cactgaattt attagacaaa cttacgaatg cttaaacttct      1489
ttacacagca taggtgaaaa tcatatttgg gctattgtat actatgaaca atttgtaaat      1549
ctcttaattt gatgtaaata actotgaaac aagagaaaaa gtttttaact tagagtagcc      1609
gtaaaatatt gatgtgctta tataatcgct tagtttttga actgtatctg agtaacagag      1669
gcagactggt ttttaacctt cttctgcaag tttgttgacc tacatgggct aatatggata      1729
ctaaaaatac tacaattgat taagaagaaa ctagccctgt ggagtatata gatgcttttc      1789
attatacaca caaaatcccc tgaggggacat tttgaggcat gaataataaa catttttatt      1849
tcagtaactt ttccccctgt gtaagttact atgggtttgt gtacaacttc attctataga      1909
atattaagtg gaagtgggtg aattctactt ttatgttggg agtggaccaa tgcctatcaa      1969
gagtgacaaa taaagttaat gatgattcca aaaaaaaaaa a                        2010

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<210> 403
 <211> 387
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..321

<220> .
 <221> sig_peptide
 <222> 70..234
 <223> Von Heijne matrix
 score 4.09999990463257
 seq AVCAALLASHPTA/EV

<220>
 <221> polyA_signal
 <222> 364..369

<220>
 <221> polyA_site
 <222> 375..387

<400> 403
 agaaatcgta ggacttccga aagcagcggc ggcgtttgct tcactgcttg gaagtgtgag 60

tgcgcgaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att 111
 Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
 -55 -50 -45
 ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat 159
 Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
 -40 -35 -30
 ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct 207
 Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
 -25 -20 -15 -10
 gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg 255
 Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
 -5 1 5
 gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag 303
 Asp Val Ser Asn Leu Gln Ser Phe Arg Ala Ser Lys Glu Leu Lys
 10 15 20
 caa agg atg atc tct tgc tgatggattt ttttttcat gtgattgtgc 351
 Gln Arg Met Ile Ser Cys
 25
 ascataacac ttaataaaat aagaaaaaaa aaaaaa 387

 <210> 404
 <211> 983
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 38..877

 <220>
 <221> sig_peptide
 <222> 38..91
 <223> Von Heijne matrix
 score 7.40000009536743
 seq GWLVLCVLAISLA/SM

 <220>
 <221> polyA_signal
 <222> 947..952

 <220>
 <221> polyA_site
 <222> 974..983

 <400> 404
 aatccagtyg gasttgacaa caggaggcag aggcacac atg gag ggt ccc cgg gga 55
 Met Glu Gly Pro Arg Gly
 -15
 tgg ctg gtg ctc tgt gtg ctg gcc ata tgc ctg gcc tct atg gtg acc 103
 Trp Leu Val Leu Cys Val Leu Ala Ile Ser Leu Ala Ser Met Val Thr
 -10 -5 1
 gag gac ttg tgc cga gca cca gac ggg aag aaa ggg gag gca gga aga 151
 Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys Lys Ggg Glu Ala Gly Arg
 5 10 15 20
 cct ggc aga cgg ggg cgg cca ggc ctc aag ggg gag caa ggg gag ccg 199
 Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys Gly Glu Gln Gly Glu Pro
 25 30 35
 ggg gcc cct ggc atc cgg aca ggc atc caa ggc ctt aaa gga gac cag 247
 Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln Gly Leu Lys Gly Asp Gln
 40 45 50
 ggg gaa cct ggg ccc tct gga aac ccc ggc aag gtg ggc tac cca ggg 295

Gly	Glu	Pro	Gly	Pro	Ser	Gly	Asn	Pro	Gly	Lys	Val	Gly	Tyr	Pro	Gly	
		55					60						65			
ccc	agc	ggc	ccc	ctc	gga	gcc	cgt	ggc	atc	ccg	gga	att	aaa	ggc	acc	343
Pro	Ser	Gly	Pro	Leu	Gly	Ala	Arg	Gly	Ile	Pro	Gly	Ile	Lys	Gly	Thr	
		70					75						80			
aag	ggc	agc	cca	gga	aac	atc	aag	gac	cag	ccg	agg	cca	gcc	ttc	tcc	391
Lys	Gly	Ser	Pro	Gly	Asn	Ile	Lys	Asp	Gln	Pro	Arg	Pro	Ala	Phe	Ser	
		85					90								100	
gcc	att	cgg	cgg	aac	ccc	cca	atg	ggg	ggc	aac	gtg	gtc	atc	ttc	gac	439
Ala	Ile	Arg	Arg	Asn	Pro	Pro	Met	Gly	Gly	Asn	Val	Val	Ile	Phe	Asp	
							105								115	
acg	gtc	atc	acc	aac	cag	gaa	gaa	ccg	tac	cag	aac	cac	tcc	ggc	cga	487
Thr	Val	Ile	Thr	Asn	Gln	Glu	Glu	Pro	Tyr	Gln	Asn	His	Ser	Gly	Arg	
							120								130	
ttc	gtc	tgc	act	gta	ccc	gct	act	act	act	tca	cct	tcc	agg	tgc	tgt	535
Phe	Val	Cys	Thr	Val	Pro	Ala	Thr	Thr	Thr	Ser	Pro	Ser	Arg	Cys	Cys	
							135								145	
ccc	agt	ggg	aaa	tct	gcc	tgt	cca	tcg	tct	cct	cct	caa	ggg	gcc	agg	583
Pro	Ser	Gly	Lys	Ser	Ala	Cys	Pro	Ser	Ser	Pro	Pro	Gln	Gly	Ala	Arg	
							150								160	
tcc	gac	gct	ccc	tgg	gct	tct	gtg	aca	cca	cca	aca	agg	ggc	tct	tcc	631
Ser	Asp	Ala	Pro	Trp	Ala	Ser	Val	Thr	Pro	Pro	Thr	Arg	Gly	Ser	Ser	
							165								180	
agg	tgg	tgt	cag	ggg	gca	tgg	tgc	ttc	agc	agg	gtg	acc	agg			679
Arg	Trp	Cys	Gln	Gly	Ala	Trp	Cys	Phe	Ser	Cys	Ser	Arg	Val	Thr	Arg	
							185								195	
tct	ggg	tgt	aaa	aag	acc	cca	aaa	agg	gtc	aca	ttt	acc	agg	gct	ctg	727
Ser	Gly	Leu	Lys	Lys	Thr	Pro	Lys	Arg	Val	Thr	Phe	Thr	Arg	Ala	Leu	
							200								210	
agg	ccg	aca	gcg	tct	tca	gcg	gct	tcc	tca	tct	tcc	cat	ctg	cct	gag	775
Arg	Pro	Thr	Ala	Ser	Ser	Ala	Ala	Ser	Ser	Ser	Ser	His	Leu	Pro	Glu	
							215								225	
cca	ggg	aag	gac	ccc	ctc	ccc	cac	cca	cct	ctc	tgg	ctt	cca	tgc	tcc	823
Pro	Gly	Lys	Asp	Pro	Leu	Pro	His	Pro	Pro	Leu	Trp	Leu	Pro	Cys	Ser	
							230								240	
gcc	tgt	aaa	atg	ggg	gcg	cta	ttg	ctt	cag	ctg	ctg	aag	gga	ggg	ggc	871
Ala	Cys	Lys	Met	Gly	Ala	Leu	Leu	Leu	Gln	Leu	Leu	Lys	Gly	Gly	Gly	
							245								260	
tgg	ctc	tgagagcccc	aggactggct	gccccgtgac	acatgctcta	agaagctcgt										927
Trp	Leu															
ttcttagacc	tcttctcgga	ataaacatct	gtgtctgtgt	ctgtgaaaa	aaaaaa											983

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<210> 405
<211> 1614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..470

<220>
<221> sig_peptide
<222> 51..203
<223> Von Heijne matrix
      score 5.80000019073486
      seq  AVGLFPAPTECFARV

<220>
<221> polyA_signal
<222> 1585..1590

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[illegible]

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<210> 406
<211> 325
<212> PRT
<213> Homo Sapiens
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<220>
 <221> SIGNAL
 <222> -26...-1

<400> 406
 Met Ala Thr Pro Leu Pro Pro Pro Ser Pro Arg His Leu Arg Leu Leu
 -25 -20 -15
 Arg Leu Leu Leu Ser Gly Leu Val Leu Gly Ala Ala Leu Arg Gly Ala
 -10 -5 1 5
 Ala Ala Gly His Pro Asp Val Ala Ala Cys Pro Gly Ser Leu Asp Cys
 10 15 20
 Ala Leu Lys Arg Arg Ala Arg Cys Pro Pro Gly Ala His Ala Cys Gly
 25 30 35
 Pro Cys Leu Gln Pro Phe Gln Glu Asp Gln Gln Gly Leu Cys Val Pro
 40 45 50
 Arg Met Arg Arg Pro Pro Gly Gly Gly Arg Pro Gln Pro Arg Leu Glu
 55 60 65 70
 Asp Glu Ile Asp Phe Leu Ala Gln Glu Leu Ala Arg Lys Glu Ser Gly
 75 80 85
 His Ser Thr Pro Pro Leu Pro Lys Asp Arg Gln Arg Leu Pro Glu Pro
 90 95 100
 Ala Thr Leu Gly Phe Ser Ala Arg Gly Gln Gly Leu Glu Leu Gly Leu
 105 110 115
 Pro Ser Thr Pro Gly Thr Pro Thr Pro His Thr Ser Leu Gly
 120 125 130
 Ser Pro Val Ser Ser Asp Pro Val His Met Ser Pro Leu Glu Pro Arg
 135 140 145 150
 Gly Gly Gln Gly Asp Gly Leu Ala Leu Val Leu Ile Leu Ala Phe Cys
 155 160 165
 Val Ala Gly Ala Ala Leu Ser Val Ala Ser Leu Cys Trp Cys Arg
 170 175 180
 Leu Gln Arg Glu Ile Arg Leu Thr Gln Lys Ala Asp Tyr Ala Thr Ala
 185 190 195
 Lys Ala Pro Gly Ser Pro Ala Ala Pro Arg Ile Ser Pro Gly Asp Gln
 200 205 210
 Arg Leu Ala Gln Ser Ala Glu Met Tyr His Tyr Gln His Gln Arg Gln
 215 220 225 230
 Gln Met Leu Cys Leu Glu Arg His Lys Glu Pro Pro Lys Glu Leu Asp
 235 240 245
 Thr Ala Ser Ser Asp Glu Glu Asn Glu Asp Gly Asp Phe Thr Val Tyr
 250 255 260
 Glu Cys Pro Gly Leu Ala Pro Thr Gly Glu Met Glu Val Arg Asn Pro
 265 270 275
 Leu Phe Asp His Ala Ala Leu Ser Ala Pro Leu Pro Ala Pro Ser Ser
 280 285 290
 Pro Pro Ala Leu Pro
 295

<210> 407
 <211> 302
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 407
 Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
 -15 -10 -5
 Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu

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[illegible]

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<210> 408
<211> 249
<212> PRT
<213> Homo Sapiens
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      100              105              110
Val Thr Ala Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile
      115              120              125
Asn Leu Lys Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr
      130              135              140              145
Asp Pro Gln Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser
      150              155              160
Asp Pro Thr Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile
      165              170              175
Ile Asn Lys Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val
      180              185              190
Ser Ser Leu Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile
      195              200              205
His Ser Leu Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln
      210              215              220              225
His Lys Thr Gln Leu Gln Thr Leu Ile
      230

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<210> 409

<211> 84

<212> PRT

<213> Homo Sapiens

<400> 409

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Met Lys Val Lys Ile Lys Cys Trp Asn Gly Val Ala Thr Trp Leu Trp
1      5      10      15
Val Ala Asn Asp Glu Asn Cys Gly Ile Cys Arg Met Ala Phe Asn Gly
      20      25      30
Cys Cys Pro Asp Cys Lys Val Pro Gly Asp Asp Cys Pro Leu Val Trp
      35      40      45
Gly Gln Cys Ser His Cys Phe His Met His Cys Ile Leu Lys Trp Leu
      50      55      60
His Ala Gln Gln Val Gln Gln His Cys Pro Met Cys Arg Gln Glu Trp
      65      70      75      80
Lys Phe Lys Glu

```

<210> 410

<211> 554

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -13...-1

<220>

<221> UNSURE

<222> 259

<223> Xaa = Asp,His,Asn,Tyr

<400> 410

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Met Leu Tyr Leu Gln Gly Trp Ser Met Pro Ala Val Ala Glu Val Lys
      -10      -5      1
Leu Arg Asp Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met
      5      10      15
Tyr Asn Tyr Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr
      20      25      30      35
Ile Asp Thr Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr
      40      45      50
Ala Leu Gly Lys Pro Arg Glu Val Phe Arg Leu Pro Thr Asp Leu Thr
      55      60      65

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Aly	Cys	Asp	Asn	Arg	Leu	Cys	Ala	Ser	Ile	His	Phe	Ser	Ser	Ser	Thr
Trp	Val	Thr	Leu	Ser	Asp	Gly	Thr	Gly	Arg	Leu	Tyr	Val	Ile	Gly	Thr
85						90	75				95	80			
Gly	Glu	Arg	Gly	Asn	Ser	Ala	Ser	Glu	Lys	Trp	Glu	Ile	Met	Phe	Asn
100					105					110					115
Glu	Glu	Leu	Gly	Asp	Pro	Phe	Ile	Ile	Ile	His	Ser	Ile	Ser	Leu	Leu
				120					125					130	
Asn	Ala	Glu	Glu	His	Ser	Ile	Ala	Thr	Leu	Leu	Leu	Arg	Ile	Glu	Lys
			135					140					145		
Glu	Glu	Leu	Asp	Met	Lys	Gly	Ser	Gly	Phe	Tyr	Val	Ser	Leu	Glu	Trp
							155					160			
Val	Thr	Ile	Ser	Lys	Lys	Asn	Gln	Asp	Asn	Lys	Lys	Tyr	Glu	Ile	Ile
						170					175				
Lys	Arg	Asp	Ile	Leu	Arg	Gly	Lys	Ser	Val	Pro	His	Tyr	Ala	Ala	Ile
180					185					190					195
Lys	Pro	Asp	Gly	Asn	Gly	Leu	Met	Ile	Val	Ser	Tyr	Lys	Ser	Leu	Thr
				200					205					210	
Phe	Val	Gln	Ala	Gly	Gln	Asp	Leu	Glu	Glu	Asn	Met	Asp	Glu	Asp	Ile
				215				220					225		
Ser	Glu	Lys	Ile	Lys	Glu	Pro	Leu	Tyr	Tyr	Trp	Gln	Gln	Thr	Glu	Asp
						235					240				
Asp	Leu	Thr	Val	Thr	Ile	Arg	Leu	Pro	Glu	Asp	Ser	Thr	Lys	Glu	Xaa
						250					255				
Ile	Gln	Ile	Gln	Phe	Leu	Pro	Asp	His	Ile	Asn	Ile	Val	Leu	Lys	Asp
260					265					270					275
His	Gln	Phe	Leu	Glu	Gly	Lys	Leu	Tyr	Ser	Ser	Ile	Asp	His	Glu	Ser
				280					285					290	
Ser	Thr	Trp	Ile	Lys	Glu	Ser	Asn	Ser	Leu	Glu	Ile	Ser	Leu	Ile	
				295			300					305			
Lys	Lys	Asn	Glu	Gly	Leu	Thr	Trp	Pro	Glu	Leu	Val	Ile	Gly	Asp	Lys
				310			315					320			
Gln	Gly	Glu	Leu	Ile	Arg	Asp	Ser	Ala	Gln	Cys	Ala	Ala	Ile	Ala	Glu
						330					335				
Arg	Leu	Met	His	Leu	Thr	Ser	Glu	Glu	Leu	Asn	Pro	Asn	Pro	Asp	Lys
340					345					350					355
Glu	Lys	Pro	Pro	Cys	Asn	Ala	Gln	Glu	Leu	Glu	Glu	Cys	Asp	Ile	Phe
				360					365					370	
Phe	Glu	Glu	Ser	Ser	Ser	Leu	Cys	Arg	Phe	Asp	Gly	Asn	Thr	Leu	Lys
				375				380					385		
Thr	Thr	His	Val	Val	Asn	Leu	Gly	Ser	Asn	Gln	Tyr	Leu	Phe	Ser	Val
							395					400			
Ile	Val	Asp	Pro	Lys	Glu	Met	Pro	Cys	Phe	Cys	Leu	Arg	His	Asp	Val
						410					415				
Asp	Ala	Leu	Leu	Trp	Gln	Pro	His	Ser	Ser	Lys	Gln	Asp	Asp	Met	Trp
420															

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<210> 411
 <211> 99
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 411
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -45 -40 -35
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
 -30 -25 -20
 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
 -15 -10 -5
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
 5 10 15
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 20 25 30
 Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 35 40 45
 Glu Val Leu
 50

<210> 412
 <211> 90
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 412
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20
 Ala Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala
 -15 -10 -5
 Gln Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu
 5 10 15
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
 20 25 30
 Val Tyr Leu Ser Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
 35 40 45
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
 50 55

<210> 413
 <211> 115
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -46...-1

<400> 413
 Met Lys Thr Leu Phe Asn Pro Ala Pro Ala Ile Ala Asp Leu Asp Pro
 -45 -40 -35
 Gln Phe Tyr Thr Leu Ser Asp Val Phe Cys Cys Asn Glu Ser Glu Ala

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-30          -25          -20          -15
Glu Ile Leu Thr Gly Leu Thr Val Gly Ser Ala Ala Asp Ala Gly Glu
Ala Ala Leu Val Leu Leu Lys Arg Gly Cys Gln Val Val Ile Ile Thr
Leu Gly Ala Glu Gly Cys Val Val Leu Ser Gln Thr Glu Pro Glu Pro
Lys His Ile Pro Thr Glu Lys Val Lys Ala Val Asp Thr Thr Cys Arg
Pro Gly Ser Arg Pro Lys Ser Glu Ala Ala Ser Val Lys Lys Gln Lys
His Tyr Lys

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<210> 414
<211> 66
<212> PRT
<213> Homo Sapiens

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<220>
<221> SIGNAL
<222> -19..-1

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<400> 414
Met Lys Pro Leu Leu Val Val Phe Val Phe Leu Phe Leu Trp Asp Pro
Val Leu Ala Gly Ile Asn Ser Leu Ser Ser Glu Met His Lys Lys Cys
Tyr Lys Asn Gly Ile Cys Arg Leu Glu Cys Tyr Glu Ser Glu Met Leu
Val Ala Tyr Cys Met Phe Gln Leu Glu Cys Cys Val Lys Gly Asn Pro
Ala Pro

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<210> 415
<211> 133
<212> PRT
<213> Homo Sapiens

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<220>
<221> SIGNAL
<222> -21..-1

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<400> 415
Met Ser Cys Ser Leu Lys Phe Thr Leu Ile Val Ile Phe Phe Tyr Cys
Trp Leu Ser Ser Ser His Glu Glu Leu Glu Gly Gly Thr Ser Lys Ser
Phe Asp Leu His Thr Val Ile Met Leu Val Ile Ala Gly Gly Ile Leu
Ala Ala Leu Leu Leu Ile Val Val Val Leu Cys Leu Tyr Phe Lys
Ile His Asn Ala Leu Lys Ala Ala Lys Glu Pro Glu Ala Val Ala Val
Lys Asn His Asn Pro Asp Lys Val Trp Trp Ala Lys Asn Ser Gln Ala
Lys Thr Ile Ala Thr Glu Ser Cys Pro Ala Leu Gln Cys Cys Glu Gly
Tyr Arg Met Cys Ala Ser Phe Asp Ser Leu Pro Pro Cys Cys Cys Asp
Ile Asn Glu Gly Leu

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<210> 416
 <211> 140
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -70..-1

<400> 416
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
 -70 -65 -60 -55
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
 -50 -45 -40
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
 -35 -30 -25
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
 -20 -15 -10
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
 -5 1 5 10
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser
 15 20 25
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
 30 35 40
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
 45 50 55
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys
 60 65 70

<210> 417
 <211> 233
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 417
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala

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130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 418
 <211> 83
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 418
 Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu
 -25 -20 -15
 Val Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val
 -10 -5 1
 Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
 5 10 15
 Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
 20 25 30 35
 Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
 40 45 50
 Val Thr Lys

<210> 419
 <211> 215
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 419
 Met Val Ser Ala Leu Arg Gly Ala Pro Leu Ile Arg Val His Ser Ser
 -40 -35 -30
 Pro Val Ser Ser Pro Ser Val Ser Gly Pro Arg Arg Leu Val Ser Cys
 -25 -20 -15 -10
 Leu Ser Ser Gln Ser Ser Ala Leu Ser Gln Ser Gly Gly Gly Ser Thr
 -5 1 5
 Ser Ala Ala Gly Ile Glu Ala Arg Ser Arg Ala Leu Arg Arg Arg Trp
 10 15 20
 Cys Pro Ala Gly Ile Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys
 25 30 35
 Leu Leu Pro Ser Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala
 40 45 50 55
 Arg Val Leu His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu
 60 65 70
 Ala Asp Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala
 75 80 85
 Ala Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
 90 95 100

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Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn
 105 110 115
 Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp
 120 125 130 135
 Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly
 140 145 150
 Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys Asp Leu Thr Glu
 155 160 165
 Trp Val Asp Gly Cys Asp Phe
 170

<210> 420
 <211> 417
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 420
 Met Met Gly Ser Pro Val Ser His Leu Leu Ala Gly Phe Cys Val Trp
 -20 -15 -10 -5
 Val Val Leu Gly Trp Val Gly Gly Ser Val Pro Asn Leu Gly Pro Ala
 1 5 10
 Glu Gln Glu Gln Asn His Tyr Leu Ala Gln Leu Phe Gly Leu Tyr Gly
 15 20 25
 Glu Asn Gly Thr Leu Thr Ala Gly Gly Leu Ala Arg Leu Leu His Ser
 30 35 40
 Leu Gly Leu Gly Arg Val Gln Gly Leu Arg Leu Gly Gln His Gly Pro
 45 50 55 60
 Leu Thr Gly Arg Ala Ala Ser Pro Ala Ala Asp Asn Ser Thr His Arg
 65 70 75
 Pro Gln Asn Pro Glu Leu Ser Val Asp Val Trp Ala Gly Met Pro Leu
 80 85 90
 Gly Pro Ser Gly Trp Gly Asp Leu Glu Glu Ser Lys Ala Pro His Leu
 95 100 105
 Pro Arg Gly Pro Ala Pro Ser Gly Leu Asp Leu Leu His Arg Leu Leu
 110 115 120
 Leu Leu Asp His Ser Leu Ala Asp His Leu Asn Glu Asp Cys Leu Asn
 125 130 135 140
 Gly Ser Gln Leu Leu Val Asn Phe Gly Leu Ser Pro Ala Ala Pro Leu
 145 150 155
 Thr Pro Arg Gln Phe Ala Leu Leu Cys Pro Ala Leu Leu Tyr Gln Ile
 160 165 170
 Asp Ser Arg Val Cys Ile Gly Ala Pro Ala Pro Ala Pro Gly Asp
 175 180 185
 Leu Leu Ser Ala Leu Leu Gln Ser Ala Leu Ala Val Leu Leu Ser
 190 195 200
 Leu Pro Ser Pro Leu Ser Leu Leu Leu Arg Leu Leu Gly Pro Arg
 205 210 215 220
 Leu Leu Arg Pro Leu Leu Gly Phe Leu Gly Ala Leu Ala Val Gly Thr
 225 230 235
 Leu Cys Gly Asp Ala Leu Leu His Leu Leu Pro His Ala Gln Glu Gly
 240 245 250
 Arg His Ala Gly Pro Gly Gly Leu Pro Glu Lys Asp Leu Gly Pro Gly
 255 260 265
 Leu Ser Val Leu Gly Gly Leu Phe Leu Leu Phe Val Leu Glu Asn Met
 270 275 280
 Leu Gly Leu Leu Arg His Arg Gly Leu Arg Pro Arg Cys Cys Arg Arg
 285 290 295 300

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Ile Cys Arg Leu Arg Tyr Gly Asn Pro Asp Ala Lys Pro Thr Lys Ala
 15 20 25
 Asp Ile Thr Leu Ser Gly Cys Ala Ser Gly Leu Val Arg Val Phe Leu
 30 35 40
 Thr Ser Pro Thr Glu Val Ala Lys Val Arg Leu Gln Thr Gln Thr Gln
 45 50 55 60
 Ala Gln Lys Gln Gln Arg Leu Leu Ser Ala Ser Gly Pro Leu Ala Val
 65 70 75
 Pro Pro Met Cys Pro Val Pro Pro Ala Cys Pro Glu Pro Lys Tyr Arg
 80 85 90
 Gly Pro Leu His Cys Leu Ala Thr Val Ala Arg Glu Glu Gly Leu Cys
 95 100 105
 Gly Leu Tyr Lys Gly Ser Ser Ala Leu Val Leu Arg Asp Gly His Ser
 110 115 120
 Phe Ala Thr Tyr Phe Leu Ser Tyr Ala Val Leu Cys Glu Trp Leu Ser
 125 130 135 140
 Pro Ala Gly His Ser Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly
 145 150 155
 Gly Cys Ala Gly Val Leu Ala Trp Ala Val Ala Thr Pro Met Asp Val
 160 165 170
 Ile Lys Ser Arg Leu Gln Ala Asp Gly Gln Gly Gln Arg Tyr Arg
 175 180 185
 Gly Leu Leu His Cys Met Val Thr Ser Val Arg Glu Glu Gly Pro Arg
 190 195 200
 Val Leu Phe Lys Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val
 205 210 215 220
 Asn Met Val Val Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg
 225 230 235
 Gly Leu Leu Thr
 240

<210> 424

<211> 114

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -49..-1

<400> 424

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35
 Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
 -30 -25 -20
 Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
 -15 -10 -5
 Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
 1 5 10 15
 Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met
 20 25 30
 Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly
 35 40 45
 Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr
 50 55 60
 Ser Asp
 65

<210> 425

<211> 382

<212> PRT

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<220>
 <221> SIGNAL
 <222> -197...-1

<220>
 <221> UNSURE
 <222> -88
 <223> Xaa = Ala,Asp,Gly,Val

<220>
 <221> UNSURE
 <222> -109
 <223> Xaa = Asp,Glu

<400> 426
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 -195 -190 -185
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 -180 -175 -170
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 -165 -160 -155 -150
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Ala Lys Ile Leu
 -145 -140 -135
 Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala
 -130 -125 -120
 Met Val Leu Asp Gln Ile Glu Ala Xaa Leu Glu Lys Arg Lys Leu Glu
 -115 -110 -105
 Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Xaa Phe Thr
 -100 -95 -90
 Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu
 -85 -80 -75 -70
 Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln
 -65 -60 -55
 Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu
 -50 -45 -40
 Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe
 -35 -30 -25
 Arg Leu Val Lys Arg Lys Pro Ser Phe Phe Gly Ala Ser Phe Leu
 -20 -15 -10
 Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys
 -5 1 5 10
 Lys Lys Tyr Ile
 15

<210> 427
 <211> 287
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 427
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Leu Ser Ala Arg Ser Pro Gly Lys His

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140 145 150
 Ile His Phe Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro
 155 160 165
 Glu Met Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile
 170 175 180
 Asp Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser
 185 190 195
 Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala Ala
 200 205 210 215
 Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly Asp Thr
 220 225 230
 Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly Ser Ser Phe
 235 240 245
 Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly Glu Ser Arg Leu
 250 255 260
 Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys Trp Leu Trp Glu Pro
 265 270 275
 Thr Ala Pro Glu Lys Gly Lys Glu
 280 285

<210> 429

<211> 226

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 429

Met Glu Thr Val Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile Phe
 -25 -20 -15
 Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg Tyr Cys
 -10 -5 1
 Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro Ile Val Asp
 5 10 15
 Leu Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser Glu Leu Glu Leu
 20 25 30 35
 Asp Asp Val Val Ile Thr Asn Pro His Ile Glu Ala Ile Leu Glu Asn
 40 45 50
 Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu Met Ser His Cys Ile Ala
 55 60 65
 Ile Leu Lys Ile Cys His Thr Leu Thr Glu Lys Leu Val Ala Met Thr
 70 75 80
 Met Gly Ser Gly Ala Lys Met Lys Thr Ser Ala Ser Val Ser Asp Ile
 85 90 95
 Ile Val Val Ala Lys Arg Ile Ser Pro Arg Val Asp Asp Val Val Lys
 100 105 110 115
 Ser Met Tyr Pro Pro Leu Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr
 120 125 130
 Ala Leu Leu Leu Ser Val Ser His Leu Val Leu Val Thr Arg Asn Ala
 135 140 145
 Cys His Leu Thr Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala
 150 155 160
 Ala Glu Glu His Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu
 165 170 175
 Pro Asp Lys Gly Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser
 180 185 190 195
 Ala Ile

<210> 430

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<211> 406
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 430
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
 -35 -30 -25 -20
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5
 Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
 15 20 25
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 30 35 40 45
 Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp
 50 55 60
 Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro
 65 70 75
 Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu
 80 85 90
 Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly
 95 100 105
 Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile
 110 115 120 125
 Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His
 130 135 140
 Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe
 145 150 155
 Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg
 160 165 170
 Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly
 175 180 185
 Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr
 190 195 200 205
 Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile
 210 215 220
 Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp
 225 230 235
 Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser
 240 245 250
 Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro
 255 260 265
 Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg
 270 275 280 285
 Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe
 290 295 300
 Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp
 305 310 315
 Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro
 320 325 330
 Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met
 335 340 345
 Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser
 350 355 360 365
 Glu Tyr Gln Ser Ile Asn
 370

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<210> 431
 <211> 120
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -57..-1

<400> 431
 Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
 -55 -50 -45
 Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 -40 -35 -30
 Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 -25 -20 -15 -10
 Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 -5 1 5
 Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 10 15 20
 Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 25 30 35
 Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
 40 45 50 55
 Asp Asp Ile Pro Asp Phe Asp Asp
 60

<210> 432
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 432
 Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu
 -35 -30 -25
 Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr
 -20 -15 -10 -5
 Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly
 1 5 10
 Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro
 15 20 25
 Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu
 30 35 40
 Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro
 45 50 55 60
 Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr
 65 70 75
 Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp
 80 85 90
 Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro
 95 100 105
 Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly
 110 115 120
 Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser
 125 130 135 140
 Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr

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145 150 155
 Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly
 160 165 170
 Gly Ser

 <210> 433
 <211> 251
 <212> PRT
 <213> Homo Sapiens

 <220>
 <221> SIGNAL
 <222> -243...-1

 <400> 433
 Met Ala His Arg Leu Gln Ile Arg Leu Leu Thr Trp Asp Val Lys Asp
 -240 -235 -230
 Thr Leu Leu Arg Leu Arg His Pro Leu Gly Glu Ala Tyr Ala Thr Lys
 -225 -220 -215
 Ala Arg Ala His Gly Leu Glu Val Glu Pro Ser Ala Leu Glu Gln Gly
 -210 -205 -200
 Phe Arg Gln Ala Tyr Arg Ala Gln Ser His Ser Phe Pro Asn Tyr Gly
 -195 -190 -185 -180
 Leu Ser His Gly Leu Thr Ser Arg Gln Trp Trp Leu Asp Val Val Leu
 -175 -170 -165
 Gln Thr Phe His Leu Ala Gly Val Gln Asp Ala Gln Ala Val Ala Pro
 -160 -155 -150
 Ile Ala Glu Gln Leu Tyr Lys Asp Phe Ser His Pro Cys Thr Trp Gln
 -145 -140 -135
 Val Leu Asp Gly Ala Glu Asp Thr Leu Arg Glu Cys Arg Thr Arg Gly
 -130 -125 -120
 Leu Arg Leu Ala Val Ile Ser Asn Phe Asp Arg Arg Leu Glu Gly Ile
 -115 -110 -105 -100
 Leu Glu Gly Leu Gly Leu Arg Glu His Phe Asp Phe Val Leu Thr Ser
 -95 -90 -85
 Glu Ala Ala Gly Trp Pro Lys Pro Asp Pro Arg Ile Phe Gln Glu Ala
 -80 -75 -70
 Leu Arg Leu Ala His Met Glu Pro Val Val Ala Ala His Val Gly Asp
 -65 -60 -55
 Asn Tyr Leu Cys Asp Tyr Gln Gly Pro Arg Ala Val Gly Met His Ser
 -50 -45 -40
 Phe Leu Val Val Gly Pro Gln Ala Leu Asp Pro Val Val Arg Asp Ser
 -35 -30 -25 -20
 Val Pro Lys Glu His Ile Leu Pro Ser Leu Ala His Leu Leu Pro Ala
 -15 -10 -5
 Leu Asp Cys Leu Glu Gly Ser Thr Pro Gly Leu
 1 5

 <210> 434
 <211> 126
 <212> PRT
 <213> Homo Sapiens

 <220>
 <221> SIGNAL
 <222> -24...-1

 <400> 434
 Met Asp Lys Ser Leu Leu Leu Glu Leu Pro Ile Leu Leu Cys Cys Phe
 -20 -15 -10
 Arg Ala Leu Ser Gly Ser Leu Ser Met Arg Asn Asp Ala Val Asn Glu

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Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
 40 45 50
 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
 55 60 65
 Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Gly Tyr
 70 75 80
 Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
 85 90 95 100
 Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
 105 110 115
 Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
 120 125 130
 Ser Tyr Pro Leu Thr Thr Ile Ala Thr Leu Thr Ser Ala Ser Trp Cys
 135 140 145
 Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
 150 155 160
 Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
 165 170 175 180
 Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
 185 190

<210> 437
 <211> 352
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 437
 Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 -20 -15 -10
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 -5 1 5
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 10 15 20 25
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
 30 35 40
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 45 50 55
 Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
 60 65 70
 Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
 75 80 85
 Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
 90 95 100 105
 Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
 110 115 120
 Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
 125 130 135
 Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
 140 145 150
 Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
 155 160 165
 Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
 170 175 180 185
 Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
 190 195 200
 Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
 205 210 215

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Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
 220 225 230
 Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
 235 240 245
 Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
 250 255 260 265
 Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
 270 275 280
 Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
 285 290 295
 Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 300 305 310
 Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 315 320 325

<210> 438

<211> 385

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -184...-1

<400> 438

Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val
 -180 -175 -170
 Tyr Phe Ile Gly Ala His Lys Ile Pro Asn Ala Asn Met Asn Glu Asp
 -165 -160 -155
 Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
 -150 -145 -140
 Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp
 -135 -130 -125
 Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn
 -120 -115 -110 -105
 Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His
 -100 -95 -90
 Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys
 -85 -80 -75
 Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly
 -70 -65 -60
 Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys
 -55 -50 -45
 Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro
 -40 -35 -30 -25
 Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu
 -20 -15 -10
 Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile
 -5 1 5
 Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr
 10 15 20
 Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Tyr Pro Ser Glu
 25 30 35 40
 Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn
 45 50 55
 His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile
 60 65 70
 Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala
 75 80 85
 Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp
 90 95 100

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Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp
 105 110 115 120
 Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln
 125 130 135
 Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr
 140 145 150
 Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met
 155 160 165
 Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln
 170 175 180
 Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser
 185 190 195 200
 Leu

<210> 439
 <211> 69
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 439
 Met Asn Leu Met Trp Thr Leu Leu Leu Phe Leu Leu Leu Asp Val Thr
 -20 -15 -10
 Val Phe Ile Pro Ala Leu Pro Phe Ser Thr Arg His Ile Asp Asn Pro
 -5 1 5
 Arg Ser Trp Val Pro Arg Gly His His Arg Tyr Cys Asp Val Met Met
 10 15 20 25
 Arg Arg Arg Trp Leu Ile Tyr Arg Gly Lys Cys Glu Gln Ile His Thr
 30 35 40
 Phe Ile His Arg Ile
 45

<210> 440
 <211> 108
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 440
 Met Asn Lys Thr His Lys Asp Cys Ser Ser Pro Gln Tyr Ser Ile Tyr
 -45 -40 -35
 Asn Ile Leu Asn Glu Leu Pro Thr Arg Pro Ile Ile Leu Ser Cys Ser
 -30 -25 -20
 Gln Ile Ser Cys Leu Leu Leu Val Ser Thr Trp Ser Ala Asp Leu Met
 -15 -10 -5
 Ser Tyr Arg Pro Val Thr Lys Pro Ser Gln Arg Cys Thr Ser Pro Ala
 1 5 10 15
 Gln Ser Met Thr Val Asn Leu Thr Lys Asp Val Gly Phe Tyr Glu Asp
 20 25 30
 Thr Gln Ser Ile Arg Ile Thr Leu Ser Glu Ile Ser Gln Ala Gln Lys
 35 40 45
 Asp Thr Tyr Phe Ile Ile Ser Cys Ile Cys Gly Ile
 50 55

<210> 441

Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
 -85 -80 -75
 Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
 -70 -65 -60
 Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
 -55 -50 -45
 Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
 -40 -35 -30 -25
 Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
 -20 -15 -10
 Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
 -5 1 5
 Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
 10 15 20
 Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
 25 30 35 40
 Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
 45 50 55
 Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
 60 65 70
 Leu Pro Gly Glu Met Glu Lys Gln Lys
 75 80

<210> 444
 <211> 82
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<400> 444
 Met Lys Ala Val Trp His Phe Cys Leu Ser His Lys Ser Ser Leu Val
 -55 -50 -45
 Ile Val Leu Lys Thr Ala Gly Trp Ile Pro Gln Ala Gly Thr Leu Ile
 -40 -35 -30 -25
 Pro Gly Ser Arg Glu Glu Ser Arg Ser Asp Ser Gln Met Ile Met Leu
 -20 -15 -10
 Val Cys Phe Asn Leu Ser Arg Gly Cys Leu Lys Lys Val Phe Ile Ile
 -5 1 5
 Ser Val Leu Pro Asp Pro Glu Thr Ile Leu Leu Gly Lys Thr Val Gly
 10 15 20
 Ile Ala
 25

<210> 445
 <211> 251
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 445
 Met Asp Lys Val Gln Ser Gly Phe Leu Ile Leu Phe Leu Phe Leu Met
 -20 -15 -10 -5
 Glu Cys Gln Leu His Leu Cys Leu Pro Tyr Ala Asp Gly Leu His Pro
 1 5 10
 Thr Gly Asn Ile Thr Gly Leu Pro Gly Ser Phe Asn His Trp Phe Tyr

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      15          20          25
Val Thr Gln Gly Glu Leu Lys Ser Cys Phe Arg Gly Asp Lys Lys Lys
  30          35          40
Val Ile Thr Phe His Arg Lys Lys Phe Ser Phe Gln Gly Ser Lys Arg
  45          50          55
Ser Gln Pro Pro Arg Asn Ile Thr Lys Glu Pro Lys Val Phe Phe His
      65          70          75
Lys Thr Gln Leu Pro Gly Ile Gln Gly Ala Ser Arg Ser Thr Ala
      80          85          90
Ala Ser Pro Thr Asn Pro Met Lys Phe Leu Arg Asn Lys Ala Ile Ile
      95          100          105
Arg His Arg Pro Ala Leu Val Lys Val Ile Leu Ile Ser Ser Val Ala
     110          115          120
Phe Ser Ile Ala Leu Ile Cys Gly Met Ala Ile Ser Tyr Met Ile Tyr
     125          130          135
Arg Leu Ala Gln Ala Glu Glu Arg Gln Gln Leu Glu Ser Leu Tyr Lys
      145          150          155
Asn Leu Arg Ile Pro Leu Leu Gly Asp Glu Glu Glu Gly Ser Glu Asp
     160          165          170
Glu Gly Glu Ser Thr His Leu Leu Pro Lys Asn Glu Asn Glu Leu Glu
     175          180          185
Lys Phe Ile His Ser Val Ile Ile Ser Lys Arg Ser Lys Asn Ile Lys
     190          195          200
Lys Lys Leu Lys Glu Glu Gln Asn Ser Val Thr Glu Asn Lys Thr Lys
     205          210          215
Asn Ala Ser His Asn Gly Lys Met Glu Asp Leu
      225          230

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<210> 446

<211> 305

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 446

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Met Ser Phe Leu Arg Ile Thr Pro Ser Thr His Ser Ser Val Ser Ser
      -30          -25          -20
Gly Leu Leu Arg Leu Ser Ile Phe Leu Leu Ser Phe Pro Asp Ser
      -15          -10          -5
Asn Gly Lys Ala Ile Trp Thr Ala His Leu Asn Ile Thr Phe Gln Val
      1          5          10
Gly Asn Glu Ile Thr Ser Glu Leu Gly Glu Ser Gly Val Phe Gly Asn
     15          20          25
His Ser Pro Leu Glu Arg Val Ser Gly Val Val Ala Leu Pro Glu Glu
      35          40          45
Trp Asn Gln Asn Ala Cys His Pro Leu Thr Asn Phe Ser Arg Pro Lys
      50          55          60
Gln Ala Asp Ser Trp Leu Ala Leu Ile Glu Arg Gly Gly Cys Thr Phe
      65          70          75
Thr His Lys Ile Asn Val Ala Ala Glu Lys Gly Ala Asn Gly Val Ile
      80          85          90
Ile Tyr Asn Tyr Gln Gly Thr Gly Ser Lys Val Phe Pro Met Ser His
      95          100          105
Gln Gly Thr Glu Asn Ile Val Ala Val Met Ile Ser Asn Leu Lys Gly
      115          120          125
Met Glu Ile Leu His Ser Ile Gln Lys Gly Val Tyr Val Thr Val Ile
      130          135          140
Ile Glu Val Gly Arg Met His Met Gln Trp Val Ser His Tyr Ile Met

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145 150 155
 Tyr Leu Phe Thr Phe Leu Ala Ala Thr Ile Ala Tyr Phe Tyr Leu Asp
 160 165 170
 Cys Val Trp Arg Leu Thr Pro Arg Val Pro Asn Ser Phe Thr Arg Arg
 175 180 185 190
 Arg Ser Gln Ile Lys Thr Asp Val Lys Lys Ala Ile Asp Gln Leu Gln
 195 200 205
 Leu Arg Val Leu Lys Glu Gly Asp Glu Glu Leu Asp Leu Asn Glu Asp
 210 215 220
 Asn Cys Val Val Cys Phe Asp Thr Tyr Lys Pro Gln Asp Val Val Arg
 225 230 235
 Ile Leu Thr Cys Lys His Phe Phe His Lys Ala Cys Ile Asp Pro Trp
 240 245 250
 Leu Leu Ala His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys
 255 260 265 270
 Thr

<210> 447
 <211> 61
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 447
 Met Thr Asp Leu Asp Leu Met Ile Asn Phe Thr Phe Pro Ile Gln Trp
 -40 -35 -30
 Val Asn Gln Asn Arg Met Ala Tyr Tyr Ser Leu Lys Pro Leu Leu Pro
 -25 -20 -15
 Cys Ser Ser Val Leu Thr Cys Gly Gln Ala Ser Gln Asp Leu Leu Thr
 -10 -5 1 5
 Ser Ala Thr Ser Val Thr Gly Met Glu Lys Ile Glu Ala
 10 15

<210> 448
 <211> 113
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 448
 Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
 -15 -10 -5 1
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
 5 10 15
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
 20 25 30
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
 35 40 45
 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
 50 55 60 65
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
 70 75 80
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
 85 90 95
 Thr

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<210> 449
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 449
 Met Glu Arg Pro Arg Ser Pro Gln Cys Ser Ala Pro Ala Ser Ala Ser
 -30 -25 -20 -15
 Ala Ser Val Thr Leu Ala Gln Leu Leu Gln Leu Val Gln Gln Gly Gln
 -10 -5 1
 Glu Leu Pro Gly Leu Glu Lys Arg His Ile Ala Ala Ile His Gly Glu
 5 10 15
 Pro Thr Ala Ser Arg Leu Pro Arg Arg Pro Lys Pro Trp Glu Ala Ala
 20 25 30
 Ala Leu Ala Glu Ser Leu Pro Pro Pro Thr Leu Arg Ile Gly Thr Ala
 35 40 45 50
 Pro Ala Glu Pro Gly Leu Val Glu Ala Ala Thr Ala Pro Ser Ser Trp
 55 60 65
 His Thr Val Gly Pro
 70

<210> 450
 <211> 97
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -90...-1

<220>
 <221> UNSURE
 <222> -39
 <223> Xaa = His,Gln

<400> 450
 Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
 -90 -85 -80 -75
 Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Pro Met Gly
 -70 -65 -60
 Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Leu Gln
 -55 -50 -45
 Tyr Gly Trp Xaa Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
 -40 -35 -30
 Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
 -25 -20 -15
 Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp Asp Met Leu
 -10 -5 1 5
 Thr

<210> 451
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<220>

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<221> SIGNAL
<222> -25..-1

<400> 451
Met Val Asp Arg Glu Leu Ala Asp Ile His Glu Asp Ala Lys Thr Cys
-25 -20 -15 -10
Leu Val Leu Cys Ser Arg Val Leu Ser Val Ile Ser Val Lys Glu Ile
-5 1 5
Lys Thr Gln Leu Ser Leu Gly Arg His Pro Ile Ile Ser Asn Trp Phe
10 15 20
Asp Tyr Ile Pro Ser Thr Arg Tyr Lys Asp Pro Cys Glu Leu Leu His
25 30 35
Leu Cys Arg Leu Thr Ile Arg Asn Gln Leu Leu Thr Asn Asn Met Leu
40 45 50 55
Pro Asp Gly Ile Phe Ser Leu Leu Ile Pro Ala Arg Leu Gln Asn Tyr
60 65 70
Leu Asn Leu Glu Ile
75

<210> 452
<211> 132
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> -101..-1

<400> 452
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
-100 -95 -90
Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val Thr Ser
-85 -80 -75 -70
Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr Ile Val Ile
-65 -60 -55
Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile Leu Leu Tyr Val
-50 -45 -40
Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe Trp Pro Leu Leu Asp
-35 -30 -25
Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met Leu Ile Val Ser Val
-20 -15 -10
Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val
-5 1 5 10
Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile
15 20 25
Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro
30 35 40
Val His Glu Lys Lys Glu Val Leu
45 50

<210> 453
<211> 209
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> -86..-1

<400> 453
Met Leu Ser Pro Thr Phe Val Leu Trp Asp Val Gly Tyr Pro Leu Tyr

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-85 -80 -75
 Thr Tyr Gly Ser Ile Cys Ile Ile Ala Leu Ile Ile Trp Gln Val Lys
 -70 -65 -60 -55
 Lys Ser Cys Gln Lys Leu Ser Leu Val Pro Asn Arg Ser Cys Cys Arg
 -50 -45 -40
 Cys His Arg Arg Val Gln Gln Lys Ser Gly Asp Arg Thr Ser Arg Ala
 -35 -30 -25
 Arg Arg Thr Ser Gln Glu Glu Ala Glu Lys Leu Trp Lys Leu Leu Phe
 -20 -15 -10
 Leu Met Lys Ser Gln Gly Trp Ile Pro Gln Glu Gly Ser Val Arg Arg
 -5 1 5 10
 Ile Leu Cys Ala Asp Pro Cys Cys Gln Ile Cys Asn Val Met Ala Leu
 15 20 25
 Glu Ile Lys Gln Leu Leu Ala Glu Ala Pro Glu Val Gly Leu Asp Asn
 30 35 40
 Lys Met Lys Leu Phe Leu His Trp Ile Asn Pro Glu Met Lys Asp Arg
 45 50 55
 Arg His Glu Glu Ser Ile Leu Leu Ser Lys Ala Glu Thr Val Thr Gln
 60 65 70
 Asp Arg Thr Lys Asn Ile Glu Lys Ser Pro Thr Val Thr Lys Asp His
 75 80 85 90
 Val Trp Gly Ala Thr Thr Gln Lys Thr Thr Glu Asp Pro Glu Ala Gln
 95 100 105
 Pro Pro Ser Thr Glu Glu Gly Leu Ile Phe Cys Asp Ala Pro Ser
 110 115 120
 Ala

<210> 454
 <211> 89
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 454
 Met Gly Ser Cys Ser Gly Arg Cys Ala Leu Val Val Leu Cys Ala Phe
 -20 -15 -10
 Gln Leu Val Ala Ala Leu Glu Arg Gln Val Phe Asp Phe Leu Gly Tyr
 -5 1 5 10
 Gln Trp Ala Pro Ile Leu Ala Asn Phe Val His Ile Ile Ile Val Ile
 15 20 25
 Leu Gly Leu Phe Gly Thr Ile Gln Tyr Arg Leu Arg Tyr Val Met Cys
 30 35 40
 Thr Arg Cys Gly Gln Pro Ser Gly Ser Pro Gly Thr Ser Ser Ser Ser
 45 50 55
 Ala Ser Thr Trp Lys Ser Val Ala Ser
 60 65

<210> 455
 <211> 66
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 455
 Met Lys Pro Leu Leu Val Val Phe Val Phe Leu Phe Leu Trp Asp Pro

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<220>
 <221> SIGNAL
 <222> -20...-1

<400> 458
 Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
 -20 -15 -10 -5
 Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
 1 5 10
 Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
 15 20 25
 Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
 30 35 40
 Gly Arg Lys
 45

<210> 459
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 459
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala
 175

<210> 460
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

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<400> 460

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25 -20 -15 -10
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
-5 1 5
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Gln Gln Asp
10 15 20
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa
25 30 35
Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe
40 45 50 55
Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp
60 65 70
Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr
75 80 85
Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser
90 95 100
Lys Gln Lys Ser Ile Glu Glu
105 110

<210> 461

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -70...-1

<400> 461

Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe
-70 -65 -60 -55
Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val
-50 -45 -40
Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn
-35 -30 -25
Val Val Ser Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu
-20 -15 -10
Ala Pro Phe Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val
-5 1 5 10
Gly Leu Gly Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val
15 20 25
Glu Asn Thr Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr
30 35 40
Ala Thr Ser Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp
45 50 55
Ile Thr Pro Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr
60 65 70
Lys Met Ile Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr
75 80 85 90
Val Gly Arg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val
95 100 105
Glu Thr Leu Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val
110 115 120
Ala Arg Asn Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp
125 130 135
Val Val Asn Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Glu Lys
140 145 150
Ser Glu Ser Ala Glu Leu Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu
155 160 165 170

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Asn Leu Asn Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
 175 180 185

<210> 462
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 462
 Met Pro Gly Thr Glu Val Leu Glu Gly Ala Thr Asp Gly Leu Ala Ala
 -45 -40 -35
 Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu Gly Gly Ser Val Ile Ser
 -30 -25 -20
 Met Ile Val Leu Leu Ile Cys Val Val Cys Leu Tyr Ile Val Cys Arg
 -15 -10 -5
 Cys Gly Ser His Leu Trp Arg Glu Ser His His
 1 5 10

<210> 463
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln Leu
 1 5 10 15
 Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly Asp Gly
 20 25 30
 Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala
 35 40 45
 Thr Lys Ser Asp Asp Thr Val Val Ala Ile Pro Tyr Gly Ser Arg His
 50 55 60
 Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu Tyr Leu Glu Thr Lys
 65 70 75 80
 Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr
 85 90 95
 Phe Leu Val Asp Asn Ser Ser Val Asp Phe Gln Lys Phe Pro Asp Lys
 100 105 110
 Glu Ile Leu Arg Met Ala Gly Pro Leu Thr Ala Asp Phe Ile Val Lys
 115 120 125
 Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr
 130 135 140
 Gln Pro Ile Ile His Arg Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser
 145 150 155 160
 Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp
 165 170 175
 Leu Arg Ser Asn
 180

<210> 464
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

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<211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 467
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 -40 -35 -30
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
 -25 -20 -15
 Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
 -10 -5 1 5
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
 10 15 20
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
 25 30 35
 Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
 40 45 50
 Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
 55 60 65 70
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 75 80 85
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 90 95 100
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
 105 110 115
 Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Val Leu Ala
 120 125 130
 Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 135 140 145 150
 Gly Leu Lys Arg Lys Ala Glu
 155

<210> 468
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 468
 Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 1 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 469
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 469
 Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25

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Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 470
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 470
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140
 Gln Val Ser Gln Gln Glu Glu Leu Lys
 145 150

<210> 471
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 471
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 472
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
 1 5 10 15
 Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
 20 25 30
 Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly

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35 40 45
 Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln Ala
 50 55 60
 Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp Lys
 65 70 75 80
 Leu Ala Glu Glu His Ser Ser
 85

<210> 473
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -85..-1

<400> 473
 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
 -85 -80 -75 -70
 Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
 -65 -60 -55
 Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
 -50 -45 -40
 Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu Thr
 -35 -30 -25
 Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu Ala
 -20 -15 -10
 Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu Ala
 -5 1 5 10
 Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val Tyr
 15 20 25
 Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu Glu
 30 35 40
 Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser Ala
 45 50 55
 Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val Leu
 60 65 70 75
 Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu Gln
 80 85 90
 Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu Lys
 95 100 105
 Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Thr Ser Gln
 110 115 120
 Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly Thr
 125 130 135
 Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu Arg
 140 145 150 155
 Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn
 160 165

<210> 474
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
 1 5 10 15
 His Ile Asn Ile Ser Phe His Arg
 20

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<210> 475
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
 1 5 10 15
 His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys Arg Arg
 20 25 30
 Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val Pro Gly Lys
 35 40 45
 His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser Cys Phe Asp Leu
 50 55 60
 Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val Pro Thr Ile Phe
 65 70 75 80
 Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
 85 90 95
 Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
 100 105 110
 Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
 115 120 125
 Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
 130 135 140
 Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg
 145 150 155 160
 Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
 165 170 175
 Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
 180 185 190
 Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
 195 200 205
 Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
 210 215 220
 Ser Thr Phe Ile
 225

<210> 476
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 476
 Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Ala Lys Leu Arg Gln
 65

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<210> 477
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
 1 5 10 15
 Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
 20 25 30
 Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
 35 40

<210> 478
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58..-1

<400> 478
 Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
 -55 -50 -45
 Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
 -40 -35 -30
 Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
 -25 -20 -15
 His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Leu Lys Val Lys
 -10 -5 1 5
 Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro
 10 15 20
 Cys Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala
 25 30 35
 Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His
 40 45 50
 Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu
 55 60 65 70
 Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu
 75 80 85
 Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr
 90 95 100
 Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg
 105 110 115
 Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp
 120 125 130
 Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys
 135 140 145 150
 Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg
 155 160 165
 Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
 170 175 180
 Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
 185 190 195
 Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
 200 205 210
 Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met
 215 220 225 230
 Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
 235 240 245

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Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
250 255

<210> 479
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -80...-1

<400> 479
Met Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe
-80 -75 -70 -65
Pro Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg
-60 -55 -50
Thr Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala
-45 -40 -35
Leu Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr
-30 -25 -20
Gln Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly
-15 -10 -5
Ser Thr Gln Pro Val Pro Leu Cys Ser
1 5

<210> 480
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 480
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15
Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
35 40 45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
50 55 60 65
Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu Thr Ser Glu Pro Leu
70 75 80
Thr Ala

<210> 481
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36...-1

<400> 481
Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn

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290 295 300
 His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Cys
 305 310 315 320
 His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp Arg
 325 330 335

<210> 483
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 483
 Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu
 -45 -40 -35
 Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser
 -30 -25 -20
 Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile
 -15 -10 -5 1
 Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu
 5 10 15
 Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile
 20 25 30
 Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly Glu
 35 40 45
 Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu Gln Phe
 50 55 60 65
 Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn Arg Arg Glu
 70 75 80
 Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
 85 90

<210> 484
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -73...-1

<400> 484
 Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 -70 -65 -60
 Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
 -55 -50 -45
 Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
 -40 -35 -30
 Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
 -25 -20 -15 -10
 Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
 -5 1 5
 Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
 10 15 20
 Pro Leu Gly Thr Pro
 25

<210> 485

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      1      5      10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15      20      25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30      35      40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45      50      55      60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
      65      70      75
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
      80      85      90
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile
      95      100      105
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val
      110      115      120
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser
      125      130      135      140
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly
      145      150      155
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp
      160      165      170
Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
      175      180      185
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
      190      195      200
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
      205      210      215      220
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
      225      230      235
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
      240      245      250
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
      255      260      265
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
      270      275      280

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<210> 487

<211> 390

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...1

<400> 487

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65      -60      -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50      -45      -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35      -30      -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20      -15      -10      -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
      1      5      10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15      20      25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30      35      40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys

```

45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Phe Glu
 110 115 120
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
 175 180 185
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
 190 195 200
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
 205 210 215 220
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
 225 230 235
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
 240 245 250
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
 255 260 265
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
 270 275 280
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
 285 290 295 300
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
 305 310 315
 Glu Gly Thr Ser Ala Ser
 320

<210> 488

<211> 190

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -82...-1

<400> 488

Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu

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35 40 45
 Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
 65 70 75
 Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105

<210> 489
 <211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -232..-1

<400> 489
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
 -230 -225 -220
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 -215 -210 -205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 -200 -195 -190
 Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
 -180 -175 -170
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 -165 -160 -155
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 -150 -145 -140
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 -135 -130 -125
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 -120 -115 -110
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
 -100 -95 -90
 Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
 -85 -80 -75
 Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
 -70 -65 -60
 Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
 -55 -50 -45
 Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
 -40 -35 -30
 Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
 -20 -15 -10
 Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
 -5 1 5
 Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
 10 15 20
 Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40
 Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys
 45 50

<210> 490
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 490

```
Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
1      5      10      15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20      25      30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35      40      45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50      55      60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65      70      75      80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85      90      95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
100      105      110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
115      120      125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
130      135      140
His His Cys Val Arg Glu Gly Ser Gly
145      150
```

<210> 491

<211> 49

<212> PRT

<213> Homo sapiens

<400> 491

```
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Lys Ile Trp Leu Leu
1      5      10      15
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
20      25      30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
35      40      45
Cys
```

<210> 492

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 492

```
Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
      -20      -15      -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
      -5      1      5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
10      15      20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25      30      35      40
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
45      50      55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
60      65      70
Pro Pro Arg
75
```

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<210> 493
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 493
 Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
 -35 -30 -25
 Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
 -20 -15 -10
 Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
 -5 1 5 10
 Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
 15 20 25
 Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
 30 35 40
 Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
 45 50 55

<210> 494
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 494
 Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
 -20 -15 -10
 Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
 -5 1 5
 Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
 10 15 20 25
 Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
 30 35 40
 Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
 45 50 55
 Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
 60 65 70
 Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
 75 80 85
 Gln Lys Leu Ala Lys Lys Met Phe Phe
 90 95

<210> 495
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 495
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 1 5 10 15
 Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 20 25 30

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Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
 35 40 45
 Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
 50 55

<210> 496
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 496
 Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
 -10 -5 1
 Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
 5 10 15
 Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
 20 25 30
 Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
 35 40 45 50
 Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
 55 60 65
 Tyr Arg Ile Cys Asp Leu
 70

<210> 497
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 497
 Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
 -55 -50 -45
 Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
 -40 -35 -30
 Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
 -25 -20 -15
 Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
 -10 -5 1 5
 Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
 10 15 20
 Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
 25 30 35
 Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
 40 45 50
 Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
 55 60 65 70
 Ser Leu Gln Asp Ala Leu Leu Leu Leu Met Gly Leu Gly Pro Leu
 75 80 85
 Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Gly Leu Ala Phe Cys
 90 95 100
 Leu His Pro Trp Ala
 105

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<210> 498
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 498
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 499
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 499
 Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
 -20 -15 -10
 Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
 -5 1 5 10
 Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys
 15 20 25
 Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe
 30 35 40
 Cys Gly Asn Ile Cys Met Ser Ile Leu
 45 50

<210> 500
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 500
 Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser
 1 5 10 15
 Ile Ser Lys Arg Glu Gln Leu Glu Gln Val Pro Glu Asn Tyr Phe
 20 25 30
 Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr
 35 40 45
 Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp
 50 55 60
 Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu
 65 70 75 80
 Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
 85 90 95
 Gly Tyr

Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val Asn His Leu Lys Ala
 65 70 75 80
 Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu Pro Thr Thr Val Glu
 85 90 95
 Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn Thr Leu Asn Ser Val
 100 105 110
 His Leu Ala Val Glu Ala Leu Gln Lys Thr Val Asp Glu His Lys Lys
 115 120 125
 Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln His Phe Leu Lys Glu
 130 135 140
 Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro Ser Ala Thr Ser Glu
 145 150 155 160
 Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys Gln Met Gly Asp Arg
 165 170 175
 Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln Val Thr Asn Arg Thr
 180 185 190
 Asp Thr Val Lys Ile Gln Lys Lys Lys
 195 200

<210> 506

<211> 379

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 506

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 -35 -30 -25
 Gly Ala Gln Lys Ala Ala Leu Val Leu Ser Ala Cys Leu Val Thr
 -20 -15 -10
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 -5 1 5 10
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 15 20 25
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 30 35 40
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 45 50 55
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
 60 65 70 75
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
 80 85 90
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
 95 100 105
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
 110 115 120
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
 125 130 135
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
 140 145 150 155
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
 160 165 170
 Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
 175 180 185
 Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
 190 195 200
 Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
 205 210 215

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Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
 220 225 230 235
 Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
 240 245 250
 Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
 255 260 265
 Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
 270 275 280
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 285 290 295
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 300 305 310 315
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Leu Ser Gly Met
 320 325 330
 Gly Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 335 340

<210> 507

<211> 112

<212> PRT

<213> Homo sapiens

<400> 507

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
 1 5 10 15
 Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
 20 25 30
 Glu Asp Val Leu Glu Glu Cys Met Ser Leu Pro Lys Leu Ser Ser Tyr
 35 40 45
 Ser Gly Trp Val Val Glu His Val Leu Pro His Met Gln Glu Asn Gln
 50 55 60
 Pro Leu Ser Glu Thr Ser Pro Ser Ser Thr Ser Ala Ser Ala Leu Asp
 65 70 75 80
 Gln Pro Ser Phe Val Pro Lys Ser Pro Asp Ala Ser Ser Ala Phe Ser
 85 90 95
 Pro Ala Ser Pro Ala Thr Pro Asn Gly Thr Lys Gly Lys Lys Lys
 100 105 110

<210> 508

<211> 43

<212> PRT

<213> Homo sapiens

<400> 508

Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser
 1 5 10 15
 Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn
 20 25 30
 Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
 35 40

<210> 509

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 509

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Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 510
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 510
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
 -15 -10 -5
 Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
 1 5 10
 Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
 15 20 25 30
 Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
 35 40 45
 Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Ala Asp
 50 55 60
 Val Thr Glu Glu Glu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
 65 70 75
 Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
 80 85 90
 Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
 95 100 105 110
 Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr
 115 120 125
 Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
 130 135 140
 Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
 145 150 155
 Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
 160 165 170
 Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
 175 180 185 190
 His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Ala Glu Val
 195 200 205
 Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
 210 215 220
 Arg Thr Ala Trp
 225

<210> 511
 <211> 353
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

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<400> 511
Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-30 -25 -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
-15 -10 -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
1 5 10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15 20 25 30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
35 40 45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
50 55 60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
65 70 75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
80 85 90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
95 100 105 110
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
115 120 125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
130 135 140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
145 150 155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
160 165 170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
175 180 185 190
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
195 200 205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
210 215 220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
225 230 235
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
240 245 250
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
255 260 265 270
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
275 280 285
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
290 295 300
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
305 310 315
Leu

<210> 512
<211> 30
<212> PRT
<213> Homo sapiens

<400> 512
Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
1 5 10 15
Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys
20 25 30

<210> 513
<211> 112
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 513

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Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
      -45      -40      -35
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
      -30      -25      -20
Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
      -15      -10      -5
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
1      5      10      15
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
      20      25      30
Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
      35      40      45
Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
      50      55      60
```

<210> 514

<211> 54

<212> PRT

<213> Homo sapiens

<400> 514

```
Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
1      5      10      15
Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
      20      25      30
Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
      35      40      45
Ser Ser Gly His Leu Pro
      50
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<210> 515

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 515

```
Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val
      -20      -15      -10
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
      -5      1      5      10
Lys Lys Gln Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
      15      20      25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
      30      35      40
Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Ile Thr Glu Glu Asp
      45      50      55
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
      60      65      70      75
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser Lys
      80      85      90
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Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 516
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 516
 Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
 -25 -20 -15 -10
 Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
 -5 1 5
 Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
 10 15 20
 Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
 25 30 35
 Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
 40 45 50 55
 Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Gly
 60 65 70
 Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
 75 80 85
 Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly
 90 95 100
 Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
 105 110 115
 Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
 120 125 130 135
 Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
 140 145 150
 Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
 155 160 165
 Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
 170 175 180
 Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
 185 190 195
 Asn Ala Tyr Val
 200

<210> 517
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 517
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser

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<220>
 <221> SIGNAL
 <222> -27...-1

<400> 520
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser
 10

<210> 521
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 521
 Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
 1 5 10 15
 Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
 20 25 30
 Asp Leu Lys Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
 35 40 45
 Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
 50 55 60
 Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Gly
 65 70 75 80
 Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
 85 90 95
 Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
 100 105 110
 Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
 115 120 125
 His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
 130 135 140
 Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
 145 150

<210> 522
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 522
 Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
 1 5 10 15
 Asp Thr Trp Lys Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
 20 25 30
 Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
 35 40 45
 Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
 50 55 60
 Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
 65 70 75 80
 Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
 85 90 95
 Lys Gln Thr Ser Val
 100

<210> 523

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<211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 523

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Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
   -20                               -15                -10
Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
   -5                               1                   5                10
Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
                               15                20                25
Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser
   30                               35                40
Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys Lys Ala Ser
   45                               50                55
Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys Lys Lys Cys
   60                               65                70
Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu Val Glu Arg
   75                               80                85
Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp Ser Ala Glu
                               95                100                105
Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro Ile Asn Ser
   110                               115                120
Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys Ala Trp Lys
   125                               130                135
Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly Ser Thr Ser
   140                               145                150
Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg Asn Arg Gln
   155                               160                165
Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro Gln Val Pro
   175                               180                185
Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu Val Ser Pro
   190                               195                200
Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala Leu Arg Ala
   205                               210                215
Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr Leu Asn Glu
   220                               225                230
Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu Phe Gln Glu
   235                               240                245
Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln Ser Gln Val
   255                               260                265
Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg Asp Leu Arg
   270                               275                280
Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys Gly Asp Cys
   285                               290                295
Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe Asp Leu Ala
   300                               305                310
Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln Val Pro Leu
   315                               320                325
Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser Leu Met Gly
   335                               340                345
Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val Leu Lys Pro
   350                               355                360
Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe Glu Asp Val
   365                               370                375
Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys Ile Val Ser
   380                               385                390

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Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe Gln Lys Thr
 395 400 405 410
 Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly Leu Gln Leu
 415 420 425
 Gln Pro Cys Leu Tyr Lys Arg Arg
 430

<210> 524
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 524
 Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
 1 5 10 15
 Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
 20 25 30
 Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
 35 40 45
 Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
 50 55 60
 Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
 65 70 75
 Val Glu
 80

<210> 525
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 525
 Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
 -25 -20 -15
 Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
 -10 -5 1
 Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
 5 10 15
 Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
 20 25 30 35
 Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
 40 45 50
 Asn Ala Ser

<210> 526
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

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<222> -23...-1

<400> 526

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
60 65 70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
75 80 85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
90 95 100 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
110 115 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
125 130 135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
140 145 150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
155 160 165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
170 175 180 185
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
190 195 200
Arg Lys Ser Arg Thr
205

<210> 527

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 527

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
-20 -15 -10
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
-5 1 5 10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
15 20 25
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
30 35 40
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
45 50 55
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
60 65 70 75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
80 85 90
Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
95 100 105
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu

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110 115 120
 Asn Asp Phe Ser Gln Glu Ser Ser
 125 130

<210> 528
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 528
 Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
 -50 -45 -40
 Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
 -35 -30 -25
 Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
 -20 -15 -10
 Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
 -5 1 5 10
 Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
 15 20 25
 Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu
 30 35 40
 Ala Gly Met Pro Ser Pro Glu Trp Thr Lys Arg Lys Lys Gln Thr Leu
 45 50 55
 Lys Ile Gly His Gly Gly Thr Leu Asp Ser Ala Ala Arg Gly Val Leu
 60 65 70
 Val Val Gly Ile Gly Ser Gly Thr Lys Met Leu Thr Ser Met Leu Ser
 75 80 85 90
 Gly Ser Lys Arg Tyr Thr Ala Ile Gly Glu Leu Gly Lys Ala Thr Asp
 95 100 105
 Thr Leu Asp Ser Thr Gly Lys Val Thr Glu Glu Lys Pro Tyr Gly Met
 110 115 120
 Asn Leu Ile
 125

<210> 529
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92...-1

<400> 529
 Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu
 -90 -85 -80
 Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro
 -75 -70 -65
 Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp
 -60 -55 -50 -45
 Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr
 -40 -35 -30
 Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala
 -25 -20 -15
 Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val
 -10 -5 1

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Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val
 5 10 15 20
 Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr Phe
 25 30 35
 Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu Cys
 40 45 50
 His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu Thr
 55 60 65
 Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn
 70 75 80
 Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala
 85 90 95 100
 Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln
 105 110 115
 Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu
 120 125 130
 His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala Asp
 135 140 145
 Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu Thr
 150 155 160
 Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
 165 170 175

<210> 530
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 530
 Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val
 -20 -15 -10
 Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala
 -5 1 5 10
 Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser
 15 20 25
 Phe Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile
 30 35 40
 Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe
 45 50 55
 His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu
 60 65 70
 Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile
 75 80 85 90
 Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn
 95 100 105
 Ser Ala Pro Lys Ser Asn Val
 110

<210> 531
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

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<400> 531
 Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -35 -30 -25
 Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
 -20 -15 -10
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 -5 1 5 10
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 15 20 25
 Glu Val Leu

<210> 532
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 532
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Tyr
 60 65 70

<210> 533
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 533
 Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Pro Pro
 -20 -15 -10
 Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
 -5 1 5 10
 Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
 15 20 25
 Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
 30 35 40
 Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
 45 50 55
 Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
 60 65 70 75
 Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe

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80										85					90				
Thr	Glu	Thr	Met	95	Ser	Ser	Leu	Ser	Pro	Gly	Arg	Pro	Trp	Gln	Thr	Lys			
Leu	Ser	Ser	Ala	Gly	Leu	Ile	Tyr	Leu	His	Phe	Gly	His	Lys	Leu	Leu				
Ala	Gln	Leu	Leu	Gly	Thr	Ser	Glu	Glu	Asp	Ser	Met	Val	Gly	Thr	Leu				
Tyr	Asp	Lys	Met	Tyr	Glu	Asn	Phe	Val	Glu	Glu	Val	Asp	Ala	Val	Asp				
Asn	Gly	Ile	Ser	Gln	Trp	Ala	Glu	Gly	Glu	Pro	Arg	Tyr	Ala	Leu	Thr				
Thr	Thr	Leu	Ser	Ala	Arg	Val	Ala	Arg	Leu	Asn	Pro	Thr	Trp	Asn	His				
Pro	Asp	Gln	Asp	Thr	Glu	Ala	Gly	Phe	Lys	Arg	Ala	Met	Asp	Leu	Val				
Gln	Glu	Glu	Phe	Leu	Gln	Arg	Glu	Asp	Phe	Tyr	Gln	His	Ser	Trp	Leu				
Pro	Ala	Arg	Ala	Leu	Val	Glu	Glu	Ala	Leu	Ala	Gln	Arg	Phe	Gln	Val				
220	Asp	Pro	Ser	Gly	Glu	Ile	Val	Glu	Leu	Ala	Lys	Gly	Ala	Cys	Pro				
Lys	Glu	His	Leu	Tyr	His	Leu	Glu	Ser	Gly	Leu	Ser	Pro	Pro	Val	Ala				
Ile	Phe	Phe	Val	Ile	Tyr	Thr	Asp	Gln	Ala	Gly	Gln	Trp	Arg	Ile	Gln				
Cys	Val	Pro	Lys	Glu	Pro	His	Ser	Phe	Gln	Ser	Arg	Leu	Pro	Leu	Pro				
Glu	Pro	Trp	Arg	Gly	Leu	Arg	Asp	Glu	Ala	Leu	Asp	Gln	Val	Ser	Gly				
300	Ile	Pro	Gly	Cys	Ile	Phe	Val	His	Ala	Ser	Gly	Phe	Ile	Gly	Gly				
Arg	Thr	Arg	Glu	Gly	Ala	Leu	Ser	Met	Ala	Arg	Ala	Thr	Leu	Ala	Gln				
Arg	Ser	Tyr	Leu	Pro	Gln	Ile	Ser												
		350					355												

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<210> 534
<211> 211
<212> PRT
<213> Homo sapiens
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85 90 95
 His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
 100 105 110
 Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115 120 125 130
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
 135 140 145
 Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
 150 155 160
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
 165 170 175
 Arg Gln Leu
 180

<210> 535
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 535
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
 25 30 35
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 536
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 536
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
 -40 -35 -30
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
 -25 -20 -15
 Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
 -10 -5 1 5

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Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser
 10 15 20
 Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser
 25 30 35
 Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Thr Ala Arg Ala Leu
 40 45 50
 Cys Leu Gly Cys Ser Cys Cys Thr Glu Arg Leu Leu Leu Pro Pro Pro
 55 60 65 70
 Ser Leu Leu Ser Leu Glu Ala Pro Ala Ser Thr
 75 80

<210> 537
 <211> 346
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 537
 Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
 -15 -10 -5
 Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
 1 5 10
 Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
 15 20 25
 Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
 30 35 40 45
 Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
 50 55 60
 Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
 65 70 75
 Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
 80 85 90
 Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
 95 100 105
 Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
 110 115 120 125
 Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
 130 135 140
 Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
 145 150 155
 Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
 160 165 170
 Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
 175 180 185
 Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
 190 195 200 205
 Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
 210 215 220
 His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Phe Phe Ser
 225 230 235
 Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
 240 245 250
 Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
 255 260 265
 Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
 270 275 280 285
 Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
 290 295 300

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Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
 305 310 315
 Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
 320 325

<210> 538
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 538
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
 30 35 40
 Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
 45 50 55 60
 Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
 65 70 75
 Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
 80 85 90
 Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
 95 100 105
 Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
 110 115 120
 Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
 125 130 135 140
 Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
 145 150 155
 His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu
 160 165 170
 Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys
 175 180 185
 Pro Lys
 190

<210> 539
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 539
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr

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      30              35              40
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45      50      55
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
      65      70      75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
      80      85      90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
      95      100      105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
      110      115      120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
      125      130      135      140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
      145      150      155
His Leu Leu Ala Asp Thr Met Leu
      160

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<210> 540
<211> 227
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -22..-1

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<400> 540
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
      -20      -15
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
      -5      1      5      10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
      15      20      25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
      30      35      40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
      45      50      55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
      60      65      70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
      75      80      85      90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
      95      100      105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
      110      115      120
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
      125      130      135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
      140      145      150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
      155      160      165      170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
      175      180      185
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
      190      195      200
Ala Ala Cys
      205

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<210> 541
<211> 74

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 541
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
-40 -35 -30
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
-25 -20 -15 -10
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
-5 1 5
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
10 15 20
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
25 30

<210> 542
<211> 73
<212> PRT
<213> Homo sapiens

<400> 542
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
1 5 10 15
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
20 25 30
Lys Lys Phe Leu Glu Ser Asp Asp Lys Met Val Lys Lys Ile Ala
35 40 45
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
50 55 60
Asn Leu Leu Glu Val Cys Lys Lys Lys
65 70

<210> 543
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 543
Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
-15 -10 -5
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
1 5 10 15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
20 25 30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
35 40 45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
50 55 60
Lys Asn
65

<210> 544
<211> 119

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56...-1

<400> 544
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys Lys
60

<210> 545
<211> 54
<212> PRT
<213> Homo sapiens

<400> 545
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

<210> 546
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 546
Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
-10 -5 1
Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
5 10 15
Arg Gly Gly Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
20 25 30
Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
35 40 45 50
Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
55 60 65
Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met

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70 75 80
 Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
 85 90 95
 Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
 100 105 110
 Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
 115 120 125 130
 Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
 135 140 145
 Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
 150 155 160
 Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
 165 170 175
 Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
 180 185 190
 Gln Glu
 195

<210> 547

<211> 108

<212> PRT

<213> Homo sapiens

<400> 547

Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 548

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 548

Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
 -15 -10 -5
 Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
 1 5 10
 Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
 15 20 25

<210> 549

<211> 36

<212> PRT

<213> Homo sapiens

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<400> 549
 Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
 1 5 10 15
 Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
 20 25 30
 Phe Phe Gln Ile
 35

<210> 550
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 550
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
 Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
 Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
 Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
 Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
 Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80
 Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
 85 90 95
 Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu
 100 105 110 115
 Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
 120 125 130
 Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
 135 140 145
 Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
 150 155 160
 Trp Gln Arg Arg Asp Tyr Leu Leu Val Met Glu Gly Thr Asp Asp
 165 170 175
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
 180 185 190 195
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
 200 205 210
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
 215 220 225
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
 230 235 240
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
 245 250 255
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
 260 265 270 275
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
 280 285 290
 Lys Lys Lys

<210> 551
 <211> 106

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 551
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
-30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
-15 -10 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
20 25 30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
35 40 45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
50 55 60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65 70

<210> 552
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 552
Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
-15 -10 -5
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
1 5 10
Gln Leu Ser Asp Lys Val His Asn Asp Ile
15 20

<210> 553
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 553
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
30 35 40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg

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65 70 75
 Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile
 80 85 90
 Ile Asp Lys Thr Thr
 95

<210> 554
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 554
 Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
 -35 -30 -25
 Gln His Xaa Xaa Ala Xaa Xaa Leu Val Phe Asn Phe Leu Leu Ile
 -20 -15 -10
 Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
 -5 1 5 10
 Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
 15 20 25
 Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
 30 35 40
 Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
 45 50 55
 Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
 60 65 70 75
 His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
 80 85 90
 Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe
 95 100 105
 His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
 110 115 120
 Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
 125 130 135
 Ile Gly
 140

<210> 555
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 555
 Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val
 -25 -20 -15
 Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser
 -10 -5 1 5
 Met Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe Ile
 10 15 20
 Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala
 25 30 35
 Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
 40 45 50

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 558
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
-20 -15 -10
Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
-5 1 5
Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
10 15 20 25
Arg Lys Ser Cys His Asp Trp Ile Gly Pro Asp Lys Tyr Ser Asn
30 35 40
Leu Arg Pro Val His Phe Tyr Ile Pro Asn Glu Ser Pro Leu Glu
45 50 55
Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
60 65 70
Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
75 80 85
Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
90 95 100 105
Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
110 115 120
Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
125 130 135
Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
140 145 150
Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
155 160 165
Asn
170

<210> 559
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 559
Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
-10 -5 1
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
5 10 15
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
20 25 30
Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
35 40 45 50
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
55 60 65
Phe Gly

<210> 560
<211> 198
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 560

Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
-20 -15 -10
Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
-5 1 5 10
Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
15 20 25
Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu Thr Lys Ala Arg
30 35 40
Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
45 50 55
Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
60 65 70 75
Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu Gln Ala Xaa Ala Thr
80 85 90
Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
95 100 105
Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa Ala Trp Leu Gly Pro
110 115 120
Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro Pro Xaa Lys Gln Asn
125 130 135
His Ile Leu Trp Ala Leu Thr Gly His Val Xaa Arg Gln Xaa Arg Glu
140 145 150 155
Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile Gln Glu Lys Leu His
160 165 170
Thr Ala Ala Leu Pro Ala
175

<210> 561

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 561

Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
-55 -50 -45 -40
Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
-35 -30 -25
Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
-20 -15 -10
Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
-5 1 5
Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
10 15 20 25
Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
30 35 40
Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
45 50 55
Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
60 65 70
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile

75 80 85
 Pro Phe Ala Arg Asp Ala Val Lys Xaa Cys Phe Ala Val Cys Leu Ala
 90 95 100 105

<210> 562
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 562
 Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
 -15 -10 -5
 Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
 1 5 10
 Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
 15 20 25 30
 Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
 35 40 45
 Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
 50 55 60
 Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
 65 70 75
 Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 80 85 90

<210> 563
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 563
 Met Ile Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu
 -20 -15 -10
 Phe Pro Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp
 -5 1 5 10
 Leu Tyr Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser
 15 20 25
 Gln Lys Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
 30 35 40

<210> 564
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 564
 Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
 -15 -10 -5 1
 Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn

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<210> 565
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 565
 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 -20 -15 -10
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
 -5 1 5 10
 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 15 20 25
 Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 30 35 40
 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Leu Glu Gly
 45 50 55
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys
 60 65 70 75
 Ala Ala His Pro Thr Asp Asp Thr Thr Leu Ser Glu Arg Pro Ser
 80 85 90
 Pro Ser Thr Xaa Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu
 95 100 105
 Val Phe Met Arg Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly
 110 115 120
 Asn Xaa Gly Cys Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser
 125 130 135
 Ser Ser Pro Val Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile
 140 145 150 155
 Ile Ala Gly Glu Ser Ile Arg Asn Arg Ser
 160 165

<210> 566
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 566
 Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
 -25 -20 -15
 Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys Arg Pro Val Leu Gln Asn
 -10 -5 1 5
 Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser Leu Glu Val Pro Thr Gly
 10 15 20
 Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly Pro Gly Leu Xaa Gly Ala
 25 30 35
 Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu Met Gly Arg Gln Arg Thr
 40 45 50
 Arg Lys Val Lys Gly Pro Ala Trp Xaa His Thr Ala Asn Gln Glu Leu
 55 60 65 70
 Asn Arg Met Arg Ser Leu Ser Ser Gly Ser Val Pro Val Gly His Leu
 75 80 85

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Glu Gly Gly Thr Val Lys Leu Gln Lys Asp Thr Gly Leu His Ser Cys
 90 95 100
 Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr Pro Ala Ser Val Leu Ala
 105 110 115
 Asp Ala Cys Pro Gly Phe His Asp Val Xaa Val Gln Xaa Ala Leu Phe
 120 125 130
 Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys Thr His Phe Cys Leu Ser
 135 140 145 150
 Ile Xaa Leu

<210> 567
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<400> 567
 Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
 -55 -50 -45 -40
 Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
 -35 -30 -25
 Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
 -20 -15 -10
 Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
 -5 1 5
 Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
 10 15 20 25
 Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
 30 35 40
 Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
 45 50 55
 Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
 60 65 70
 Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
 75 80 85
 Pro Gly Cys Tyr Arg Tyr
 90 95

<210> 568
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 568
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys
 -30 -25 -20
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
 -15 -10 -5 1
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 5 10 15
 Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu
 20 25 30
 Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln Ala Ser

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<221> SIGNAL
<222> -30...-1

<400> 572
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys Trp Leu Glu Val Glu
-30 -25 -20 -15
Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn Ala Ser Ala Ile Ser
-10 -5 1
Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp Arg Arg Glu Ser
5 10 15

<210> 573
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 573
Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
-25 -20 -15
Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
-10 -5 1
Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
5 10 15 20
Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa
25 30 35
Ser

<210> 574
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 574
Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
-20 -15 -10
Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
-5 1 5
Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
10 15 20
Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
25 30 35 40
Trp Gly Gln Gly Thr His Ser Ser Leu
45

<210> 575
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

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<400> 575
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
 -15 -10 -5
 Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
 1 5 10
 Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
 15 20 25 30
 Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
 35 40

<210> 576
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93...-1

<400> 576
 Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
 -90 -85 -80
 Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val
 -75 -70 -65
 Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
 -60 -55 -50
 Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
 -45 -40 -35 -30
 Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
 -25 -20 -15
 Val Leu Leu Leu Arg Gln Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu
 -10 -5 1
 Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu
 5 10 15
 Gln Xaa Ala Glu Phe Glu Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys
 20 25 30 35
 Pro Ile Leu Xaa Val Thr Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly
 40 45 50
 Gly Thr Ala Lys Leu Leu Asn Lys Val Ile Cys Ile Ile Leu Arg Asn
 55 60 65
 Gly Lys Ser Leu Ile Leu Ser Cys His Cys Leu Gly Trp Arg Asn Lys
 70 75 80
 Ser Gly Arg Phe Val Ser Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
 85 90 95

<210> 577
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -72...-1

<400> 577
 Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
 -70 -65 -60
 Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
 -55 -50 -45
 Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
 -40 -35 -30 -25

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Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
 -20 -15 -10
 Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
 -5 1 5
 Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
 10 15 20
 Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
 25 30 35 40
 Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln
 45 50 55
 His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn Gln Lys Thr Leu
 60 65 70
 Phe Ser Met Val Gly
 75

<210> 578

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 578

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
 -20 -15 -10 -5
 Leu Ala Gln Ala Leu Asp Cys His Val Cys Ala Tyr Asn Gly Asp Asn
 1 5 10
 Cys Phe Asn Pro Met Arg Cys Pro Ala Met Val Ala Tyr Cys Met Thr
 15 20 25
 Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys Val Ser Lys Ser Cys
 30 35 40
 Val Pro Arg Cys Phe Glu Xaa Cys Val
 45 50

<210> 579

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 579

Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Xaa Lys Leu Arg Gln
 65

<210> 580

<211> 78

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 580
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
-20 -15 -10
Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
-5 1 5 10
Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
15 20 25
Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg Ser Leu Asn Gln Glu
30 35 40
Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr Ser Ile Thr
45 50 55

<210> 581
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 581
Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu Pro Leu Ser
-25 -20 -15
Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser
-10 -5 1
Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val Pro Glu Pro
5 10 15 20
Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg
25 30 35
Thr

<210> 582
<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 582
Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu Glu Leu Thr
-25 -20 -15
Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr Asn Lys Phe
-10 -5 1 5
Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile Phe Ile Gly
10 15 20
Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu Ser Lys Asn
25 30 35
Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile Leu Val His
40 45 50
Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly Asp Ala Pro
55 60 65

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Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile Lys Ser Ser
 70 75 80 85
 Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu Gly Asn Ser
 90 95 100
 Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu Tyr Ser Glu
 105 110 115
 Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln Ser Ile Cys
 120 125 130
 Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu His Trp Gln
 135 140 145
 Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile Ser Phe Phe
 150 155 160 165
 Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly Ser Asp Tyr
 170 175 180
 Arg Ser Ile

<210> 583
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -80...-1

<400> 583
 Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
 -80 -75 -70 -65
 Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
 -60 -55 -50
 Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
 -45 -40 -35
 Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
 -30 -25 -20
 Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
 -15 -10 -5
 Thr Ser Thr Pro Ser Ala Lys Ile Gln Ser Leu Gln Ile Asp Leu Pro
 1 5 10 15
 Gly Gly Trp Arg Leu Ala Thr Asp Arg Ile Phe Thr Leu Ser Pro Val
 20 25 30
 Pro Met Asp Xaa Pro Leu Ile Leu His Gln Leu
 35 40

<210> 584
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 584
 Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
 -25 -20 -15
 Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
 -10 -5 1 5
 Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
 10 15 20
 Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp Val Leu

Val Arg
60

<210> 587
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 587
Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu
-15 -10 -5 1
Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
5 10 15
Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
20 25 30
Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
35 40 45
Asp Phe Ser Ser Phe Thr
50 55

<210> 588
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45...-1

<400> 588
Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
-45 -40 -35 -30
Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
-25 -20 -15
Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
-10 -5 1
Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
5 10 15

<210> 589
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22...-1

<400> 589
Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
-20 -15 -10
Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
-5 1 5 10
Asn Pro Phe Leu Trp Lys Leu
15

<210> 590

<211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 590
 Met Ala Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala
 -20 -15 -10
 Phe Pro Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly
 -5 1 5
 Lys Pro Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg
 10 15 20 25
 Ile Trp Pro

<210> 591
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 591
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Xaa Xaa Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 592
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 592
 Met Asp Glu Tyr Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly
 -30 -25 -20
 Gln Met Phe Thr Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys
 -15 -10 -5
 Gln Arg Phe Phe Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser
 1 5 10 15
 Thr Val Thr Pro Ser Trp Arg Leu Cys Leu Val Ser
 20 25

<210> 593

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<211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -79...-1

<400> 593
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 -75 -70 -65
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 -45 -40 -35
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 -15 -10 -5 1
 Pro Ser Ser Lys Ala Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa
 5 10 15
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 20 25 30
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa
 35 40 45
 Arg His Xaa Gln Xaa His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 50 55 60 65
 Cys Thr Xaa Cys Gly Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln
 70 75 80
 His Tyr Ile Arg His Ala Arg Gly Gly Leu
 85 90

<210> 594
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<400> 594
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45
 Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe

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65 70 75
 Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105

<210> 595
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 595
 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
 -60 -55 -50 -45
 Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
 -40 -35 -30
 Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
 -25 -20 -15
 Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
 -10 -5 1
 Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
 5 10 15 20
 Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys
 25 30 35
 Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser
 40 45 50
 Ser Lys

<210> 596
 <211> 161
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -108...-1

<400> 596
 Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln Ser Pro Gln Ala Leu
 -105 -100 -95
 Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr Leu
 -90 -85 -80
 Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His Leu
 -75 -70 -65
 Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu Ala
 -60 -55 -50 -45
 His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser Ser
 -40 -35 -30
 Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr Ala
 -25 -20 -15
 Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Ser Leu Tyr Ser
 -10 -5 1
 His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr Pro Arg Ser Gly Thr
 5 10 15 20
 Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln Asn Thr Pro Lys Ile
 25 30 35

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Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met
 40 45 50
 Leu

<210> 597
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 597
 Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
 -20 -15 -10
 Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
 -5 1 5 10
 Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
 15 20 25
 Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
 30 35 40
 Leu Arg Met
 45

<210> 598
 <211> 332
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 598
 Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp
 -30 -25 -20
 Thr Arg Gln Leu Pro Leu Leu Thr Ser Ala Leu His Gly Leu Gln Gln
 -15 -10 -5
 Gln His Pro Ala Phe Ser Gly Val Ala Arg Leu Ala Lys Arg Trp Val
 1 5 10 15
 Arg Ala Gln Leu Leu Gly Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu
 20 25 30
 Val Ala Ala Ala Leu Phe Leu His Pro Glu Pro Phe Thr Pro Pro Ser
 35 40 45
 Ser Pro Gln Val Gly Phe Leu Arg Phe Leu Phe Leu Val Ser Thr Phe
 50 55 60
 Asp Trp Lys Asn Asn Pro Leu Phe Val Asn Leu Asn Asn Glu Leu Thr
 65 70 75 80
 Val Glu Glu Gln Val Glu Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala
 85 90 95
 Gln Leu Pro Val Met Val Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser
 100 105 110
 Val Trp Thr Gln Asp Gly Pro Ser Ala Gln Ile Leu Gln Gln Leu Val
 115 120 125
 Val Leu Ala Ala Glu Xaa Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp
 130 135 140
 Pro Arg Gly Pro Gly Asp Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp
 145 150 155 160
 Ile Tyr Asp Val Leu Ile Arg Leu Ser Pro Arg His Ile Pro Arg His

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165 170 175
 Arg Gln Ala Val Asp Ser Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu
 180 185 190
 Ser Gln Pro Gly Pro Ser Ser Leu Met Pro Val Leu Gly Xaa Asp Pro
 195 200 205
 Pro Gln Leu Tyr Leu Thr Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala
 210 215 220
 Leu Phe Phe Tyr Asp Gln His Gly Gly Glu Val Ile Gly Val Leu Trp
 225 230 235 240
 Lys Pro Thr Ser Phe Gln Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys
 245 250 255
 Gly Arg Met Val Met Ser Arg Gly Gly Glu Leu Val Met Val Pro Asn
 260 265 270
 Val Glu Ala Ile Leu Glu Asp Phe Ala Val Leu Gly Glu Gly Leu Val
 275 280 285
 Gln Thr Val Glu Ala Arg Ser Glu Arg Trp Thr Val
 290 295 300

<210> 599
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 599
 Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser Phe His
 -15 -10 -5
 Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser Arg His
 1 5 10
 His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu Glu Asn
 15 20 25
 Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys Ile Val
 30 35 40 45
 Gly

<210> 600
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 600
 Met Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser
 -30 -25 -20 -15
 Thr Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val
 -10 -5 1
 Arg Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala
 5 10 15
 Glu Glu Gln Lys Xaa Ser Gly Ile Met
 20 25

<210> 601
 <211> 85
 <212> PRT
 <213> Homo sapiens

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<220>
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 <222> -17...-1

<400> 601
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 -15 -10 -5
 Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser
 1 5 10 15
 Asp Ser Asp Glu Leu Ala Ser Gly Xaa Phe Val Phe Pro Tyr Trp Tyr
 20 25 30
 Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
 35 40 45
 Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
 50 55 60
 Leu Pro Ser Glu Lys
 65

<210> 602
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -17...-1

<400> 602
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 -15 -10 -5
 Gly Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser
 1 5 10 15
 Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
 20 25 30
 Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
 35 40 45
 Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
 50 55 60
 Leu Pro Ser Glu Lys
 65

<210> 603
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -29...-1

<400> 603
 Met Thr Cys Arg Gly Ser Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser
 -25 -20 -15
 Glu Leu Ser Leu Leu Pro Ser Ser Leu Trp Val Leu Ala Thr Ser Ser
 -10 -5 1
 Pro Thr Ile Thr Ile Ala Leu Ala Met Ala Ala Gly Asn Leu Cys Pro
 5 10 15
 Leu Pro Ser Ser Xaa Arg Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln
 20 25 30 35
 Gln Xaa Ala Leu Leu

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<210> 604
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -56...-1

<400> 604
 Met Val Pro Trp Pro Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile
 -55 -50 -45
 Ser Arg Phe Pro Phe Leu Pro Thr His Asp Pro Pro Thr Pro Ala His
 -40 -35 -30 -25
 Trp Ser Pro Ala Ser His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu
 -20 -15 -10
 Thr Leu Ala Leu Leu Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys
 -5 1 5
 Lys Leu Ala Gly Gln Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu
 10 15 20
 Pro Leu Thr Leu Trp Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr
 25 30 35 40
 Val Ala Gln Lys Lys Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro
 45 50 55
 Val Pro Ser Trp Val Gln Phe Phe Leu Gly
 60 65

<210> 605
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -30...-1

<400> 605
 Met Ala Cys Glu Thr His Gly Val Leu Val Pro Ala His Leu Ser Gly
 -30 -25 -20 -15
 Leu Ile Thr Cys Leu Leu Ala Phe Trp Val Pro Ala Ser Cys Ile Gln
 -10 -5 1
 Arg Cys Ser Gly Ser Pro Leu Pro Leu
 5 10

<210> 606
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -36...-1

<400> 606
 Met Ala Pro His Thr Ala Ser Phe Gly Val Cys Pro Leu Leu Ser Val
 -35 -30 -25
 Thr Arg Val Val Ala Thr Glu His Trp Leu Phe Leu Ala Ser Leu Ser
 -20 -15 -10 -5
 Gly Ile Lys Thr Tyr Gln Ser Tyr Ile Ser Val Phe Cys Lys Val Thr

Leu Ile

1 5 10

<210> 607
 <211> 136
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -18...-1

<400> 607
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 -15 -10 -5
 Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 1 5 10
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 15 20 25 30
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Ala Thr Leu
 35 40 45
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 50 55 60
 Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
 65 70 75
 Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
 80 85 90
 Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg Xaa Glu Asn Xaa
 95 100 105 110
 Met Pro Gly Leu Ser Gly Val Leu
 115

<210> 608
 <211> 194
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -65...-1

<400> 608
 Met Gln Asp Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser
 -65 -60 -55 -50
 Val Ser Ser Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr
 -45 -40 -35
 Arg Asn Leu Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys
 -30 -25 -20
 Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu
 -15 -10 -5
 Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala
 1 5 10 15
 Gly Leu Asp Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met
 20 25 30
 Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp
 35 40 45
 Asp Gly Ser Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp
 50 55 60
 Cys Arg Arg Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys
 65 70 75

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Ser Ala Leu Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa
 80 85 90 95
 Lys Ile Val Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys
 100 105 110
 Lys His Cys Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu
 115 120 125
 Val Ser

<210> 609
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 609
 Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
 Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
 Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
 -35 -30 -25
 Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10
 Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Val Xaa
 15 20 25
 Lys Xaa Ser Glu Glu Gly Arg Met Gly Gln Xaa Gly Glu Glu Xaa Xaa
 30 35 40
 Asn Ser Leu Asn Phe Pro Xaa Ala Ser Leu Leu Xaa Leu Ile Cys Gln
 45 50 55
 Xaa Gln Gly Phe Asn Gly Glu Ser Cys Ser Pro Val Gly
 60 65 70

<210> 610
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 610
 Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
 Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
 Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Xaa Lys Val Ile
 -35 -30 -25
 Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10
 Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
 15 20 25
 Ile Ser Gly Ser Leu Ser Ile Ala Thr Lys Lys Arg Leu Thr Asn Leu

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30 35 40
 Leu Val His Thr Thr Leu Val Gly Ser Ile Leu Ser Ala Leu Ser Ala
 45 50 55
 Leu Val Gly Phe Ile Xaa Leu Ser Val Lys Gln Ala Thr Leu Asn Pro
 60 65 70 75
 Ala Ser Leu Xaa Cys Glu Leu Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa
 80 85 90
 Tyr Val Xaa Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr
 95 100 105
 Thr Ala Lys Ala Xaa Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys
 110 115 120
 Thr Leu Leu Glu Phe Cys Xaa Xaa Val Leu Thr Ala Val Leu Arg Trp
 125 130 135
 Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro Xaa
 140 145 150 155
 Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Asp Cys
 160 165 170
 Gly Tyr Glu Glu Leu Leu Thr Ser
 175

<210> 611
 <211> 49
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 611
 Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
 -35 -30 -25
 Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
 -20 -15 -10 -5
 Cys Leu Leu Ser Phe Gln Val Phe Lys Lys Lys Arg Lys Leu Xaa Leu
 1 5 10
 Phe

<210> 612
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 612
 Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
 -10 -5 1
 Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser Ala
 5 10 15
 Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
 20 25 30
 Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
 35 40 45 50
 Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
 55 60 65
 His Arg Ile Cys Asp Leu
 70

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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

Met	Thr	Arg	Leu	Cys	Leu	Pro	Arg	Pro	Glu	Ala	Arg	Glu	Asp	Pro	Ile
			-55					-50					-45		
Pro	Val	Pro	Pro	Arg	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Ser	Gly	Ser	Pro
		-40					-35					-30			
Val	Arg	Pro	Pro	Val	Ser	Thr	Trp	Gly	Pro	Ser	Trp	Ala	Gln	Leu	Leu
	-25					-20					-15				
Asp	Ser	Val	Leu	Trp	Leu	Gly	Ala	Leu	Gly	Leu	Thr	Ile	Gln	Ala	Val
-10					-5					1				5	
Phe	Ser	Thr	Thr	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Val	Ser	Phe	Leu	
			10					15				20			
Thr	Phe	Asp	Leu	Leu	His	Arg	Pro	Ala	Val	Thr	Leu	Cys	His	Ser	Ala
		25					30					35			
Asn	Phe	Ser	Pro	Gly	Ala	Arg	Val	Arg	Gly	Pro	Val	Lys	Val	Leu	Asp
	40					45					50				
Ser	Arg	Arg	Leu	Tyr	Ser	Cys	Lys	Trp	Val	Gln	Ser	Gln	Asp	Asn	Leu
55					60					65				70	
Ala	Ser	Arg	Lys	His	Cys	Cys	Cys	Cys	Ser	Trp	Gly	Trp	Ala	Arg	Ser
				75					80					85	

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<222> -16..-1
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<210> 615
<211> 162
<212> PRT
<213> Homo sapiens
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<222> -15...-1

<400> 617

Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
-15 -10 -5 1
Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
5 10 15
Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
20 25 30
Val Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile
35 40 45
Gln Val Pro Arg Arg Ala Gly
50 55

<210> 618

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 618

Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
-20 -15 -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
-5 1 5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
10 15 20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25 30 35 40
Arg Cys Glu Thr Phe Val Phe Ser Ser Cys Asn Gly Asn Leu Asn Asn
45 50 55
Phe Lys Leu Lys Ile Glu Arg Glu Val Xaa Cys Val Ala Lys Tyr Lys
60 65 70
Pro Pro Arg
75

<210> 619

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 619

Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
-25 -20 -15 -10
Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
-5 1 5
Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Gln Arg Phe Phe Ala
10 15 20
Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
25 30 35
Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
40 45 50 55
Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
60 65 70

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35
Xaa Leu Ser Lys Arg Asp
50 55

45

<210> 622
<211> 381
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33...-1

<400> 622
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
-30 -25 -20
Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
-15 -10 -5
Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
1 5 10 15
Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
20 25 30
Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
35 40 45
Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
50 55 60
Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys Gly Glu Thr Met
65 70 75
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
80 85 90 95
Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr
100 105 110
Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu Asn Leu Xaa Gln
115 120 125
Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr
130 135 140
Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu
145 150 155
Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile
160 165 170 175
Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg Phe Leu Ile Gly
180 185 190
Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly
195 200 205
Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala
210 215 220
Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp
225 230 235
Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr
240 245 250 255
Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
260 265 270
Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
275 280 285
Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile Xaa Glu Glu Val
290 295 300
Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
305 310 315
Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
320 325 330 335
Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu

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<210> 626
<211> 242
<212> PRT
<213> Homo sapiens
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<220>
 <221> SIGNAL
 <222> -30...-1

<400> 626
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35 40 45 50
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 55 60 65
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 70 75 80
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 85 90 95
 Pro Xaa Glu Gly Xaa Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 100 105 110
 Glu Lys Glu Ala Leu Val Pro Xaa Gln Lys Ala Thr Asp Ser Phe His
 115 120 125 130
 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
 135 140 145
 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Xaa Glu
 150 155 160
 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
 165 170 175
 His Lys Asp Xaa Leu Xaa Xaa Gly Thr Glu Ser Ser Ser His Ser Arg
 180 185 190
 Leu Ser Pro Arg Lys Xaa His Leu Leu Tyr Ile Leu Xaa Pro Ser Arg
 195 200 205 210
 Gln Leu

<210> 627
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 627
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu
 25 30 35

Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 628
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -61...-1

<400> 628
 Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr
 -60 -55 -50
 Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro
 -45 -40 -35 -30
 Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala
 -25 -20 -15
 Leu Leu Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg
 -10 -5 1
 Pro Asp Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro
 5 10 15
 His Pro Cys Ala Thr Tyr Pro Pro Xaa
 20 25

<210> 629
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -26...-1

<400> 629
 Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
 -25 -20 -15
 Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
 -10 -5 1 5
 Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
 10 15 20
 Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
 25 30 35
 Phe Asp Leu Asp Met Asp His Thr Ile
 40 45

<210> 630
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -34...-1

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<400> 630
 Met Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser
 -30 -25 -20
 Trp Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser
 -15 -10 -5
 Ser Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys
 1 5 10
 Ala Ile Ile Leu Met Lys
 15 20

<210> 631
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -38...-1

<400> 631
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
 -35 -30 -25
 Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
 -20 -15 -10
 Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
 -5 1 5 10
 Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala Val Leu Trp
 15 20 25
 Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn Gln Trp Gln
 30 35 40
 His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser Ala Gln Ala
 45 50 55
 Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp Ile Pro Xaa
 60 65 70
 Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80

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 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -37...-1

<400> 632
 Met Ser Thr Val Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile
 -35 -30 -25
 Cys Pro Ala Pro Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu
 -20 -15 -10
 Ser Pro Gly Ile Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp
 -5 1 5 10
 Tyr Pro Ala Leu Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe
 15 20 25
 Val Lys Gly His Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn
 30 35 40
 Cys Val Val Leu Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His
 45 50 55
 Gln Thr Arg Ser Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu

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60 65 70 75
 Gln Glu Lys Val Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His
 80 85 90
 Lys Glu Lys Arg Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg
 95 100 105
 Ala Lys Glu Thr Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu
 110 115 120
 Ser Ser Lys Lys Val His
 125

<210> 633
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 633
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
 105 110 115
 Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
 135 140 145 150
 Arg Asn Trp Glu

<210> 634
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -64..-1

<400> 634
 Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
 -60 -55 -50
 Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
 -45 -40 -35
 Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val
 -30 -25 -20

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<400> 636
Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
-60 -55 -50 -45
Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
-40 -35 -30
Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
-25 -20 -15
Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
-10 -5 1
Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala Pro
5 10 15 20
Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg Ala
25 30 35
Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa Thr
40 45 50
Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile Val
55 60 65
Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa Phe
70 75 80
Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val Leu
85 90 95 100
Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr His
105 110 115
Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro Trp
120 125 130
Glu

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<210> 637
<211> 107
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -28...-1

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<400> 637
Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg
-25 -20 -15
Phe Leu Ser Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser
-10 -5 1
Trp Asp Val Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile
5 10 15 20
Arg Ala Val Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys
25 30 35
Val Glu Phe Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val
40 45 50
Tyr Ser Leu Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu
55 60 65
Ala Glu Arg Lys Ser Pro Glu Ile Ser Trp Gly
70 75

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<210> 638
<211> 121
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -13...-1

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<400> 638
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
 -10 -5 1
 Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
 5 10 15
 Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
 20 25 30 35
 Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr
 40 45 50
 Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg
 55 60 65
 Met Xaa Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
 70 75 80
 Thr Glu Phe Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
 85 90 95
 Phe Leu Ile Pro Asn Leu Ala Leu Asn
 100 105

<210> 639
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 639
 Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
 -15 -10 -5
 Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
 1 5 10 15
 Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Ile
 20 25

<210> 640
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 640
 Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
 -10 -5 1
 Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
 5 10 15
 Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
 20 25 30 35
 Thr Val Tyr Ser Ser Ala Pro Phe His Ala Pro Leu Pro Val Gln Asn
 40 45 50
 Ser Leu Trp Gly His Pro Leu His Gly Cys Ser Trp Gln Cys His His
 55 60 65
 Pro Gln Gly Gln Asn Leu Gln Pro Ala Ser Leu Xaa Thr His Leu Ser
 70 75 80
 Lys Pro Lys Arg His Phe Xaa Lys Lys Xaa Cys Gln Ala
 85 90 95

<210> 641
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 641
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu
 25 30 35
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn
 40 45 50 55
 Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85
 Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr Gly Thr Phe Glu
 90 95 100

<210> 642
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 642
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Xaa
 -10 -5 1
 Xaa Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
 70 75 80
 Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
 85 90 95
 Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val
 100 105 110
 Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
 115 120 125 130
 Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
 135 140 145

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Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
 150 155 160
 Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
 165 170 175
 Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
 180 185 190
 Val Lys Cys Lys Phe Leu Tyr Asn
 195 200

<210> 643
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 643
 Met Thr Phe Arg His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met
 -20 -15 -10
 Ala Thr Cys Thr Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys
 -5 1 5 10
 Ser Leu Thr Ser Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu
 15 20 25
 Ile Lys Phe Gly Tyr Asp Arg Lys Ser Thr Ile Lys Ser
 30 35 40

<210> 644
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 644
 Met Phe Leu Lys Ser Gly Ala Gly Leu Ser Ser Cys Leu Leu Pro Leu
 -15 -10 -5
 Cys Trp Leu Glu Arg Lys Asp His Gly Arg Arg Pro Ser Xaa His Pro
 1 5 10
 Gly Arg
 15

<210> 645
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 645
 Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
 -50 -45 -40
 Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
 -35 -30 -25
 Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
 -20 -15 -10

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Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
 -5 1 5 10
 Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
 15 20 25
 Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
 30 35 40
 Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
 45 50 55
 Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
 60 65 70
 Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
 75 80 85 90
 Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
 95 100 105
 Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
 110 115 120
 Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
 125 130 135
 Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
 140 145 150
 Ile Ile Arg Lys Cys Phe Ile
 155 160

<210> 646
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 646
 Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
 -15 -10 -5
 Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10

<210> 647
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 647
 Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
 -20 -15 -10
 Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
 -5 1 5
 Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
 10 15 20
 Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
 25 30 35 40
 Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
 45 50 55
 Tyr Trp Asp Asn Leu
 60

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<210> 648
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 648
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 649
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 649
 Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
 -40 -35 -30
 Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
 -25 -20 -15
 Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Asn Thr Ala Val
 -10 -5 1 5
 Lys His Ser Ile Gln Lys Asn Cys Met Xaa Leu Val Leu Gly Lys Leu
 10 15 20
 Leu Ser Gln

<210> 650
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 650
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
 -15 -10 -5 1
 Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
 5 10 15
 Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
 20 25 30
 Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr Ser Ser Ala
 35 40 45

<210> 651
 <211> 179

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -58...-1

<400> 651
Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
-55 -50 -45
Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
-40 -35 -30
Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
-25 -20 -15
Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10 -5 1 5
Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
10 15 20
Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile
25 30 35
Tyr Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa
40 45 50
Xaa Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser
55 60 65 70
His Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro
75 80 85
Thr Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Ile Leu Lys
90 95 100
Xaa Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly
105 110 115
Gln Val Asn
120

<210> 652
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -71...-1

<400> 652
Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
-70 -65 -60
Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55 -50 -45 -40
Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
-35 -30 -25
Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu Leu
-20 -15 -10
Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His Gln
-5 1 5
Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr Trp
10 15 20 25
Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu His
30 35 40
Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu Ala
45 50 55
Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Tyr Pro Asp
60 65 70

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<222> -18...-1

<400> 657

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
-15 -10 -5
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
1 5 10
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
15 20 25 30
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
35 40 45
Lys Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu
50 55 60
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
65 70 75
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met
80 85 90
Leu Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
95 100 105 110
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
115 120 125
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
130 135 140
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
145 150 155
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
160 165 170
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
175 180 185 190
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
195 200 205
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
210 215 220
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
225 230

<210> 658

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 658

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-20 -15 -10
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
-5 1 5 10
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
15 20 25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
30 35 40
Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Ile Thr Glu Glu Asp
45 50 55
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
60 65 70 75
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
80 85 90
Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile

95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 659
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 659
 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
 -25 -20 -15 -10
 Leu Leu Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -5 1 5
 Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
 10 15 20
 Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 25 30 35
 Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 40 45 50 55
 Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 60 65 70
 Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
 75 80 85
 Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
 90 95 100
 Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
 105 110 115
 Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
 120 125 130 135
 Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
 140 145 150
 Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
 155 160 165
 Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
 170 175 180
 Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
 185 190 195
 Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
 200 205 210

<210> 660
 <211> 208
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92...-1

<400> 660
 Met Arg Glu Pro Gln Lys Arg Thr Ala Thr Ile Ala Lys Xaa Xaa Ala
 -90 -85 -80
 Xaa Glu Gly Leu Arg Asp Pro Tyr Gly Arg Leu Cys Gly Ser Glu His
 -75 -70 -65

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Pro Arg Arg Pro Pro Glu Arg Pro Glu Glu Asp Pro Ser Thr Pro Glu
 -60 -55 -50 -45
 Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr Ala Gln Ala Gln
 -40 -35 -30
 Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr Lys Lys Ser Leu
 -25 -20 -15
 Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly Asn Ser Ala Lys
 -10 -5 1
 Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly Met Gln Pro Gly
 5 10 15 20
 Arg Xaa His Ser Ile Phe Gly Asp Pro Lys Lys Ile Val Thr Glu Xaa
 25 30 35
 Phe Val Arg Arg Gly Tyr Leu Ile Tyr Xaa Pro Val Pro Arg Xaa Ser
 40 45 50
 Pro Val Glu Tyr Xaa Phe Phe Trp Gly Pro Arg Ala His Val Glu Ser
 55 60 65
 Ser Xaa Leu Lys Xaa Xaa His Phe Val Ala Arg Val Arg Asn Arg Cys
 70 75 80
 Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser Asp Asp Ala
 85 90 95 100
 Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Xaa Gly Tyr Ser Ala Pro
 105 110 115

<210> 661
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...1

<400> 661
 Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
 -35 -30 -25
 Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
 -20 -15 -10
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
 -5 1 5
 Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
 10 15 20 25
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 30 35 40
 Arg Leu Leu Thr His Trp
 45

<210> 662
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...1

<400> 662
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser

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<220>
<221> SIGNAL
<222> -16..-1
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<210> 664
<211> 130
<212> PRT
<213> Homo sapiens
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[illegible]

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<220>
<221> SIGNAL
<222> -84..-1
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<400> 665
 Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu
 -80 -75 -70
 Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr
 -65 -60 -55
 Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly
 -50 -45 -40
 Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu
 -35 -30 -25
 Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu
 -20 -15 -10 -5
 Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr
 1 5 10
 Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly
 15 20 25
 Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val
 30 35 40
 Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala Ala Leu His
 45 50 55 60
 Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Xaa Val Xaa
 65 70 75
 Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg
 80 85 90
 Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr
 95 100 105
 Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser
 110 115 120
 His
 125

<210> 666
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 666
 Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
 -15 -10 -5
 Ala His Pro Pro Gln Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp
 1 5 10 15
 Val Gly Ile Cys

<210> 667
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 667
 Met Met Ser Ser Glu Leu Arg Arg Asn Pro His Phe Leu Lys Ser Asn
 -25 -20 -15
 Leu Phe Leu Gln Leu Leu Val Ser His Glu Ile Val Cys Ala Thr Glu
 -10 -5 1

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Thr Val Thr Thr Asn Phe Leu Arg His Glu Lys Ala
5 10 15

<210> 668
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -52...-1

<400> 668
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
-50 -45 -40
Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
-35 -30 -25
Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
-20 -15 -10 -5
Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
1 5 10
Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
15 20 25
Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp Ser Trp
30 35 40
Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val Arg Arg
45 50 55 60
His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu Asp Pro
65 70 75
Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
80 85 90
Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala Xaa Xaa
95 100 105
Thr Arg Ser
110

<210> 669
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47...-1

<400> 669
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
-45 -40 -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
-30 -25 -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
-15 -10 -5 1
Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys Gly Xaa Asn Thr
5 10 15

<210> 670
<211> 218
<212> PRT
<213> Homo sapiens

<220>

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<221> SIGNAL
<222> -50...-1

<400> 670

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Met His His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
-50          -45          -40          -35
Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
          -30          -25          -20
Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
          -15          -10          -5
Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
          1          5          10
Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys Tyr Ala Val Ser Ser
          15          20          25          30
Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Xaa Lys Gln
          35          40          45
Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro Xaa Gln Asp Leu Lys
          50          55          60
Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys Gly Ser Glu Asn Ser
          65          70          75
Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile Asn Xaa Gly Gly Asp
          80          85          90
Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly Ser Xaa His Met Gly
          95          100          105          110
Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala Asp Asn Gly Asp Asp
          115          120          125
Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro Glu Ser Xaa Gln Phe
          130          135          140
Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp Phe Ser Gly His Pro
          145          150          155
Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
          160          165

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<210> 671

<211> 216

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 671

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Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val
-15          -10          -5          1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
          5          10          15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
          20          25          30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
          35          40          45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys
          50          55          60          65
Ile Asn Ser Phe Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met
          70          75          80
Xaa Thr Lys Tyr Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln
          85          90          95
Gln Ser Trp Pro Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu
          100          105          110
Ser Xaa Pro Leu Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn
          115          120          125

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Gly Pro Gly Thr Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly
 130 135 140 145
 Ile Leu Gly Ile Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys
 150 155 160
 Arg Val Lys Thr Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser
 165 170 175
 Asn Tyr Phe Ile Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys
 180 185 190
 Ser Val Tyr Leu Gly Arg Ile Val
 195 200

<210> 672
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 672
 Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
 -15 -10 -5
 Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
 1 5 10
 Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu Ala
 15 20 25
 Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile
 30 35 40 45
 Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile Pro
 50 55 60
 Val Ser Gly Ser Lys Ser Glu Gly Leu Tyr Val His Ser Ser Arg
 65 70 75
 Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu
 80 85 90
 Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly
 95 100 105
 Asp Glu Val Lys Lys Glu
 110 115

<210> 673
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 673
 Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
 -15 -10 -5
 Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
 1 5 10 15
 Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
 20 25 30
 Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser Thr
 35 40 45
 Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val His
 50 55 60
 His Arg Glu Gly Asp

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65

<210> 674
 <211> 292
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 674
 Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe
 -25 -20 -15
 Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr
 -10 -5 1
 Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr
 5 10 15
 Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr
 20 25 30 35
 Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu
 40 45 50
 Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe Pro Lys Asn
 55 60 65
 Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Xaa His
 70 75 80
 Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His His Cys Val
 85 90 95
 Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa Phe Leu Ile
 100 105 110 115
 Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser
 120 125 130
 Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu
 135 140 145
 Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val Phe
 150 155 160
 Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu
 165 170 175
 Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr Leu Leu Phe
 180 185 190 195
 Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg
 200 205 210
 Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro
 215 220 225
 Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His Gly Leu Arg
 230 235 240
 Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg
 245 250 255
 Lys Lys Gln Glu
 260

<210> 675
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<400> 675

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Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
 -55 -50 -45
 Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Asn Pro Ser
 -40 -35 -30 -25
 Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
 -20 -15 -10
 Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly
 -5 1 5
 Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala Gly Pro
 10 15 20
 Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly Pro Leu
 25 30 35 40
 Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser Cys Gly
 45 50 55
 Ala His Pro Lys Val Leu Lys Val Ala Leu
 60 65

<210> 676

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 676

Met Leu Xaa Leu Ser Arg Ala Thr Lys Xaa Gly Arg Ala Arg Trp Leu
 -25 -20 -15
 Met Pro Val Ile Pro Ala Leu Gln Glu Ala Xaa Ala Gly Gly Ser Arg
 -10 -5 1
 Gly Gln Glu Phe Glu Thr Ser Leu Ala Asn Met Glu Thr Glu Ala Gly
 5 10 15 20
 Glu Leu Leu Lys Pro Arg Arg Arg Arg Leu Gln
 25 30

<210> 677

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 677

Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

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<210> 678
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 678
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

<210> 679
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 679
 Met Ser Leu Thr Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
 -25 -20 -15 -10
 Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
 -5 1 5
 Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
 10 15 20
 Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 25 30 35
 Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 40 45 50 55
 Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
 60 65 70
 Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
 75 80

<210> 680
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 680
 Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp

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Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr Gly
 -40 -35 -30
 Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp Leu
 -25 -20 -15 -10
 Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys Asn
 -5 1 5
 Thr Lys Gly Asn Thr Leu Lys Glu Trp Ile Ala Tyr Ile Cys Xaa
 10 15 20
 Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile His
 25 30 35
 Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu Val
 40 45 50 55
 Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val Gly
 60 65 70
 Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa Val
 75 80 85
 Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa Asp
 90 95 100
 Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu Pro
 105 110 115
 Leu Ser Val Thr Cys Thr Pro
 120 125

<210> 683
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 683
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
 35 40 45 50
 Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
 Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
 85 90 95
 Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
 100 105 110
 Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
 115 120 125

<210> 684
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

09973667.01501

<400> 684
 Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg Leu His
 -10 -5 1
 Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser Arg Asn
 5 10 15
 Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser Gln Thr
 20 25 30
 Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
 35 40 45

<210> 685
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 685
 Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg
 -35 -30 -25
 Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile
 -20 -15 -10 -5
 Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg
 1 5 10
 Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys
 15 20 25
 Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Xaa Xaa Leu Gly
 30 35 40
 Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn Xaa
 45 50 55 60
 Ala Ala Ser Xaa Gln
 65

<210> 686
 <211> 341
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 686
 Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu
 -55 -50 -45 -40
 Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His Leu Cys
 -35 -30 -25
 Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala Ala Leu
 -20 -15 -10
 Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val Asp Val
 -5 1 5
 Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys Gln Arg
 10 15 20 25
 Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met Pro Asn
 30 35 40
 Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser Arg Lys
 45 50 55
 Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln Gly Asp
 60 65 70

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<222> -26...-1

<400> 688

Met Glu Glu Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys
-25 -20 -15
Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
-10 -5 1 5
Ser Val Arg Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
10 15 20
Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
25 30 35
Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
40 45 50

<210> 689

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44...-1

<400> 689

Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys Ile
-40 -35 -30
Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala Gly Ile
-25 -20 -15
Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala Val Val Tyr
-10 -5 1
Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys Gly Val Phe
5 10 15 20
Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
25 30 35
Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
40 45 50
Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
55 60 65
Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn Thr Asp Val
70 75 80
Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile Phe Phe Ser
85 90 95 100
Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp Thr
105 110

<210> 690

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 690

Met Asn Trp Glu Leu Leu Leu Trp Leu Val Leu Cys Ala Leu Leu
-25 -20 -15
Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
-10 -5 1
Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
5 10 15 20

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Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
 25 30 35
 Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 40 45 50
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 55 60 65
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
 70 75 80
 Thr Asp Thr Gly Ser His Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly
 85 90 95 100
 Ile Trp

<210> 691
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -62...-1

<400> 691
 Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
 -60 -55 -50
 Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
 -45 -40 -35
 Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
 -30 -25 -20 -15
 Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
 -10 -5 1
 Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu
 5 10 15
 Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro
 20 25 30
 Val Gln Ser Asn Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys
 35 40 45 50
 Thr Ile Gly Asn Asn Gly Asn Gln Ser His Lys Met Thr Thr Ser Arg
 55 60 65
 Cys Val Arg Leu Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val
 70 75 80
 Trp Ile Ser Glu Gln Pro Phe Leu Val Thr Tyr Leu Trp Gln Tyr
 85 90 95
 Met Pro Thr Trp Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg
 100 105 110
 Ile Glu Asn Phe Lys Ser Gly Val Asp Ala Xaa Ser Ser Tyr Phe Lys
 115 120 125 130
 Ile Phe Lys Thr Lys His Asp
 135

<210> 692
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 692
 Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu

<400> 696
 Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 Thr Phe Ala His
 20

<210> 697
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -97..-1

<400> 697
 Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50
 Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
 -45 -40 -35
 Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
 -30 -25 -20
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
 -15 -10 -5
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
 1 5 10 15
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
 20 25

<210> 698
 <211> 230
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 698
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg

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75 80 85
 Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
 90 95 100
 Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
 105 110 115 120
 Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
 125 130 135
 Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile
 140 145 150
 Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser
 155 160 165
 Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser
 170 175 180
 Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr
 185 190 195 200
 Ser Leu Thr Gly Tyr Val
 205

<210> 699
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 699
 Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Ala Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Gly Ser Ile Cys
 35 40

<210> 700
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 700
 Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
 -30 -25 -20
 Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
 -15 -10 -5
 Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
 1 5 10 15
 Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
 20 25 30
 Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
 35 40 45
 Asp Pro Lys Arg Lys Thr Lys Cys
 50 55

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THESE

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<400> 701
Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
      -30      -25      -20      .
Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
      -15      -10      -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1      5      10      15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
      20      25      30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
      35      40      45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
      50      55      60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65      70

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<220>
<221> SIGNAL
<222> -21..-1
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Met	Trp	Trp	Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val
-20						-15					-10				
Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr
-5					1			5						10	
Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr
			15					20					25		
Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala
		30				35						40			
Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala
		45				50					55				
Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu
60					65					70				75	
Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe
				80					85					90	
Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr
			95					100						105	
Phe	Gly	Met	Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr
		110					115					120			
Gln	Met	Gln	Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu
		125				130					135				
Leu	Leu	Val	Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys
140					145					150				155	
Ser	Ser	Val	Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys
			160						165					170	
Leu	His	Trp	Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr

175 180 185
 Thr Ala Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu
 190 195 200
 Thr Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
 205 210 215
 Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn
 220 225 230 235
 Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile Arg
 240 245

<210> 703
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 703
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 704
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46...-1

<400> 704
 Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile
 -45 -40 -35
 Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys
 -30 -25 -20 -15
 Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu
 -10 -5 1
 Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu
 5 10 15
 Lys Tyr His Trp Pro
 20

<210> 705
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

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<400> 705

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
-25 -20 -15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
-10 -5 1
Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
5 10 15 20
Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
25 30 35
Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
40 45 50
Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Tyr
55 60 65
Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
70 75 80
Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe
85 90 95 100
Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys
105 110 115
Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val
120 125 130
Val Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu
135 140 145
Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg
150 155 160
Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn
165 170 175 180
Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu
185 190 195
Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys
200 205 210
Tyr Trp Gly Lys Phe Tyr Met Pro Lys Arg Val
215 220

<210> 706

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 706

Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
-45 -40 -35
Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
-30 -25 -20
Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
-15 -10 -5
Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
1 5 10 15
Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
20 25 30
Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
35 40 45
Glu Val Leu
50

<210> 707

<211> 81

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31...-1

<400> 707
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
-30 -25 -20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15 -10 -5 1
Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
5 10 15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
20 25 30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
35 40 45
Leu
50

<210> 708
<211> 150
<212> PRT
<213> Homo sapiens

<400> 708
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
1 5 10 15
Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
20 25 30
Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
35 40 45
Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
50 55 60
Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
65 70 75 80
Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
85 90 95
Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
100 105 110
Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His
115 120 125
Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser
130 135 140
Val Ser Thr Lys Lys Lys
145 150

<210> 709
<211> 273
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45...-1

<400> 709
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
-45 -40 -35 -30
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg

95 100 105
 Gln Ala Val Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys
 110 115 120
 Leu Glu Ala Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val
 125 130 135
 Gln Thr Glu Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser
 140 145 150 155
 Ile Leu Asn Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu
 160 165 170
 Glu Lys Lys Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val
 175 180 185
 Gln Gln Lys Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg
 190 195 200
 Ser Gln Trp Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met
 205 210 215
 Lys Trp Ser Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys
 220 225 230 235
 Lys Leu Lys Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln
 240 245 250
 Met Phe Arg Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr
 255 260 265
 Leu Asn Ser Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln
 270 275 280
 Arg Gln Val Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr
 285 290 295
 Gly Val Leu Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu
 300 305 310 315
 Val Asp Val Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg
 320 325 330
 Thr Tyr Ser Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg
 335 340 345
 Gln Asn Leu Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile
 350 355 360
 Gly Leu Gln Asn Lys Cys Lys Tyr Gly Ala Lys Lys Lys
 365 370 375

<210> 711
 <211> 393
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 711
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 1 5 10
 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 15 20 25
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 30 35 40 45
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 50 55 60
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
 65 70 75
 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
 80 85 90
 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp

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95	100	105
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu		
110	115	120
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe		
	130	135
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr		
	145	150
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu		
	160	165
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met		
	175	180
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu		
190	195	200
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met		
	210	215
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe		
	225	230
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn		
	240	245
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys		
	255	260
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met		
270	275	280
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg		
	290	295
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser		
	305	310
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg		
	320	325
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu		
	335	340
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln		
350	355	360
Gly Leu Asp Tyr Phe Tyr Asp Leu Leu		
	370	

<210> 712

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 712

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr		
	-10	-5
Thr Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val		1
	5	10
Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe		15
20	25	30
Asp Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu		35
	40	45
Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile		50
	55	60
Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu		65
	70	75
Ile Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln		80
	85	90
Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp		95

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          90          95          100
Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile
      105      110      115
Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp
      120      125      130
Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys
      135      140      145
Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
      155      160      165
Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
      170      175      180
Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
      185      190      195
Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
      200      205      210
Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
      215      220      225
Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
      235      240      245
Asn Lys Lys Ala

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<210> 714
<211> 92
<212> PRT
<213> Homo sapiens

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<400> 714
Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly
1      5      10      15
Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr
      20      25      30
Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu
      35      40      45
Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys
      50      55      60
Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe
      65      70      75      80
Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
      85      90

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<210> 715
<211> 127
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -63...-1

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<400> 715
Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
      -60      -55      -50
Pro Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
      -45      -40      -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
      -30      -25      -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
      -15      -10      -5      1
Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
      5      10      15

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Ile Ser His Asp Glu Leu
160

<210> 718
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 718
Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25 -20 -15 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
-5 1 5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
10 15 20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
25 30 35
Ser Gln Gln Glu Glu Leu Lys
40 45

<210> 719
<211> 73
<212> PRT
<213> Homo sapiens

<400> 719
Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu
1 5 10 15
Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu Phe
20 25 30
Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu Gly
35 40 45
Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln Arg
50 55 60
Glu Ser Leu Thr Gly Pro Pro Tyr Leu
65 70

<210> 720
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -150..-1
<220>
<221> UNSURE
<222> -67
<223> Xaa = any one of the twenty amino acids

<400> 720
Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys Asp
-150 -145 -140 -135
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
-130 -125 -120
Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu Leu
-115 -110 -105

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Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly
 -100 -95 -90
 Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly Trp
 -85 -80 -75
 Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu
 -70 -65 -60 -55
 Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg
 -50 -45 -40
 Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr
 -35 -30 -25
 Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys
 -20 -15 -10
 Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser
 -5 1 5 10
 His Arg Ala Arg Gln Arg Lys Thr Ala
 15

<210> 721
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 721
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
 30 35 40
 Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 45 50

<210> 722
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 722
 Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
 -50 -45 -40
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -35 -30 -25
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
 -20 -15 -10
 Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
 -5 1 5 10
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
 15 20 25
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
 30 35 40

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<210> 723
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 723
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
 30 35 40
 Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
 45 50 55
 Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys
 60 65 70

<210> 724
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 724
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 20 25 30
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 35 40 45
 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 50 55 60
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70

<210> 725
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 725
 Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
 1 5 10 15
 Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
 20 25 30
 Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
 35 40 45
 Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
 50 55 60
 Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln

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<211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 728
 Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
 -20 -15 -10
 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
 -5 1 5 10
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
 15 20 25
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
 30 35 40
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
 45 50 55
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
 60 65 70

<210> 729
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 729
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
 55 60 65 70
 Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile
 75 80 85
 Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
 90 95 100
 Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
 105 110 115
 Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
 120 125 130
 Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu
 135 140 145 150
 Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
 155 160 165

<210> 730
 <211> 59

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<212> PRT
<213> Homo sapiens

<400> 730
Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu
1 5 10 15
Cys Pro Ala Glu Leu Phe Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly
20 25 30
Pro Gly Leu Asp Ile Leu Arg Cys Val Leu Ser Pro Trp Ala Ser His
35 40 45
Phe Pro Ser Leu Ser Leu Gly Val Phe Asn Leu
50 55

<210> 731
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 731
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 732
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -94..-1

<400> 732
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-90 -85 -80
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-75 -70 -65
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
-60 -55 -50
Val Leu Phe Asn Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
-45 -40 -35
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
-30 -25 -20 -15
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
-10 -5 1
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
5 10 15
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
20 25 30
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
35 40 45 50
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

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55 60 65
 Arg Arg
 <210> 733
 <211> 154
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -68..-1
 <400> 733
 Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
 -65 -60 -55
 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
 -50 -45 -40
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
 -35 -30 -25
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
 -20 -15 -10
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
 1 5 10
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
 15 20 25
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
 30 35 40
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
 45 50 55 60
 His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
 65 70 75
 Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 80 85
 <210> 734
 <211> 99
 <212> PRT
 <213> Homo sapiens
 <400> 734
 Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu His Gly
 1 5 10 15
 Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala Leu Leu
 20 25 30
 Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn Ile Thr
 35 40 45
 Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His
 50 55 60
 Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr
 65 70 75 80
 Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His
 85 90 95
 Leu Gly Asn
 <210> 735
 <211> 43
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL

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<222> -24...-1

<400> 735

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-20 -15 -10
Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
-5 1 5
Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
10 15

<210> 736

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 736

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
15 20 25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
30 35 40
Val Leu Cys Gln Lys
45

<210> 737

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 737

Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
-15 -10 -5
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
1 5 10
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15 20 25 30
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
35 40 45
Val Thr Val Gly Gly Arg Val Gly Ser Thr Phe Val Ala
50 55 60

<210> 738

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

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<400> 738
 Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
 -45 -40 -35
 Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
 -30 -25 -20
 Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
 -15 -10 -5 1
 Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
 5 10 15
 Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
 20 25 30

<210> 739
 <211> 241
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103...-1

<400> 739
 Met Trp Leu Asp Pro Val Phe Pro Leu Phe Pro Val Gly Asp His Tyr
 -100 -95 -90
 Leu Pro His Leu His Met Asp Val Leu Glu Gly Leu Ile Leu Val Leu
 -85 -80 -75
 Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
 -70 -65 -60
 Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
 -55 -50 -45 -40
 Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
 -35 -30 -25
 Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
 -20 -15 -10
 Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
 -5 1 5
 Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
 10 15 20 25
 Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
 30 35 40
 Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
 45 50 55
 Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Asn
 60 65 70
 Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro
 75 80 85
 Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr
 90 95 100 105
 Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu
 110 115 120
 Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys
 125 130 135
 Ala

<210> 740
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 740

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Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu Leu Thr Glu
 1 5 10 15
 Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn Ala Ala Ile
 20 25 30
 Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu
 35 40 45
 Phe Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg
 50 55 60
 Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly
 65 70 75 80
 Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys
 85 90 95
 Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val
 100 105 110
 Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp
 115 120 125
 Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
 130 135 140

<210> 741
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 741
 Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu
 -20 -15 -10
 Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys
 -5 1 5 10
 Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
 15 20 25
 Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
 30 35 40
 Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly Asn Thr Gln Glu
 45 50 55
 Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val Phe Val Ala Phe
 60 65 70
 Gln Thr Phe Leu Arg Gly Met Val Met Tyr Thr Ser Lys Asp Arg Tyr
 75 80 85 90
 Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser Ala Tyr Pro Ser
 95 100 105
 Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln Tyr Gln Leu Leu
 110 115 120
 Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro
 125 130 135
 Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val
 140 145 150
 Gly Arg
 155

<210> 742
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

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<222> -19...-1

<400> 742

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
-15 -10 -5
Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
1 5 10
Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
15 20 25
Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
30 35 40 45
Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
50 55 60
Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
65 70

<210> 743

<211> 125

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 743

Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
-15 -10 -5 1
Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
5 10 15
Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
20 25 30
Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile
35 40 45
Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe
50 55 60 65
Leu Arg Thr Met His His Leu Leu Leu Glu Glu Val Ile Glu Gly
70 75 80
Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly
85 90 95
Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser
100 105 110

<210> 744

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 744

Met Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr
-30 -25 -20
Phe Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu
-15 -10 -5
Leu Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn
1 5 10
Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr
15 20 25 30

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Thr Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala
 35 40 45
 Val Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val
 50 55 60
 Phe Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu
 65 70 75
 Trp Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu
 80 85 90
 Met Ile Arg Ala Cys Arg Val Asn
 95 100

<210> 745
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -53...-1

<400> 745
 Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp
 -50 -45 -40
 Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His Ile Arg Met
 -35 -30 -25
 Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu
 -20 -15 -10
 Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr
 -5 1 5 10
 Phe Val His Glu Ser Pro Ala Leu Ile Leu Phe Ala Leu Gly Ser
 15 20 25
 Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Arg His Lys Tyr Pro Leu
 30 35 40
 Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val
 45 50 55
 Ala Val Val Val Thr Phe Tyr Asp Val Tyr Ile Ile Leu Gln Ala Phe
 60 65 70 75
 Ile Leu Thr Thr Thr Val Phe Phe Gly Leu Thr Val Tyr Thr Leu Gln
 80 85 90
 Ser Lys Lys Asp Phe Ser Lys Phe Gly Ala Gly Leu Phe Ala Leu Leu
 95 100 105
 Trp Ile Leu Cys Leu Ser Gly Phe Leu Lys Phe Phe Leu Tyr Ser Glu
 110 115 120
 Ile Met Glu Leu Val Leu Ala Ala Ala Gly Ala Leu Leu Phe Cys Gly
 125 130 135
 Phe Ile Ile Tyr Asp Thr His Ser Leu Met His Lys Leu Ser Pro Glu
 140 145 150 155
 Glu Tyr Val Leu Ala Ala Ile Ser Leu Tyr Leu Asp Ile Ile Asn Leu
 160 165 170
 Phe Leu His Leu Leu Arg Phe Leu Glu Ala Val Asn Lys Lys
 175 180 185

<210> 746
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -71...-1

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<400> 746
Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
-70 -65
Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
-55 -50 -45
Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
-35 -30 -25
Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
-20 -15 -10
Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
-5 1 5
Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
10 15 20 25
Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
30 35

<210> 747
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84..-1

<400> 747
Met Ser Gly Gly Pro Glu Ala Arg Pro Pro Met Leu Val Glu Gly Gly
-80 -75 -70
Gly Pro Glu Ser Leu Gln Lys Ala Pro Cys Thr Arg Gly Pro Pro Ser
-65 -60 -55
His Pro Val Pro Pro Ala Leu Ala Phe Thr Val Gly Asn Gly Ser Gly
-50 -45 -40
Pro Gly Val Arg Cys Pro Arg Asn Met Ala Glu Gly His Pro Gly Pro
-35 -30 -25
Glu Arg Arg Gln Ser Gln Gln Gly Leu Phe Arg Ala Ala Trp Leu Pro
-20 -15 -10 -5
Gly Ser Arg Pro Ser Pro Leu Phe Cys Val Cys Ser Val Thr Ser Pro
1 5 10
Gly Trp Asp Val Pro Gln Val His Arg Val Glu Val Gly His Gly Arg
15 20 25
Arg Gln Glu Thr His Pro Val Arg Arg Arg Ala
30 35

<210> 748
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 748
Met Pro Arg Gly Arg Arg Leu Gly Met Val Phe Ala Pro Pro Arg Pro
-45 -40 -35
Gly Gln Arg Gln Ala Gly Ala Pro Trp Val Pro Glu Arg Arg Lys Arg
-30 -25 -20
Arg Pro Asp Gly Asp Thr Phe Leu Leu Ser Phe Leu Ser Thr Thr Trp
-15 -10 -5
Leu Lys Thr Trp Arg Ser Gln Gln Tyr Lys Glu Ser Lys Ser Arg Ser
1 5 10 15

Cys Ala Arg Glu Gln Met Asn Ser Ser Ser Cys
20 25

<210> 749
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 749
Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile Ser Gln
-40 -35 -30 -25
Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala Leu
-20 -15 -10
Phe Val Ala Phe Leu Leu Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser
-5 1 5
Gln Lys His Thr Arg Leu Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu
10 15 20
Asn Asp Val Gln His Gly Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu
25 30 35 40

<210> 750
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 750
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
-45 -40 -35
Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
-30 -25 -20
His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
-15 -10 -5
Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
1 5 10 15
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
20 25 30
Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
35 40 45
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Val Phe Val
50 55 60
Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
65 70 75
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
80 85 90 95
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
100 105 110
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
115 120 125
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
130 135 140
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
145 150 155
Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp

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160 165 170 175
 Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 180 185 190
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
 195 200 205
 His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
 210 215 220
 Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
 225 230 235
 Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
 240 245 250 255
 Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
 260 265 270
 Thr Pro Trp Cys Thr Phe Ser
 275

<210> 751
 <211> 235
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 751
 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe
 -20 -15 -10 -5
 Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile
 1 5 10
 Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly
 15 20 25
 Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
 30 35 40
 His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
 45 50 55 60
 Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
 65 70 75
 Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
 80 85 90
 Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
 95 100 105
 Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
 110 115 120
 Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
 125 130 135 140
 Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
 145 150 155
 Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
 160 165 170
 Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
 175 180 185
 His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
 190 195 200
 Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
 205 210 215

<210> 752
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 752
 Met Arg Val Tyr Lys Arg Thr Gln Leu Arg Gln Glu Thr Gly Pro Lys
 -30 -25 -20
 Ser Tyr Val Leu Phe Ser Ala Ser Ser Phe Pro Ser Ile Ser Gly Asn
 -15 -10 -5 1
 Ile Arg Ser Arg Asn Tyr Phe Gln Lys Gln Asn Asn His Trp Phe Gln
 5 10 15
 Thr Ser Asp Tyr
 20

<210> 753
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 753
 Met Gln Asp Glu Asp Gly Tyr Ile Thr Leu Asn Ile Lys Thr Arg Lys
 -45 -40 -35
 Pro Ala Leu Val Ser Val Gly Pro Ala Ser Ser Phe Trp Trp Arg Val
 -30 -25 -20
 Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val Val Gly Leu
 -15 -10 -5 1
 Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp
 5 10 15
 Glu Asn Gln Asp Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
 20 25 30
 Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly
 35 40 45
 His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
 50 55 60 65
 Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
 70 75 80
 Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn
 85 90 95
 Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly
 100 105 110
 Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser
 115 120 125
 Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn
 130 135 140 145
 Met Asn Cys Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys
 150 155 160
 Glu Asn Lys His Tyr Leu Met Cys Glu Arg Lys Ala Gly Met Thr Lys
 165 170 175
 Val Asp Gln Leu Pro
 180

<210> 754
 <211> 92
 <212> PRT
 <213> Homo sapiens

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235 240 245
 Glu Ser Gly Ile Cys Met Asp Ser Gly Gly Phe Arg Thr Thr Ala Ser
 250 255 260 265
 Met Val Ser Val Leu Pro Gln Asp Pro Thr Gln Pro Cys Val His Phe
 270 275 280
 Leu Thr Ala Thr Pro Asp Pro Ser Arg Ser Val Phe Lys Pro Phe Ile
 285 290 295
 Phe Gly Val Gly Val Ala Gln Ala Pro Gln Val Leu Ser Pro Thr Phe
 300 305 310
 Gly Ala Gln Asp Pro Val Arg Thr Leu Pro Arg Phe Gln Thr Gln Val
 315 320 325
 Asp Arg Arg His Thr Leu Tyr Arg Gly His Gln Ala Ala Leu Gly Leu
 330 335 340 345
 Met Glu Arg Asp Gln Asp Arg Gly Gln Gln Leu Gln Gln Lys Gln Gln
 350 355 360
 Asp Leu Glu Gln Glu Gly Leu Glu Ala Thr Gln Gly Leu Leu Ala Gly
 365 370 375
 Glu Trp Ala Pro Pro Leu Trp Glu Leu Gly Ser Leu Phe Gln Ala Phe
 380 385 390
 Val Lys Arg Glu Ser Gln Ala Tyr Ala
 395 400

<210> 756

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -62...-1

<400> 756

Met Ala Ile Phe Trp Ile Val His Ala His Phe Trp Ser Pro Leu Pro
 -60 -55 -50
 Pro Arg Leu Pro His Gly Arg Cys Cys Cys Leu Lys Ala Pro Leu Pro
 -45 -40 -35
 Pro Asp Val Gly Pro Leu Gln Val Ala Pro His Leu Phe Ser Val Pro
 -30 -25 -20 -15
 Leu His Ile Leu Thr Val Pro Leu Leu Glu Pro Ala Arg Cys Ser Gly
 -10 -5 1
 Ile Leu Val Phe Phe Leu His Gln Pro Val Ser Ser Leu Ser Phe Cys
 5 10 15
 Tyr Phe Ile Gly Gly Trp Cys
 20 25

<210> 757

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -100...-1

<400> 757

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 -100 -95 -90 -85
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
 -80 -75 -70
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
 -65 -60 -55

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Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 -50 -45 -40
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 -35 -30 -25
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 -20 -15 -10 -5
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 1 5 10
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
 15 20 25
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 30 35 40
 Gly Tyr Leu Met Gly
 45

<210> 758

<211> 187

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 758

Met Ala Asn Asn Thr Thr Ser Leu Gly Ser Pro Trp Pro Glu Asn Phe
 -35 -30 -25 -20
 Trp Glu Asp Leu Ile Met Ser Phe Thr Val Ser Met Ala Ile Gly Leu
 -15 -10 -5
 Val Leu Gly Gly Phe Ile Trp Ala Val Phe Ile Cys Leu Ser Arg Arg
 1 5 10
 Arg Arg Ala Ser Ala Pro Ile Ser Gln Trp Ser Ser Ser Arg Arg Ser
 15 20 25
 Arg Ser Ser Tyr Thr His Gly Leu Asn Arg Thr Gly Phe Tyr Arg His
 30 35 40 45
 Ser Gly Cys Glu Arg Arg Ser Asn Leu Ser Leu Ala Ser Leu Thr Phe
 50 55 60
 Gln Arg Gln Ala Ser Leu Glu Gln Ala Asn Ser Phe Pro Arg Lys Ser
 65 70 75
 Ser Phe Arg Ala Ser Thr Phe His Pro Phe Leu Gln Cys Pro Pro Leu
 80 85 90
 Pro Val Glu Thr Glu Ser Gln Leu Val Thr Leu Pro Ser Ser Asn Ile
 95 100 105
 Ser Pro Thr Ile Ser Thr Ser His Ser Leu Ser Arg Pro Asp Tyr Trp
 110 115 120 125
 Ser Ser Asn Ser Leu Arg Val Gly Leu Ser Thr Pro Pro Pro Pro Ala
 130 135 140
 Tyr Glu Ser Ile Ile Lys Ala Phe Pro Asp Ser
 145 150

<210> 759

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 759

Met Ala Thr Ala Ala Gly Ala Thr Tyr Phe Gln Arg Gly Ser Leu Phe

Leu Ser Pro Leu Phe Leu Ser His
65 70

<210> 762
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 762
Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Val Ala Leu Ser
-20 -15 -10 -5
Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
1 5 10
Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
15 20 25
Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
30 35 40
Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
45 50 55 60
Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
65 70 75
Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
80 85 90
Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile
95 100 105
Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Thr Gly Arg
110 115 120
Tyr Ser Asn Arg Leu Tyr Ala Tyr Glu Pro Ala Asp Thr Ala Leu Leu
125 130 135 140
Leu Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr Glu Leu
145 150 155

<210> 763
<211> 303
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 763
Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
-20 -15 -10 -5
Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
1 5 10
Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
15 20 25
Cys Gln Leu Pro Gly Leu Phe Ser Tyr Ala Gln His Ile Ala Ser Ile
30 35 40
Asp Gly Arg Arg Gly Leu Phe Thr Gly Leu Thr Pro Arg Leu Cys Ser
45 50 55 60
Gly Val Leu Gly Thr Val Val His Gly Lys Val Leu Gln His Tyr Gln
65 70 75
Glu Ser Asp Lys Gly Glu Glu Leu Gly Pro Gly Asn Val Gln Lys Glu
80 85 90
Val Ser Ser Ser Phe Asp His Val Ile Lys Glu Thr Thr Arg Glu Met

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95 100 105
 Ile Ala Arg Ser Ala Ala Thr Leu Ile Thr His Pro Phe His Val Ile
 110 115 120
 Thr Leu Arg Ser Met Val Gln Phe Ile Gly Arg Glu Ser Lys Tyr Cys
 125 130 135 140
 Gly Leu Cys Asp Ser Ile Ile Thr Ile Tyr Arg Glu Glu Gly Ile Leu
 145 150 155
 Gly Phe Phe Ala Gly Leu Val Pro Arg Leu Leu Gly Asp Ile Leu Ser
 160 165 170
 Leu Trp Leu Cys Asn Ser Leu Ala Tyr Leu Val Asn Thr Tyr Ala Leu
 175 180 185
 Asp Ser Gly Val Ser Thr Met Asn Glu Met Lys Ser Tyr Ser Gln Ala
 190 195 200
 Val Thr Gly Phe Phe Ala Ser Met Leu Thr Tyr Pro Phe Val Leu Val
 205 210 215 220
 Ser Asn Leu Met Ala Val Asn Asn Cys Gly Leu Ala Gly Gly Cys Pro
 225 230 235
 Pro Tyr Ser Pro Ile Tyr Thr Ser Trp Ile Asp Cys Trp Cys Met Leu
 240 245 250
 Gln Lys Gly Gly Asn Met Ser Arg Gly Asn Ser Leu Phe Phe Arg Lys
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<213> Homo sapiens

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 Lys Lys Lys Asp Val Leu Phe Thr Ser Tyr Phe Lys Thr Ile Ala Phe
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 Leu Leu Leu Tyr Val Ser Ala Gly Pro Ile Ser Arg Ile Phe Ile Arg
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 Ser Leu Glu Leu Phe Leu Met Phe Pro Ser Asn Lys His Trp Tyr Ile
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 Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Ser
 20 25 30
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

35 40 45
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 50 55 60
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Tyr
 65 70 75
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
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 Tyr Met Asp Ala Pro Lys Ala Ala Leu
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 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 20 25 30 35
 Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 40 45 50
 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
 55 60 65
 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 70 75 80
 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 85 90 95
 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 100 105 110 115
 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 120 125 130
 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys
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 Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Phe Leu Phe Gly
 -20 -15 -10 -5
 Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val
 1 5 10
 Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
 15 20 25

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Gly Phe Lys Asn Lys Thr Val Leu Asn Lys Arg Cys Lys Asp Cys Tyr
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 Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
 45 50 55 60
 Arg His Lys Gln Arg Gln Met
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 -55 -50 -45
 Leu Pro Glu Ser Pro Phe Leu Leu Ala Ser Ser Pro Leu Pro Pro Leu
 -40 -35 -30
 Pro Thr Thr Leu Arg Lys Phe Ile Pro Pro Pro Ser Leu Ile Ser Cys
 -25 -20 -15
 Thr Cys Leu Leu Leu Tyr Leu Thr His Cys Ile Leu Gly Ile Cys Phe
 -10 -5 1 5
 Ala Tyr Pro Phe Ile Leu
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 Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
 -290 -285 -280
 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
 -275 -270 -265
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
 -260 -255 -250
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
 -245 -240 -235
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
 -230 -225 -220 -215
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
 -210 -205 -200
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
 -195 -190 -185
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
 -180 -175 -170
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
 -165 -160 -155
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val

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-150 -145 -140 -135
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
 -130 -125 -120
 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
 -115 -110 -105
 Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
 -100 -95 -90
 Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
 -85 -80 -75
 Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
 -70 -65 -60 -55
 Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
 -50 -45 -40
 Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
 -35 -30 -25
 Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
 -20 -15 -10
 Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
 -5 1 5 10
 Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
 15 20 25
 Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val
 30 35 40
 Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser
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 1 5 10
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 15 20 25 30
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 35 40 45
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 50 55 60
 Glu Tyr Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 65 70 75

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<400> 771

Met Arg Glu Met Pro Val Pro Ser Leu Ile Asn Leu Ala Ala Ser Arg
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Thr Leu Ser Phe Cys Ile Ser Asp Asn His Val Ser Ser Pro Gly Pro
-5 1 5 10
Ala Asn Pro Ser Cys Gly Leu His Pro His Trp Leu Arg Pro Leu Lys
15 20 25
Leu Leu Thr Tyr Thr Cys Arg Glu Leu Lys Leu Gln Gly
30 35 40

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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
-15 -10 -5 1
Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
5 10 15
Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
20 25 30
Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
35 40 45
Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
50 55 60 65
Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
70 75 80
Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
85 90 95
Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
100 105 110
Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
115 120 125
Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
130 135 140 145
Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
150 155 160
Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
165 170 175
Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
180 185 190
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
195 200 205
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
210 215 220 225
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
230 235 240
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
245 250 255
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
260 265 270
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
275 280 285

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Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
290 295 300

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Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
-80 -75 -70
Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
-65 -60 -55
Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
-50 -45 -40
Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
-35 -30 -25 -20
Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
-15 -10 -5
Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
1 5 10
Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
15 20 25
Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
30 35 40 45
Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
50 55 60
Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
65 70 75
Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
80 85 90
Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
95 100 105
Leu Gln
110

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Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
-50 -45 -40
Thr Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg
-35 -30 -25 -20
Asp Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Ser Leu Phe Met
-15 -10 -5
Gly Phe Gly Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val

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1 5 10 15
Leu Leu Pro Asn Tyr Gln Leu Arg Gly Ser Val Pro Lys Arg Glu Lys
20 25 30
Arg Pro Lys Arg Lys His Gln His Leu Phe Thr Pro Ser Glu Arg His
35 40 45
Ser Val Cys Leu Asp Cys Leu Leu Glu Ile Ser Leu Ser Gly Lys Gln
50 55 60
Trp Arg Asn Val Ile Ser Phe Asn Cys Phe Cys Thr Thr Lys Thr Leu
65 70 75 80
Phe Trp Val Asn

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Met	Ala	Lys	Ala	Glu	Ser	Pro	Lys	Glu	His	Asp	Pro	Phe	Thr	Tyr	Asp
				1				5					10		
Tyr	Gln	Ser	Leu	Gln	Ile	Gly	Gly	Leu	Val	Ile	Ala	Gly	Ile	Leu	Phe
			15				20					25			
Ile	Leu	Gly	Ile	Leu	Ile	Val	Leu	Ser	Arg	Arg	Cys	Arg	Cys	Lys	Phe
			30				35				40				
Asn	Gln	Gln	Gln	Arg	Thr	Gly	Glu	Pro	Asp	Glu	Glu	Glu	Gly	Thr	Phe
45					50					55					60
Arg	Ser	Ser	Ile	Arg	Arg	Leu	Ser	Thr	Arg	Arg	Arg				
				65					70						

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Gly	Gly	Ala	Cys	Ile	Tyr	Lys	His	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr
5															
Arg	Gly	Glu	Met	Cys	Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu
20															
Arg	Gly	Gly	Glu	Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile
25															
30															

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35 40 45 50
 Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
 Ser Asp Ser Asp 55 Ala Ala Ile Ile His 60 Asp Phe Glu Lys Gly Met
 Thr Ala Tyr Leu Asp Leu Leu Leu Gly 75 Asn Cys Tyr Leu Met Pro Leu
 Asn Thr Ser Ile Val Met Pro Pro Glu Asn Leu Val Glu Leu Phe Gly
 Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
 Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
 Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
 Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
 Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
 Gln Glu
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 His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met Glu Tyr Tyr
 Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Gly Glu Ala Lys Asp Lys
 Ala Gly Gly Gly Gly Ser Gly Val Gly Ala Gln Gly Arg Ser His Thr
 Ser Arg Gln Glu Arg Arg Leu Gly Leu Gly Ser Asp Asp Ala Asn
 Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu Thr Gly
 Ala Gln Gln Glu Asp Val Gly Gly Leu Cys Arg Gly Asp Leu Ser Leu
 Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro Ser Ala
 Ser Pro Glu Glu Asp Gly Glu Ser Glu Asp Tyr Gln Asn Ser Ala Ser
 Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu Gln Arg
 Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp Gly Glu
 Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala
 55 60 65

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1 5 10 15
Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
20 25 30
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
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Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
50 55 60
Leu Pro Ser Glu Lys
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-35 -30 -25 -20
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
-15 -10 -5
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
1 5 10
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
15 20 25
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30 35 40 45
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
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Arg Thr Phe

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Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15 -10 -5 1

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Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
5 10 15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
20 25 30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
35 40 45
Leu
50

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-35 -30 -25
Thr His Ile Asp Val His Ile His Gln Glu Ser Ala Leu Ala Lys Leu
-20 -15 -10
Leu Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg
-5 1 5
Gly Ser Ser Arg Leu Leu Val Ala Ser Trp Val Met Gln Ile Val Leu
10 15 20 25
Gly Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr
30 35 40
Thr Leu Leu Val Thr Ser Gly Ala Ala Ile Trp Thr Gly Ala Val Ala
45 50 55
Val Leu Ala Gly Ala Ala Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr
60 65 70
Tyr Trp Ala Leu Leu Arg Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr
75 80 85
Ala Ile Ala Ala Leu Lys Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr
90 95 100 105
Ser Tyr Tyr Asn Ser Ala Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn
110 115 120
Thr Pro Ala Pro Thr Gln Ser Pro Glu Glu Val Arg Arg Leu His Leu
125 130 135
Cys Thr Ser Phe Met Asp Met Leu Lys Ala Leu Phe Arg Thr Leu Gln
140 145 150
Ala Met Leu Leu Gly Val Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala
155 160 165
Pro Leu Trp Leu Tyr Cys Trp Arg Met Phe Pro Thr Lys Gly Lys Arg
170 175 180 185
Asp Gln Lys Glu Met Leu Glu Val Ser Gly Ile
190 195

<210> 783
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 783
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu

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Asn Phe Ser Ala Asp Gln Val Thr Arg Xaa Leu Glu Asn Val Leu Ser
 50 55 60
 Gly Lys Ala
 65

<210> 787
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<220>
 <221> UNSURE
 <222> 49,74,75,88,98,104,112,114,120
 <223> Xaa = any one of the twenty amino acids

<400> 787
 Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
 -25 -20 -15
 Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
 -10 -5 1 5
 Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
 10 15 20
 Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
 25 30 35
 Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Xaa Tyr Leu Val Ile
 40 45 50
 Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
 55 60 65
 Gly Leu Cys Leu Xaa Xaa Lys Leu Gln Arg Cys Leu Pro Phe Lys His
 70 75 80 85
 Lys Leu Xaa Ile Tyr Ile Ser Glu Gly Thr His Ser Xaa Glu Glu Asp
 90 95 100
 Ile Asn Xaa Gln Ile Asn Asp Lys Glu Arg Xaa Ala Xaa Ala Met Glu
 105 110 115
 Asn Pro Xaa Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
 120 125 130

<210> 788
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 788
 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
 Pro Leu Ser Asp Val Leu Asn Thr Val His Lys
 30 35

<210> 789

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<211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<220>
 <221> UNSURE
 <222> 48
 <223> Xaa = any one of the twenty amino acids

<400> 789
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -45 -40 -35
 Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -30 -25 -20
 Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -15 -10 -5
 Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10 15
 Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
 20 25 30
 Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Xaa
 35 40 45
 Leu Leu Met Val Ala Lys Ile Gly Val Ser Met Phe Asn Arg Pro His
 50 55 60

<210> 790
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<220>
 <221> UNSURE
 <222> 27,28,43,44,49,50,52,53
 <223> Xaa = any one of the twenty amino acids

<400> 790
 Met Gly Gly Asn Gly Ser Thr Cys Lys Pro Asp Thr Glu Arg Gln Gly
 -55 -50 -45
 Thr Leu Ser Thr Ala Ala Pro Thr Thr Ser Pro Ala Pro Cys Leu Ser
 -40 -35 -30 -25
 Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys Ala Gly Val
 -20 -15 -10
 Leu Leu Thr Leu Leu Leu Ile Ala Phe Ile Phe Leu Ile Ile Lys Ser
 -5 1 5
 Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Asp Pro His Ser Asp
 10 15 20
 Pro Pro Xaa Xaa Leu Ser Ser Ile Pro Gly Glu Ser Leu Thr Tyr Ala
 25 30 35 40
 Ser Thr Xaa Xaa Gln Thr Leu Arg Xaa Xaa Glu Xaa Xaa Leu Gly
 45 50 55

<210> 791
 <211> 144

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -77..-1

<220>
<221> UNSURE
<222> -65,31,34
<223> Xaa = any one of the twenty amino acids

<400> 791
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Xaa Gly Gly Tyr
-75 -70 -65
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
-60 -55 -50
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
-45 -40 -35 -30
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
-25 -20 -15
Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
-10 -5 1
Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
5 10 15
Ile Met Lys Asp Val Pro Asp Trp Lys Val Gly Xaa Ser Val Xaa His
20 25 30 35
Thr Thr Arg Trp Val Pro Pro Leu Ile Gly Glu Leu Tyr Gly Leu Arg
40 45 50
Thr Thr Lys Glu Ala Leu His Ala Ser His Gly Phe Met Trp Tyr Thr
55 60 65

<210> 792
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<220>
<221> UNSURE
<222> 48,52,55,59,65
<223> Xaa = any one of the twenty amino acids

<400> 792
Met Glu Thr Gly Arg Leu Leu Ser Leu Ser Ser Leu Pro Leu Val Leu
-15 -10 -5
Leu Gly Trp Glu Tyr Ser Ser Gln Thr Leu Asn Leu Val Pro Ser Thr
1 5 10
Ser Ile Leu Ser Phe Val Pro Phe Ile Pro Leu His Leu Val Leu Phe
15 20 25 30
Ala Leu Trp Tyr Leu Pro Val Pro His His Leu Tyr Pro Gln Gly Leu
35 40 45
Gly Xaa His Ala Ala Xaa Ala Glu Xaa Gly Lys Arg Xaa Glu Gly Gly
50 55 60
Thr Gln Xaa Ala Leu Trp Leu Arg Val Gln Pro Ser Cys Pro Ser Pro
65 70 75
Val Cys Leu Glu Pro Val Pro Pro Arg Ser Arg Phe Leu Leu
80 85 90

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<210> 793
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 793
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala
 -35 -30 -25
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 -20 -15 -10 -5
 Thr Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg
 1 5 10
 Asp Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Ser Leu Phe Met
 15 20 25
 Gly Phe Gly Val Leu Phe Leu Leu Leu Trp Val Gly Ile Tyr Val
 30 35 40

<210> 794
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<220>
 <221> UNSURE
 <222> 81,84,87,131,135,143,156
 <223> Xaa = any one of the twenty amino acids

<400> 794
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Xaa His Ile Xaa Thr Glu Xaa Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Met Trp Tyr
 115 120 125
 Asn Phe Phe Arg Xaa Trp Asn Gly Xaa Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Xaa Gly Phe Ile Leu Gly Gly Ile Phe Val Val Gly Ser Xaa Lys Ala
 145 150 155

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Gly His Ser Ser
160

<210> 795
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<220>
<221> UNSURE
<222> 32,91,98
<223> Xaa = any one of the twenty amino acids

<400> 795
Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Phe Pro Thr Gly
-15 -10 -5
Phe Ser Ser Pro Ser Pro Ser Ala Ala Ala Ala Gln Glu Val Arg
1 5 10
Ser Ala Thr Asp Gly Asn Thr Ser Thr Thr Pro Thr Ser Ala Lys
15 20 25 30
Lys Xaa Lys Leu Asn Ser Ser Ser Ser Ser Ser Asn Ser Ser Asn
35 40 45
Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Ser Pro Pro
50 55 60
Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser Phe Cys Leu
65 70 75
Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Xaa Lys Lys Leu
80 85 90
Arg Phe Glu Xaa Thr Leu Glu Phe Val Gly Phe Asp Ala Lys Met Ala
95 100 105 110
Glu Glu Ser Ser Ser Ser Ser Ser Ser Ser Pro Thr Ala Ala Thr
115 120 125
Ser Gln Gln Gln Gln Leu Lys Asn Lys Ser Ile Leu Asn Leu Phe Cys
130 135 140
Gly Phe Gly Ala Ser Cys Lys Arg Pro Ser Gln Ile Phe Tyr His Arg
145 150 155
Leu

<210> 796
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22...-1

<400> 796
Met Gln Gly His Trp Leu Ser Ser Ala Phe Ala Leu Val Trp Leu Trp
-20 -15 -10
Leu Arg Ser Thr Gly Cys Phe Trp Trp Asp His Trp Leu Cys Lys Ser
-5 1 5 10
Arg Gln Arg Ala Val Pro Gly Cys Arg Ala Ala Leu Trp Gln Ser Ser
15 20 25
Arg Pro Gly Cys Leu Pro Ala Val Ser Gly Ser Lys Glu Arg Leu Gly
30 35 40
Phe Pro Ser Tyr Ile Trp Tyr Leu Gly Trp His Tyr Gly Asn Glu Val

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Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
 10 15 20 25
 Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
 30 35 40
 Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
 45 50 55
 Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
 60 65 70
 Thr Phe Val Ser Arg His Lys Lys Phe Asp Xaa Phe Arg Xaa Leu
 75 80 85
 Xaa Glu Asn Ala Xaa Lys Ser Leu Asn Asp Xaa Phe Val Arg Thr Tyr
 90 95 100 105
 Gly Met Leu Tyr Xaa Gln Asn Xaa Glu Val Phe Xaa Asp Leu Phe Thr
 110 115 120
 Xaa Leu Lys Arg Tyr Tyr Thr Gly Gly Asn Val Asn Leu Glu Glu Met
 125 130 135
 Leu Asn Asp Phe Trp Ala Arg Leu Leu Glu Arg Met Phe Gln Xaa Xaa
 140 145 150
 Asn Pro Gln Tyr His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys
 155 160 165
 Tyr Thr Asp Xaa Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys
 170 175 180 185
 Ile Gln Val Thr Arg Ala Phe Xaa Xaa Ala Arg Thr Phe Val Gln Gly
 190 195 200
 Leu Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ile Glu
 205 210 215
 Asn Val Leu Ser Phe Ser Leu Val Phe Leu Val Tyr Ser Val Phe Lys
 220 225 230
 Thr Asn Val
 235

<210> 799

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -62..-1

<220>

<221> UNSURE

<222> 37,43

<223> Xaa = any one of the twenty amino acids

<400> 799

Met Gly Glu Ser Ile Pro Leu Ala Ala Pro Val Pro Val Glu Gln Ala
 -60 -55 -50
 Val Leu Glu Thr Phe Phe Ser His Leu Gly Ile Phe Ser Tyr Asp Lys
 -45 -40 -35
 Ala Lys Asp Asn Val Glu Lys Glu Arg Glu Ala Asn Lys Ser Ala Gly
 -30 -25 -20 -15
 Gly Ser Trp Leu Ser Leu Leu Ala Ala Leu Ala His Leu Ala Ala Ala
 -10 -5 1
 Glu Lys Val Tyr His Ser Leu Thr Tyr Leu Gly Gln Lys Leu Gly Thr
 5 10 15
 Ser Ala Pro Pro Pro Glu Pro Leu Glu Glu Glu Val Lys Gly Val Tyr
 20 25 30
 Ser Pro Xaa Gly Ser Gly Leu Gly Xaa Pro Ser Leu Cys His Phe
 35 40 45

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<210> 800
 <211> 311
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<220>
 <221> UNSURE
 <222> 56,70,107,110,113,178,181,183,195,200,202,204,230,231,244
 <223> Xaa = any one of the twenty amino acids

<400> 800
 Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln
 -20 -15 -10
 Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe
 -5 1 5
 Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg
 10 15 20 25
 Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn
 30 35 40
 Arg Asp Leu Asn Glu Leu Glu Arg Leu Ser Asn Leu Val Gly Xaa Pro
 45 50 55
 Ser Glu Asn His Pro Leu His Asn Ser Gly Leu Leu Xaa Leu Asp Pro
 60 65 70
 Val Gln Asp Lys Thr Pro Leu Tyr Ser Gln Leu Leu Gln Ala Tyr Lys
 75 80 85
 Trp Ser Asn Lys Leu Gln Tyr His Ala Gly Leu Ala Ser Gly Leu Leu
 90 95 100 105
 Asn Xaa Gln Ser Xaa Lys Arg Xaa Ala Asn Gln Met Gly Val Ser Ala
 110 115 120
 Lys Arg Arg Pro Lys Ala Gln Pro Thr Thr Leu Val Leu Pro Pro Gln
 125 130 135
 Tyr Val Asp Asp Val Ile Ser Arg Ile Asp Arg Met Phe Pro Glu Met
 140 145 150
 Ser Ile His Leu Ser Arg Pro Asn Gly Thr Ser Ala Met Leu Leu Val
 155 160 165
 Thr Leu Gly Lys Val Leu Lys Val Xaa Val Val Xaa Arg Xaa Leu Phe
 170 175 180 185
 Ile Asp Arg Thr Ile Val Lys Gly Tyr Xaa Glu Asn Val Tyr Xaa Glu
 190 195 200
 Xaa Gly Xaa Leu Asp Ile Trp Ser Lys Ser Asn Tyr Gln Val Phe Gln
 205 210 215
 Lys Val Thr Asp His Ala Thr Thr Ala Leu Leu His Xaa Xaa Leu Pro
 220 225 230
 Gln Met Pro Asp Val Val Val Arg Ser Phe Xaa Thr Trp Leu Arg Ser
 235 240 245
 Tyr Ile Lys Leu Phe Gln Ala Pro Cys Gln Arg Cys Gly Lys Phe Leu
 250 255 260 265
 Gln Asp Gly Leu Pro Pro Thr Trp Arg Asp Phe Arg Thr Leu Glu Ala
 270 275 280
 Phe His Asp Thr Cys Arg Gln
 285

<210> 801
 <211> 91
 <212> PRT
 <213> Homo sapiens

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<220>
 <221> SIGNAL
 <222> -60..-1

<400> 801
 Met Thr Ser Leu Phe Ala Val Val Leu Gln Arg Glu Lys Glu Pro His
 -60 -55 -50 -45
 Leu Trp Leu Ser Ser Pro His Ile Arg Phe Ser Leu Arg Val Asn Lys
 -40 -35 -30
 Leu Ser Glu Leu Met Leu Gln Leu Leu Gln Phe Lys Ala Phe Pro Ser
 -25 -20 -15
 Ser Leu Val Pro Phe Phe Leu Phe Thr Cys Phe Gly His Phe Pro Ser
 -10 -5 1
 Phe Thr Thr Phe Gln Gly Phe Ile Glu Asn Asn Leu Leu Gln Asn Gln
 5 10 15 20
 Phe Asn Ser Asn Val Asp Ile Val Ala Cys Ser
 25 30

<210> 802
 <211> 287
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<220>
 <221> UNSURE
 <222> 74
 <223> Xaa = any one of the twenty amino acids

<400> 802
 Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
 -15 -10 -5
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
 1 5 10 15
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
 20 25 30
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr
 35 40 45
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met
 50 55 60
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Xaa Asn Lys Glu Asn Leu
 65 70 75
 Gln Pro Gln Asn Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu
 80 85 90 95
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala
 100 105 110
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu
 115 120 125
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser
 130 135 140
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu
 145 150 155
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala
 160 165 170 175
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln
 180 185 190
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp
 195 200 205

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Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala
 210 215 220
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Ser Thr Lys
 225 230 235
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys
 240 245 250 255
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His
 260 265 270

<210> 803
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<220>
 <221> UNSURE
 <222> 4
 <223> Xaa = any one of the twenty amino acids

<400> 803
 Met Glu His Leu Thr His Ser Ser Gln Lys Leu Gln Ala Asp Glu His
 -45 -40 -35
 Leu Thr Lys Glu Val Trp Ser Arg Leu Leu Lys Glu Lys Gly Pro Ala
 -30 -25 -20
 Gly Leu Ile Leu Cys Phe Leu Cys Leu Tyr Pro Ile Pro Leu Cys Thr
 -15 -10 -5
 Ser His Pro Val Xaa Leu Cys Ala His Pro Gln Asp Val Tyr Pro Val
 1 5 10 15
 Val Val Arg Ala Glu Ile His Ala Glu Leu Tyr Gln Glu Leu Ala Tyr
 20 25 30
 Leu Lys Thr Glu Thr Glu Ser Leu Ala His Leu Phe Ala Leu Val Pro
 35 40 45
 Gln Ala Lys Ile Lys Asn Arg Val
 50 55

<210> 804
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<220>
 <221> UNSURE
 <222> -26,-25,-24
 <223> Xaa = any one of the twenty amino acids

<400> 804
 Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu
 -35 -30 -25
 His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala
 -20 -15 -10 -5
 Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly
 1 5 10
 Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg

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Pro Leu Glu Gly Thr Thr Trp Thr His Ser Leu Lys Ala Gln Leu Leu
 30 35 40
 Ser Leu Pro Phe Trp Val Trp Thr Val Ile Phe Leu Val Pro Tyr Leu
 45 50 55
 Gln Xaa Phe Leu Phe Leu Tyr Ser Cys Thr Lys Xaa Asp Pro Lys Thr
 60 65 70
 Val Gly Tyr Cys Xaa Ile Pro Ile Cys Leu Ala Xaa Ile Xaa Asn Arg
 75 80 85
 His Gln Asp Phe Val Lys Ala Ser Asn Gln Ile Ser Lys Leu Gln Leu
 90 95 100 105
 Ile Asp Thr

<210> 807
 <211> 335
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1
 <220>
 <221> UNSURE
 <222> 70,139,141,154,156,165
 <223> Xaa = any one of the twenty amino acids

<400> 807
 Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly
 -15 -10 -5
 Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn
 1 5 10 15
 Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
 20 25 30
 Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
 35 40 45
 Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met Val
 50 55 60
 Lys Gly Val Asn Asn Xaa Pro Leu Pro Pro Gly Cys Val Ile Ser Tyr
 65 70 75 80
 Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser
 85 90 95
 Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala
 100 105 110
 Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Trp
 115 120 125
 Lys Thr Phe Gln Ser Leu Ala Pro Ala Pro Xaa Ile Xaa Cys Phe Lys
 130 135 140
 Lys Thr Leu Phe Ser Val His Ser Pro Xaa Ile Xaa Leu Ser Arg Asn
 145 150 155 160
 Asn Glu Val Asp Xaa Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
 165 170 175
 Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
 180 185 190
 Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
 195 200 205
 Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
 210 215 220
 Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
 225 230 235 240
 Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser

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245 250 255
 Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn
 260 265 270
 Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser
 275 280 285
 Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala
 290 295 300
 Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Glu Ser Trp Ile
 305 310 315

<210> 808
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 808
 Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu
 -55 -50 -45 -40
 Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His Leu Cys
 -35 -30 -25
 Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala Ala Leu
 -20 -15 -10
 Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val Asp Val
 -5 1 5
 Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys Gln Arg
 10 15 20 25
 Met Ile Ser Cys

<210> 809
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 809
 Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
 -15 -10 -5
 Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
 1 5 10
 Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
 15 20 25 30
 Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
 35 40 45
 Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly
 50 55 60
 Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile
 65 70 75
 Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln
 80 85 90
 Pro Arg Pro Ala Phe Ser Ala Ile Arg Arg Asn Pro Pro Met Gly Gly
 95 100 105 110
 Asn Val Val Ile Phe Asp Thr Val Ile Thr Asn Gln Glu Glu Pro Tyr
 115 120 125
 Gln Asn His Ser Gly Arg Phe Val Cys Thr Val Pro Ala Thr Thr Thr

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130 135 140
 Ser Pro Ser Arg Cys Cys Pro Ser Gly Lys Ser Ala Cys Pro Ser Ser
 145 150 155
 Pro Pro Gln Gly Ala Arg Ser Asp Ala Pro Trp Ala Ser Val Thr Pro
 160 165 170
 Pro Thr Arg Gly Ser Ser Arg Trp Cys Gln Gly Ala Trp Cys Phe Ser
 175 180 185 190
 Cys Ser Arg Val Thr Arg Ser Gly Leu Lys Lys Thr Pro Lys Arg Val
 195 200 205
 Thr Phe Thr Arg Ala Leu Arg Pro Thr Ala Ser Ser Ala Ala Ser Ser
 210 215 220
 Ser Ser His Leu Pro Glu Pro Gly Lys Asp Pro Leu Pro His Pro Pro
 225 230 235
 Leu Trp Leu Pro Cys Ser Ala Cys Lys Met Gly Ala Leu Leu Leu Gln
 240 245 250
 Leu Leu Lys Gly Gly Gly Trp Leu
 255 260

<210> 810

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -51...-1

<220>

<221> UNSURE

<222> 24,25,29,87

<223> Xaa = any one of the twenty amino acids

<400> 810

Met Arg Lys Asp Pro Ser Gly Ala Gly Leu Trp Leu His Ser Gly Gly
 -50 -45 -40
 Pro Val Leu Pro Tyr Val Arg Glu Ser Val Arg Asn Pro Ala Ser
 -35 -30 -25 -20
 Ala Ala Thr Pro Ser Thr Ala Val Gly Leu Phe Pro Ala Pro Thr Glu
 -15 -10 -5
 Cys Phe Ala Arg Val Ser Cys Ser Gly Val Glu Ala Leu Gly Arg Arg
 1 5 10
 Asp Trp Leu Gly Gly Gly Pro Arg Ala His Xaa Xaa Ala Thr Glu Xaa
 15 20 25
 Ser Ala Pro Lys Glu Ser Leu Gly Cys His Asp Cys His Ala Ile Lys
 30 35 40 45
 Lys Cys Arg Lys Trp Glu Val Phe Arg Met Thr His Gln Val Leu Phe
 50 55 60
 Pro Arg Val Trp Ala Leu Ser Trp Asn Pro Leu Ala Cys Thr Pro Ser
 65 70 75
 Cys Leu Gln Arg Cys Thr Cys Ile Pro Xaa Cys Ser
 80 85

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